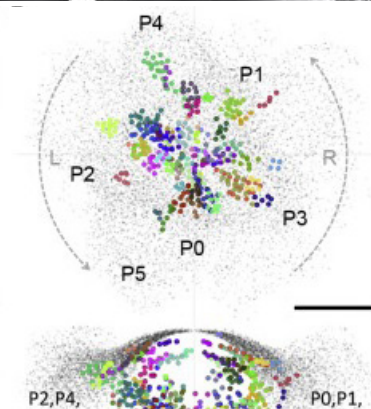
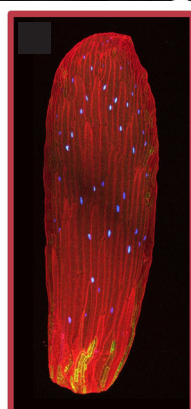
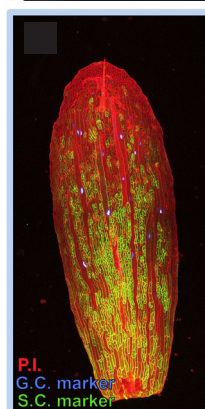


# From Bench to Bountiful Harvests

## Multinational Arabidopsis Steering Committee (MASC)

### Annual Report 2016/2017



# The Multinational Arabidopsis Steering Committee

## Annual Report 2016/2017

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Bottom Left Image: <http://dx.doi.org/10.7554/eLife.19131>  
Bottom Right Image: <https://doi.org/10.1016/j.devcel.2016.08.013>

## Further information: [www.Arabidopsisresearch.org](http://www.Arabidopsisresearch.org)

The MASC report 2016/17 and previous reports are available online at:

- > MASC, The Multinational Arabidopsis Steering Committee:  
<http://Arabidopsisresearch.org/index.php/publications/masc-reports>
- > uNASc, The Nottingham Arabidopsis Stock Centre:  
<http://Arabidopsis.info/progreports.html>
- > TAIR, The Arabidopsis Information Resource:  
[http://www.Arabidopsis.org/portals/masc/masc\\_docs/masc\\_reports.jsp](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 chair, co-chair, coordinator, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community.

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# Foreword to the Report

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). As you will read within these pages it has been another successful year for Arabidopsis research with an increase in global publications and the development of many outstanding collaborative tools that will enhance future research in Arabidopsis, other model organisms and in crop species.

MASC started in the early 1990's, when scientists from several countries formed an *ad hoc* committee to promote large-scale research with Arabidopsis. The ultimate goal was the understanding of physiological, biochemical and developmental processes of flowering plants at the molecular level, employing Arabidopsis as a model system. In order to reach this long-term goal, a commitment from the global Arabidopsis community was essential. Therefore, actively engaged researchers developed 'The Multinational Coordinated Arabidopsis - Genome Research Project' in 1990. Over time this morphed into the current incarnation of MASC which is now onto its third decade-long roadmap document entitled 'From Bench to Beautiful Harvests' (Lavagi *et al.*, 2012, *Plant Cell*, 24:2240-7). The major goal stated in this road map is to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole organism, within populations and fields of plants. All this in order to facilitate building predictive models of Arabidopsis.

An important development over the past few years has been the growing use of Arabidopsis as a model for the study of natural variation and evolutionary processes, work that has been driven forward by the participants in the 1001 Arabidopsis Genomes project. This has led to the generation of community tools such as AraGeno and AraPheno, both of which offer a gateway for a wider set of researchers to conduct investigations of this type.

Although global support for Arabidopsis research varies in a country-by-country manner, it is extremely reassuring that the three Arabidopsis seed stock centres continue to go from strength to strength. This evidenced by the appointment of Keith Slotkin as the new director of the ABRC and the announcement of continued funding for NASC until 2021. Both these developments will ensure a smooth continuation of these vital resources.

Arabidopsis remains an exemplar for plant genomic resources with the Arabidopsis Information Portal (Araport) continually adding to its portfolio of available tools. During 2016 it notably published the much

expanded Araport11 genome annotation, integrated tools from the BAR, and incorporated other public data sets. This will enable an enormous amount of expression and genome information to be located in a one-stop-shop for those who wish to interact with these resources.

Elsewhere it is gratifying that TAIR has established itself as an exemplar of a subscription-based funding model that supports their excellent biocuration (Reiser *et al* (2016) Database (Oxford) 10.1093/database/baw018). This has allowed the continued development of their Gene Ontologies and the support to fully integrate their work with the new Araport11 genome release.

MASC has undergone a significant organisational change over the past two years as it is now established as a not-for-profit organisation that is registered in Canada. MASC Inc includes Nicholas Provart as president, Siobhan Brady as treasurer, and Marília Campos as secretary. The remaining 8 Directors of MASC Inc have yet to be chosen and will be elected at the annual meeting at ICAR2017 in St Louis. Furthermore the Annual meeting will discuss the funding structure of MASC Inc and the relationship with future ICAR conferences. Moving forward MASC Inc hopes to be able to provide seed funding for future ICAR meetings even though the precise mechanisms for this interaction remain under discussion.

The 2016/2017 annual MASC report is the 5<sup>th</sup> published under the current road map. In this publication you will read about the progress of MASC activities. Members of seven of the eight MASC subcommittees, representatives of 25 from the 28 member countries and directors of resource centers and community projects have contributed to this years report. We also feature a selection of open access Arabidopsis publications that exemplify the span of research in which this model organism is important.

MASC thanks the local organisers of the 28<sup>th</sup> ICAR in St Louis for their support and all MASC members who contributed to this report.

Finally we would like to thank Loic Lepineic and all at *Science des Plantes de Saclay* for providing financial support for printing and distribution of the full report..

**The Multinational Arabidopsis Steering Committee  
June 2017**



# Executive Summary

As we enter the second 50 years of use as a model organism, research in Arabidopsis remains more highly published than any other plant species. In addition, Arabidopsis remains the most important reference plant that is used during the development of new technologies. These range from establishing bespoke phenotyping platforms through to the full development of tools that take advantage of remarkable developments across a range of 'omic techniques. In addition Arabidopsis is now often used as a tool to understand natural variation and population scale effects following the many successes of the 1001 Arabidopsis Genomes project.

Arguably the global community of Arabidopsis research can be characterised as existing at two speeds. In many countries, such as the USA, South Korea and the UK, there are major challenges when obtaining funding for Arabidopsis research given the move toward increasing support for crop species. In these locations it is uncertain how future funding schemes will support research in Arabidopsis regardless of its clear importance in providing insights into fundamental biological processes.

In other countries, such as China, the Netherlands, Chile and in Sweden, the opportunities for Arabidopsis research remain strong. Nowhere is this more clear than in China, that still sees a large increase in the number of published manuscripts that feature Arabidopsis research. In most countries there has been a plateau in the number of Arabidopsis papers but given the general stagnation in funding for basic research this can perhaps be taken as an overall positive sign. The individual Country Reports begin on Page 41 in which readers can obtain an understanding of the state of Arabidopsis research in each location.

## International Conference on Arabidopsis Research (ICAR)

MASC members are responsible for hosting the annual International Conference on Arabidopsis research in their respective home countries:

27<sup>th</sup> ICAR, Gyeongju, South Korea: June 29<sup>th</sup>-July 3<sup>rd</sup> 2016  
28<sup>th</sup> ICAR, St. Louis, Missouri, USA: June 19<sup>th</sup>-23<sup>rd</sup> 2017

Save the dates for the upcoming ICARs!  
29<sup>th</sup> ICAR, Turku, Finland: June 25<sup>th</sup>-29<sup>th</sup> 2018  
30<sup>th</sup> ICAR, Wuhan China: June/July 2019.  
31<sup>st</sup> ICAR, location TBD, The Americas. June/July 2020.

## Progress and Activities of MASC

- > MASC chair 2016/2017: Inhwan Hwang (Pohang University of Science and Technology, Republic of Korea)
- > MASC joint co-chair 2016/2017: Doris Wagner (UPenn, {Philadelphia USA})
- > MASC joint co-chair 2016/2017: Elizabeth Haswell (Washington University, St Louis, USA)
- > MASC coordinator 2017: Geraint Parry (Cardiff University, UK) funded by GARNet, BBSRC
- > 26<sup>th</sup> ICAR 2016: 954 attendees and 580 submitted poster abstracts (Figure 2, page 10)

**MASC web page:** [www.Arabidopsisresearch.org](http://www.Arabidopsisresearch.org)

## Analysis and Recommendations of MASC

By analysing the activities documented in this report it is fair to conclude that Arabidopsis research remains very active, efficient and innovative. This is a result of years of collaboration and coordination among scientists from across the globe, who did not spare efforts in promoting Arabidopsis as the model for scientific discoveries in plant biology. Still, the funding situation in several countries demonstrates a current preference for financing applied versus basic research, which lead to a few concerns regarding the future of Arabidopsis research. MASC will continue to provide a voice for the community and ensure that funding bodies and decision makers become aware of the importance of Arabidopsis not only for pioneering research, but also to serve as a pathway to translation into crops.

## MASC Subcommittees

Currently eight MASC Subcommittees monitor progress and important activities as well as discuss future directions of each of their respective fields of Arabidopsis research. Members of each subcommittee are in positions to stay in close contact with the community and promote international cooperation (pages 12-26).

In the lead up to the annual meeting that will take place at ICAR2017, there have been questions tabled about the future directions of these subcommittees. Therefore this will be a topic of conversation at the annual meeting.

Seven of the subcommittees have contributed to the 2016-2017 annual MASC report.

These are:

- Bioinformatics (page 12)
- ORFeomics (page 14)
- Metabolomics (page 16)
- Natural Variation (page 17)
- Phenomics (page 20)
- Proteomics (page 24)
- Systems and Synthetic Biology (page 25).

### Arabidopsis Community Projects and Resources

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

Information on the progress and activities of the range of community resources can be found on pages 27-34.

### Arabidopsis Scientific Highlights in 2016/2017

According to an NCBI search, Arabidopsis researchers published 4,327 peer-reviewed papers in 2016, which is a return to the numbers seen in 2013 and 2014. This is largely due to the continued increase in publications from Chinese researchers. As also shown in figure 4 (page 35) this reflects a plateauing in papers from many countries, which is significantly different to the situation in China.

In this report we highlight nine **Open Access** papers that demonstrate the breadth of research in which Arabidopsis is involved. The topics range from basic research, which adds to our understanding of the fundamental cell biology of gene regulation, includes large scale genomic studies through to translational studies that improve our understanding of plant-insect interactions. The titles of these papers are shown below:

> A noncanonical auxin-sensing mechanism is required for organ morphogenesis in Arabidopsis. *Genes and Development*.

> Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. *Cell*.

> Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis. *Cell*.

> Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. *Elife*.

> The Mitochondrial Complexome of Arabidopsis *The Plant Journal*.

> A Novel Role for Methyl Cysteinate, a Cysteine Derivative, in Cesium Accumulation in Arabidopsis. *Scientific Reports*.

> Generation of stable nulliplex autopolyploid lines of Arabidopsis using CRISPR/Cas9 genome editing. *Plant Cell Reports*.

> Quantitative monitoring of Arabidopsis growth and development using high-throughput plant phenotyping. *Scientific Data*.

> Virus Infection of Plants Alters Pollinator Preference: A Payback for Susceptible Hosts? *PLoS Pathogens*.

### Country Highlights

MASC is supported by individual countries through the election of representatives that report back each year on the progress that their colleagues have made. In addition, they provide an important commentary on the prospects for Arabidopsis research in their individual countries.

The country reports serve to highlight the exceptional numbers of research tools that have been developed for the benefit of the global Arabidopsis community, perhaps most notably from Australia, Austria and Japan.

At the present time 28 countries support MASC and from these members there have been 25 contributions to this report (page 41). We encourage researchers from other countries who are not featured in this MASC report to get involved with this process by contacting a member of the MASC Steering Committee. Providing an update for the global community not only highlights the outstanding work that is occurring in their home country but also provides an easy reference point that can be important in discussions with potential funders and other interested parties.

# Progress and Activities of MASC

In 2016, Inhwang Hwang succeeded Loïc Lepiniec to become MASC chair whilst Doris Wagner and Elizabeth Haswell became co-co-chairs (Figure 1). Doris and Elizabeth will become the new MASC chairs when Inhwang Hwang steps down following the 28<sup>th</sup> International Conference on Arabidopsis Research (ICAR) in St Louis, USA.

The proposed structure of the not-for-profit MASC Inc. includes non-paid positions for the President, Treasurer and Secretary. These Officers are supported by a Board of eight Directors, who will be elected for a 4 year term. The Country, Resource and Subcommittee representatives are proposed to become members of MASC Inc. How the new structure of MASC, Inc. will fit with the current organisation will be discussed at the MASC annual meeting in St Louis.

The MASC report was assembled by Geraint Parry who also organised the MASC annual meeting. Geraint takes on this role in addition to his current position as the GARNet coordinator in the UK. It is hoped that this role will continue for the foreseeable future, taking advantage of the full time funding provided to the UK plant science community by the Biotechnology and Biological Sciences Research Council (BBSRC). The coordinator position was established in 2002 and has been previously supported by the NSF (USA), the DFG (Germany) and by the BBSRC. The MASC coordinator provides help and coordination to MASC and the larger Arabidopsis research community. As there is no specific funding for the MASC coordinator, the usual roles have been reduced yet still include:

- Serving as executive secretary of MASC
- 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
- Organizing the MASC annual meeting during the ICAR.

MASC operates via three groups who receive continuous input from the whole Arabidopsis and plant community: MASC subcommittees, Arabidopsis community projects and resources and MASC country representatives (Figure 1).

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from seven of the eight current subcommittee chairs/co-chairs: Bioinformatics, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics and Systems and Synthetic Biology (page 12).

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

- Submission of an annual report
- Input at MASC annual meetings



**Figure 1.** Current structure of **Multinational Arabidopsis Steering Committee (MASC)**. For explanation of abbreviations see MASC Subcommittee (page 12), Arabidopsis Community Projects and Resources (page 27) and MASC Country Reports (page 41)

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

Representatives of Arabidopsis community projects and resources attend the annual MASC meeting and contribute to the annual MASC report to broadcast their progress, activities and goals to the community (page 27).

The three resource and stock centers, i.e. the Arabidopsis Biological Resource Center (ABRC, US), the Nottingham Arabidopsis Stock Centre (uNASc, UK) and the RIKEN BioResource Center (RIKEN BRC, Japan), continue to encourage donations to keep their stocks up-to-date following the newest technologies. In order to ensure a broader and more efficient distribution of resources within the community, the stock centers operate coordinately with each other, as well as with Arabidopsis online portals.

Progress of Arabidopsis informatics and data sharing resources is also highlighted in this year's report, including updates from the Arabidopsis Information Portal (Araport) and The Arabidopsis Information Resource (TAIR). Efforts of two other community projects (BAR, Gramene) with strong participation of the Arabidopsis community are also presented in the report (page 32-34).

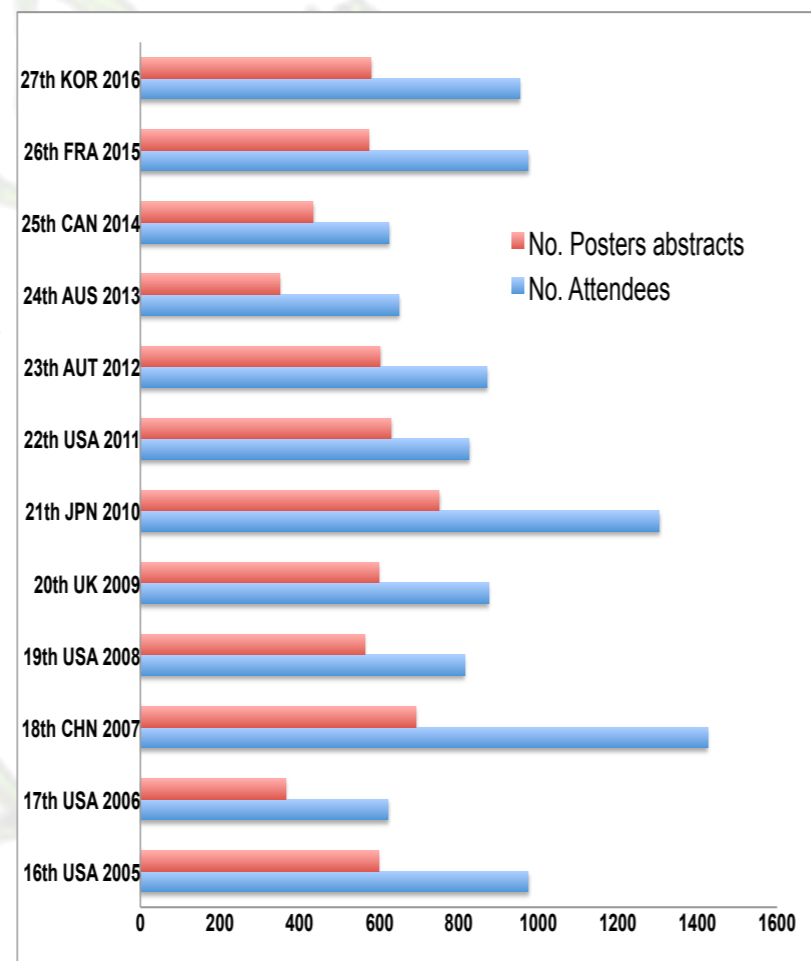
Country representatives attend the annual MASC meeting held during ICARs and contribute to the annual MASC report by submitting country reports. In 2016/2017, 25 have contributed to this year's report. Weicai Yang has stepped down as the MASC representative from China and has been kindly replaced by Yuling Jiao. Similarly Barry Pogson is no longer the representative from Australia and is replaced by Monika Murcha. MASC thanks country representatives for their valuable contributions and highly encourages researchers working on Arabidopsis to get involved in MASC activities, e.g. subcommittees, projects and resources or as country representatives.

The 27<sup>th</sup> International Conference on Arabidopsis Research (ICAR) was held in Gyeong-Ju, South Korea from June 29<sup>th</sup>- July 3<sup>rd</sup> 2016 where the organising committee was lead by Inhwang Hwang. The meeting was extremely successful and there was a great atmosphere cumulating in a very enjoyable closing ceremony featuring traditional Korean music and dance. 954 people from 29 countries attended the 27<sup>th</sup> ICAR in South Korea and over 60% of the attendees (580) submitted a poster abstract (Figure 2). On average 63% of the

attendees have presented a poster during the ICARs over the last 12 years.

Based on 185 respondents to the post-meeting survey there was an approximate even number of attendees from Asia versus the rest of the world. It is exciting to learn that around a third of attendees were PhD students, demonstrating a strong future for Arabidopsis research, particularly in the far east. Over 80% of attendees reported that they thought the meeting was 'Excellent or Good', which reflects the fantastic location and organisation of the meeting.

The success of the 27<sup>th</sup> ICAR was in part also due to efforts of many MASC members who were involved in the program: This included the organisation of ABRC and NASC booths, RIKEN booth, TAIR booth and these community workshops: "Bioinformatics and Data resources (Eva Huala: TAIR)", "Emerging Genomics Techniques and the Future of Research using Arabidopsis (Siobhan Brady and Cranos Williams)", "CO2 acquisition in C3 and C4 Plants (Inhwang Hwang)".



**Figure 2.** Number of attendees (blue) and number of posters presented (red) at the International Conference on Arabidopsis Research since 2005, when information about posters became available.

## Analysis and Recommendations by MASC

Compiled by Geraint Parry with input from Elizabeth Haswell and Nick Provart.

The main objective of MASC is to promote and facilitate research in Arabidopsis, a powerful reference system for plant molecular and genetic approaches. By publishing this annual report we bring together in one place information about the remarkable progress that has been made across all facets of research in this dynamic of plant science research community.

One aspect of the Arabidopsis community that is strongly highlighted throughout this report is the continued development of shared resources. In 2016 the 1001 Arabidopsis Genomes Consortium published their most complete work which, alongside the publication of the 1001 Epigenomes provides an enormous resource of information about natural variation throughout global Arabidopsis accessions. As appropriate for such a community-driven project all of the information from these papers are publically available and the project has generated additional resources including the AraPheno and AraGeno projects.

The integration of the 1001 Arabidopsis Genome data into Araport demonstrates the parallel thinking from the leaders of these resources. This type of interaction was further demonstrated in 2016 with the integration of the BAR ePlant visualisation tool into Araport. As genome resources from other plants are beginning to increase in complexity it is important that Araport interacts with these tools in order to aid cross-fertilisation of research between models and crop species.

In many countries over the past few years, it has become increasingly difficult to convince funding organisations that Arabidopsis research is a vital part of the generation of resources for crop science. By integrating Arabidopsis-facing resources with the nascent genomic tools from other organisms will ensure that Arabidopsis remains relevant as plant scientists attempt to tackle the challenges of global food security by utilising current and novel crop models.

Although certain country representatives, (such as from Ireland and Italy) report significant challenges in obtaining funding for basic research focussed on Arabidopsis, fortunately it appears that this is not a global problem. In addition to the continued productivity in China (Figure 4 on page 35) other countries such as The Netherlands, Sweden, Finland, Chile, New Zealand and Israel report positive developments in the availability of funding to

support basic science that encompasses Arabidopsis research. Hopefully the collaborative nature of the Arabidopsis research community means that colleagues in countries with a healthy funding situation can support publications and resource-building in countries where funding is currently more challenging to obtain. Hopefully the general high tide of Arabidopsis productivity will raise overall global research funding prospects.

The 25 country reports contained in this MASC report demonstrate that there are excellent resources being developed all around the world. This is a fantastic situation, yet the community must be wary of duplicating efforts, especially as funding resources are finite. Hopefully this report can provide a unique global perspective that distributes important information that can reduce any unnecessary repetition of effort.

MASC members are responsible for deciding upon the location of the annual ICAR meeting. Since 2007 they have been hosted on a three-year cycle between Asia, North America and Europe. Inevitably the location of ICAR dictates where the majority of attendees reside. Whereas the 2016 ICAR in South Korea has almost 1000 attendees from 29 countries, it unfortunately appears that political changes will impact the number of overseas attendees at the upcoming meeting in St. Louis. Hopefully the number of attendees will again increase for the 2018 ICAR in Turku, Finland.

Whether there is scope for increasing the breadth of meeting venues for future ICARs is open for debate. It is possible there could be the opportunity to take the meeting to South America, India or to Africa, as that would surely encourage Arabidopsis research in those regions.

In conclusion, the results obtained this year demonstrate that Arabidopsis research remains very active, efficient and innovative with thriving research communities in many countries. The most numerous research outputs have moved east away from traditional strengths, yet in the USA and Western Europe research is underpinned by broad community resources that have been developed over the past decade or longer. It will be exciting to discover the directions that research will take as new group leaders emerge in countries with currently healthy funding situations.

There is no doubt that as these tools are generated, the new MASC Inc organisation will continue to promote and interact with these exciting resources.

# Reports of the MASC Subcommittees

## Bioinformatics

<http://Arabidopsisresearch.org/index.php/subcommittees/bioinformatics>



Compiled by Nicholas Provart with input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community.

**Araport.org** Araport officially released the Araport11 protein coding gene set containing 27,655 loci with 48,359 transcripts to NCBI in June 2016 (Cheng *et al.*, 2017). Of TAIR10 protein-coding gene models, 68.9% (24,385/35,385) have been updated among which 4.7% (1,191) and 95.3% (24,367) have altered CDS and UTR sequences respectively. The number of genes in Araport11 with splice variants (10,696; 38.7%) is much higher than reported in TAIR10 (20.8%). Also in the area of splice isoform prediction, John Brown and colleague (Zhang *et al.*, 2016b) have created AtRTD2, a new reference transcript data set for RNA-seq analysis created from 285 RNA-seq data sets in the Sequence Read Archive at NCBI and by merging information from Araport 11. A total of 13,524 protein-coding genes have at least one alternatively spliced transcript in AtRTD2 such that 60.23% of the 22,453 protein-coding, intron-containing genes in Arabidopsis undergo alternative splicing.

Eva Huala and colleagues at TAIR have successfully moved to a subscription-based model, and their non-profit organization, Phoenix Bioinformatics, continues TAIR's annotation work (Reiser *et al.*, 2016). They released the 9th public release of new annotations in January 2017, containing annotations and other data added through the end of December 2016. Subscribers (and students in courses) can access 627 new gene symbols and 696 new/updated gene summaries added in the past year. In this time TAIR also added 8,890 new GO and PO annotations, generated by TAIR curators, TAIR community, UniProt and the GO consortium, to 4,883 loci, incorporating experiment-based data from 1,542 research articles. Finally TAIR linked 2,572 articles to 3,808 loci, and added 243 new alleles and 213 new phenotypes to TAIR from the literature.

Aleksy Penin and colleagues at the Russian Academy of Science published an RNA-seq atlas covering 79 organs and developmental stages from Arabidopsis, which is sure to be a highly-cited work (Klepikova *et al.*, 2016), as was the Affymetrix-based version published by Schmid *et al.* more than a decade ago (2005). Klepikova *et al.* report 37, 873 previously unreported splice junctions not in the TAIR10 database. Lida Zhang and colleagues

at Shanghai Jiao Tong University have inferred 316,747 high-confidence interactions among 12,574 Arabidopsis proteins from both three-dimensional structures and functional evidence (Zhang *et al.*, 2016a), and Ziding Zhang's group at the China Agricultural University have created AraPPISite, a database of fine-grained protein-protein interaction site annotations for Arabidopsis (Li *et al.*, 2016).

Other "big data" papers include Vincent Colot and colleagues' analysis of the Arabidopsis "mobilome" covering 211 Arabidopsis accessions from around the globe, in which they identified thousands of recent transposition events involving half of the 326 TE families in Arabidopsis (Quadrana *et al.*, 2016). Works from the Ecker Lab at the Salk Institute that will be useful for gene regulatory network reconstruction include a 21 transcription factor ChIP-seq/RNA-seq experiment for TFs involved in ABA response (Song *et al.*, 2016), and O'Malley *et al.*'s DAP-Seq effort to map the binding specificity of 529 TFs from Arabidopsis (2016). A test with native genomic DNA from Arabidopsis leaves revealed methylation sensitivities for 76% of the TFs surveyed.

Tools for exploring existing gene expression data include an update to AtCAST3.0 for identifying experiments having similar transcriptional responses as one's own (Kakei and Shimada, 2015), updates to Takeshi Obayashi and colleagues' ATTED-II to include RNA-seq data sets for gene-by-gene coexpression analyses (Aoki *et al.*, 2016), and a user-friendly extension of the Bio-Analytic Resource's Expression Angler to pictographically describe the kind of expression pattern for genes one is interested in identifying (Austin *et al.*, 2016). Kento Yano's group at Meiji University have published three useful papers: PlantExpress, for comparing gene expression networks between rice and Arabidopsis (Kudo *et al.*, 2017); CATchUP, a database of spatio-temporally-regulated genes for 8 species, including Arabidopsis (Nakamura *et al.*, 2017); and sets of reference genes based on RNA-seq data for Arabidopsis and crop species (Kudo *et al.*, 2016).

A good overview of several plant genomic databases is provided in volume 1533 of *Methods in Molecular Biology* (Plant Genomics Databases - Methods and Protocols | Aalt-Jan van Dijk | Springer), including chapters on ENSEMBL Plants, the BAR, PLAZA, Plant Promoter DB and many others. A similar collection providing a good overview of plant bioinformatic resources is available in the open-access *Current Plant Biology* special edition on genomic resources and databases (Naithani and Van de Peer, 2016). The 2017 *Nucleic Acids Research* database issue (Volume 45 Issue D1 | *Nucleic Acids Research* | Oxford Academic) contains

updates or reports on 13 plant databases. Of note here: PlantTFDB and AraPheno, a database of Arabidopsis phenotypes.

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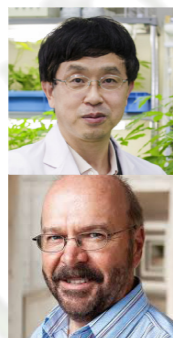
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## Clone-Based Functional Genomics Resources (ORFeomics)

<http://Arabidopsisresearch.org/index.php/subcommittees/orfeomics>

By Motoaki Seki (Chair) and Joe Ecker (Co-Chair) with contributions from subcommittee members, Masatomo Kobayashi (RIKEN BRC), Satoshi Iuchi (RIKEN BRC), Erich Grotewold (ABRC) and Debbie Christ (ABRC)



### Progress Towards Goals of the Subcommittee

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

### Future Goals of the Subcommittee

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

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

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.

### Tools and Resources

We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Please see the table on page 15). **The revised clones are shown in red.** New clones include pIX-HALO vector ones for 768 transcription factor genes.

### Selected Publications

O'Malley, R.C., Huang, S.C., Song, L., Lewsey, M.G., Bartlett, A., Nery, J.R., Gallia, M., Gallavotti, A. and Ecker, J.R. (2016) Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell* 165:1280–1292.

Yazaki, J., Gallia, M., Kima, A.Y., Nito, K., Alemand, F., Changb, K.N., Carvunis, A.R., Quana, R., Nguyen, H., Song, L., Alvarez, J.M., Huang, S.S.C., Chen, H., Ramachandran, N., Altmann, S., Gutiérrez, R.A., Hille, D.E., Schroeder, J.L., Chory, J., LaBaer, J., Vidal, M., Braun, P. and Ecker, J. R. (2016) Mapping transcription factor interactome networks using HaloTag protein arrays. *Proc. Natl. Acad. Sci. USA* 113:E4238-4247.

Creator	Format	Focus	Validation	Scale	URL	Stock Center
<b>ORF clones</b>						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14,398	<a href="http://signal.salk.edu/cdnastatus.html">signal.salk.edu/cdnastatus.html</a> <a href="http://methylo.me.salk.edu/cgi-bin/clones.cgi">http://methylo.me.salk.edu/cgi-bin/clones.cgi</a>	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	<a href="http://signal.salk.edu/cdnastatus.html">signal.salk.edu/cdnastatus.html</a> <a href="http://methylo.me.salk.edu/cgi-bin/clones.cgi">http://methylo.me.salk.edu/cgi-bin/clones.cgi</a>	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	<a href="http://interactome.dfci.harvard.edu/A_thaliana/host.php">http://interactome.dfci.harvard.edu/A_thaliana/host.php</a>	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	<a href="http://www.tigr.org/tdb/hypos/">www.tigr.org/tdb/hypos/</a>	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar <i>et al.</i>	Gateway expression	TAP-tagged TFs	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	<a href="http://gabi.rzpd.de/materials/">gabi.rzpd.de/materials/</a>	GABI/
Dinesh-Kumar <i>et al.</i>	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	<a href="http://plants.gersteinlab.org/">plants.gersteinlab.org/</a>	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	<a href="http://urgv.evry.inra.fr/ATOMEdb">http://urgv.evry.inra.fr/ATOMEdb</a>	ABRC, CNRGV
Doonan <i>et al.</i>	Gateway Expression	GFP fusions		155		ABRC
Callis <i>et al.</i>	Gateway entry	Protein ubiquitination	Full sequence	111	<a href="http://plantsubq.genomics.purdue.edu">plantsubq.genomics.purdue.edu</a>	ABRC
Sheen <i>et al.</i>	Expression	Epitope tagged MAPK	Full sequence	100	<a href="http://genetics.mgh.harvard.edu/sheenweb/category_genes.html">genetics.mgh.harvard.edu/sheenweb/category_genes.html</a>	ABRC
Steve Clouse	Gateway expression	N-terminal Flag/His tagged kinases		855 (73 new in 2015)	<a href="http://www4.ncsu.edu/~sclouse/Clouse2010.htm">http://www4.ncsu.edu/~sclouse/Clouse2010.htm</a>	ABRC
Frommer <i>et al.</i>	Gateway entry, no stop	Membrane and signaling proteins	5' and 3' end seq.	2,712	<a href="http://associomics.org">http://associomics.org</a>	ABRC
Frommer <i>et al.</i>	Gateway Expression (mbSUS clones)	Membrane and signaling proteins	5' and 3' end seq.	5,414	<a href="http://associomics.org">http://associomics.org</a>	ABRC
AIST/RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	1,998		BRC
RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	399		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 <i>et al.</i>	pIX-HALO vector	Transcription factor	Full sequence	768		ABRC
Guillaume Pilot	pDONRZEO vector	Membrane protein	5' and 3' end seq	192		ABRC
Pruneda-Paz <i>et al.</i>	Gateway Entry, no stop	Transcription factor	Full sequence	1,956		ABRC
Pruneda-Paz <i>et al.</i>	Gateway Destination, no stop, pDEST22	Transcription factor	Full sequence	1,956		ABRC
Lao <i>et al.</i>	Gateway DONR, no stop, pDONR223	glycosyltransferases	Full sequence	429	<a href="http://gt.jbei.org/">http://gt.jbei.org/</a>	ABRC
Amita Kaundal <i>et al.</i>	Gateway DONR, no stop, pDONR201			26		ABRC
<b>cDNA clones</b>						
RIKEN/SSP/Salk	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	22,671	<a href="http://www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml">www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml</a>	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	<a href="http://gabi.rzpd.de/materials/">gabi.rzpd.de/materials/</a>	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	<a href="http://www.genoscope.cns.fr/Arabidopsis">www.genoscope.cns.fr/Arabidopsis</a>	CNRGV



## Metabolomics

<http://Arabidopsisresearch.org/index.php/subcommittees/metabolomics>

Kazuki Saito (chair) and Wolfram Weckwerth (co-chair) with contributions from subcommittee members and the wider Arabidopsis community



### Conferences and Workshops

- 2016/6/27-30  
Metabolomics 2016 in partnership with Plant Metabolomics Forum, Dublin, Ireland
- 2016/7/24-27  
9th Joint Natural Products Conference 2016, Copenhagen, Denmark
- 2016/8/6-10  
55th Annual Meeting of the Phytochemical Society of North America, Davis, US
- 2016/11/21-24  
International PSE Symposium, Plant Omics and Biotechnology for Human Health, Gent, Belgium
- 2017/6/26-29  
Metabolomics 2017, Brisbane, Australia
- 2017/7/9-14  
Gordon Research Conference, Plant Metabolic Engineering, Waterville Valley, NH, US
- 2017/7/16-20  
The 4th International Conference on Plant Metabolism (ICPM 2017), Dalian, China

### Selected Publications

- Arthur S Edison, Robert D Hall, Christophe Junot, Peter D Karp, Irwin J Kurland, Robert Mistrik, Laura K Reed, Kazuki Saito, Reza M Salek, Christoph Steinbeck, Lloyd W Sumner, Mark R Viant (2016) The Time Is Right to Focus on Model Organism Metabolomes. *Metabolites*, 6, 8; doi:10.3390/metabo6010008
- Takayuki Tohge, Regina Wendenburg, Hirofumi Ishihara, Ryo Nakabayashi, Mutsumi Watanabe, Ronan Sulpice, Rainer Hoefgen, Hiromitsu Takayama, Kazuki Saito, Mark Stitt, Alisdair R. Fernie (2016) Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. *Nature Commun.*, 7, 12399 doi:10.1038/ncomms12399
- Hiroshi Tsugawa, Tobias Kind, Ryo Nakabayashi, Daichi Yukihiro, Wataru Tanaka, Tomas Cajka, Kazuki Saito, Oliver Fiehn, Masanori Arita (2016) Hydrogen rearrangement rules: computational MS/MS fragmentation and structure elucidation using MS-FINDER software. *Anal. Chem.*, 88, 7946-7958

## Analysis and Recommendations

### Progress Towards Goals of the Subcommittee

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. For this purpose we plan to establish a website for the initial process of consolidating Arabidopsis metabolomics activities making them more visible for the community.

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

### Future Goals of the Subcommittee

To realize the goals, we aimed to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. This subcommittee website has been launched at [www.masc-metabolomics.org](http://www.masc-metabolomics.org). 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 metabolomics data in available databases.

### Tools and Resources

[www.masc-metabolomics.org](http://www.masc-metabolomics.org)  
Metabolomics subcommittee website

<http://prime.psc.riken.jp/>  
Metabolomic characterization of 50 Arabidopsis mutants and the database as a functional genomics tool (MeKO), Arabidopsis metabolome expression databases 'AtMetExpress development', 'AtMetExpress 20 ecotypes' and 'ReSpect for Phytochemicals'. MS-DIAL: data independent MS/MS deconvolution for comprehensive metabolome analysis.

[www.plantmetabolomics.org](http://www.plantmetabolomics.org)  
A web portal of Arabidopsis Metabolomics Consortium that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants.

<http://mmcd.nrmfam.wisc.edu/>  
The Madison-Qingdao metabolomics consortium database has emphasis on Arabidopsis and contains both NMR and MS data of metabolites.

MetaboLights (<http://www.ebi.ac.uk/metabolights>) is a database for Metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments and is a collaborative multi-laboratory effort including groups specialising in plant metabolism.

## Natural Variation

<http://Arabidopsisresearch.org/index.php/subcommittees/>

J. Chris Pires (chair), Brian Dilkes (co-chair) with contributions from subcommittee members and the wider Arabidopsis community



### Conferences and Workshops

In addition to regular annual meetings (ASPB, ICAR, PAG), the following conferences are planned for 2017-2018:

BrassiBase workshop held in Heidelberg in October 2017. Detailed information is found on [www.ruhr-uni-bochum.de/dfg-spp1529](http://www.ruhr-uni-bochum.de/dfg-spp1529).

Plant Genome Evolution in Spain in October 2017  
<https://www.elsevier.com/events/conferences/plant-genome-evolution>

Brassica 2018 will meet in St. Malo, France - this and other Brassica conference announcements can be found at <http://www.brassica.info/info/events.php>

### Selected Publications

- 1001 Genomes Consortium (2016). 1,135 genomes reveal the global pattern of polymorphism in Arabidopsis. *Cell* 166, 481-491.
- Cheng F, Sun R, Hou X, Zheng H, Zhang F, Zhang Y, Liu B, Liang J, Zhuang M *et al.* (2016). Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in *Brassica rapa* and *Brassica oleracea*. *Nature Genetics* doi: 10.1038.ng.3634.

Golicz AA, Bayer PE, Barker GC, Edger PP, Kim H-R, Martinez PA, Chan CKK, Severn-Ellis A, McCombie R, Parkin IAP, Paterson AH, Pires JC, Sharpe AG, Tang H, Teakle GR, Town CD, Batley J, and Edwards D. (2016). The pangenome of an agronomically important crop plant *Brassica oleracea*. *Nature Communications* 7: 13390.

Kawakatsu T., Huang S.-S.C., Jupe F, Sasaki E., Schmitz RJ, Ulrich MA, Castanon R, Nery JR, Barragan C, He Y, *et al.* (2016). Epigenomic diversity in a global collection of Arabidopsis accessions. *Cell* 166, 492-505.

Novikova P, Hohmann N, Nizhynska V, Lanz C, Tsuchimatsu T, Muir G, Guggisberg A, Paape T, Schmid K, Fedorenko O, Holm S, Säll T, Schlötterer C, Marhold K, Widmer A, Sese J, Shimizu KK, Weigel D, Krämer U, Koch MA, Nordborg M. (2016) Sequencing of the genus Arabidopsis reveals a complex history of non-bifurcating speciation and abundant trans-specific polymorphisms. *Nature Genetics*. doi:10.1038/ng.3617.

## Analysis and Recommendations

### Progress Towards Goals of the Subcommittee

(A) Build a predictive model of an Arabidopsis plant from its molecular parts  
 • Progress was made in expanding epigenomic insights in Arabidopsis (Kawakatsu *et al.* 2016).

(B) Exploit the wealth of natural variation that exists in Arabidopsis and related species to further our understanding of adaptation and evolution  
 • Progress in the natural variation of Arabidopsis was made with the sequencing of 1,135 genomes (The 1001 Arabidopsis Genomes Consortium 2016), and several closely related species of Arabidopsis (Novikova *et al.* 2016).  
 • Progress in comparative genomics was made in sequencing additional genomes.

Major milestones were made in sequencing the economically important genus Brassica, including the publication of hundreds of accessions of *Brassica rapa*, *Brassica oleracea*, and associated pan-genomes (Cheng *et al.* 2016, Golicz *et al.* 2016). These studies in comparative genomics and natural variation illuminated several aspects of Brassicaceae biology.

(E) Deepen international cooperation and coordination  
 • Progress was made toward international cooperation and coordination at various meetings, including the annual meetings of the Brassicales Map Alignment Project (BMAP, see <http://www.brassica.info/resource/sequencing/bmap.php>) and the Multinational Brassica Genome Project (MBGP, <http://www.brassica.info/info/about-mbgp.php#meetings>).

The BMAP species sequenced soon to be on Phytozome include one genome in the Cleomaceae (*Cleome violacea*) and 18 genomes in the Brassicaceae: *Cakile maritima*, *Caulanthus amplexicaulis*, *Crambe hispanica*, *Descurainia (two species)*, *Diptychocarpus strictus*, *Eruca vesicaria*, *Euclidium syriacum*, *Iberis amara*, *Isatis tinctoria*, *Lepidium sativum*, *Lunaria annua*, *Malcomia martima*, *Myagrum perfoliatum*, *Rorippa islandica*, *Sinapis alba*, *Stanleya pinnata*, and *Thlaspi arvense*.

(F) Subcommittee specific goals (if applicable)

- Progress was made toward agreeing on gene naming conventions across the Brassica species, with planned discussions among the Arabidopsis and Brassica communities to coordinate various standards and ontologies, as well as conventions for annotation, pan-genomes, ancestral genomes, and other -omics efforts within and across species in the Brassicales.

In conclusion, the results obtained over the past year demonstrate that research in natural variation and comparative genomes remains very active, efficient and innovative (for example, we had many more than five publications to choose from for our section). The impacts on the future of the MASC, its objectives, activities, organization and funding model will be discussed during ICAR 2017 in St. Louis, Missouri.

### Future Goals of the Subcommittee

(A) Build a predictive model of an Arabidopsis plant from its molecular parts

Future goals include building predictive models with insights from:

- Studying natural variation within Arabidopsis and comparisons to other related species of plants.
- Developing systems biology and -omics resources parallel to those available in Arabidopsis in crops like Brassica and Camelina and phylogenetically related model species that exhibit traits not present in Arabidopsis (e.g., both C3 and C4 photosynthesis in Cleome, woodiness in Caper).

(B) Exploit the wealth of natural variation that exists in Arabidopsis to further our understanding of adaptation and evolution

Future goals include:

- Exploring the variation in Arabidopsis and related species at numerous levels of biological organization to infer biological networks from various -omics datasets, including genomic, epigenomic, proteomic, metabolomic, ionomic, interactomic, and phenomic.
- Analyzing Arabidopsis ecotypes and related plant species in association with their rhizosphere, endophyte and epiphyte communities in various ecological and agricultural settings.
- Integrating studies across species and environments by analyzing and classifying natural diversity in the Brassicaceae, dissecting the genomic basis of diversified traits, and developing the infrastructure to maximize common benefits from genetic, genomic, ecological and systematics tools.
- Generating a multi-locus nuclear phylogeny of all the genera and species of the Brassicales for comparative biology, and to quickly identify transcriptome variation, life history traits, and genome size for future candidates of species for genome sequencing.
- Developing computational resources to understand and utilize the natural variation of Arabidopsis and

related species. This will include interactions among the all the MASC subcommittees with the 1001 Arabidopsis Genomes project, Multinational Brassica Genome Project (MBGP), and Brassicales Map Alignment Project (BMAP) to consider natural variation and comparative -omics in the roadmap. Ensure that the Arabidopsis Information Portal (AIP) be built to work for Brassica and other plant species.

- Creating germplasm resources that are publicly available (e.g., Brassica diversity sets) and create a database for managing diversity (e.g., Brassibase, see brassica.info)

(C) Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa

Future goals include

- Pursuing systems biology research programs and analyze -omics datasets in other plant systems using key knowledge gained through the analysis of Arabidopsis, starting with the crop Brassicas (vegetables and oilseeds), biofuel crops (e.g., Camelina), and other economically important species (e.g., horseradish, wasabi, etc.).
- Establishing data standards and ontologies to provide uniform data on growth conditions and experimental metadata to enable modeling from controlled environments to the field.
- Developing high-throughput methods in the lab and the field for measuring phenotypes and identifying QTLs that have subtle effects. Develop appropriate open access informatics and data infrastructure for storage, retrieval and analysis of natural variation and QTL. Establish accessible statistical and computational methods for the analysis of natural variation and QTL data.

(D) Build the IAIC and develop efficient informatics tools and repositories further

Future goals include:

- Integrating -omics data and informatics infrastructure in Arabidopsis with other species.
- Developing international standards for population genomics (Arabidopsis 1001 genomes, Brassica 100 genomes) and comparative genomics (BMAP 100 genomes) to maintain high-quality reference genomes and re-sequenced genomes.
- Developing open access ontology-driven database tools and promote the adoption of uniform vocabularies and machine-readable formats for describing experimental data and metadata. Subcommittee member Nicholas Provart has developed an Arabidopsis-centric view of BMAP data via a tool called GeneSlider at the Bio-Analytic Resource (BAR). The current version of tool will include predicted transcription factor binding sites with links to Regulome (genome-wide DNase I sensitivity data), see Waese *et al.*, 2016 and URL: <https://goo.gl/QhMDOh>

Furthermore, the Provart Lab's ePlant (Waese *et al.*, 2017, in revision) displays non-synonymous polymorphisms from the 1001 Proteomes site (Joshi *et al.*, 2012) on

documented or predicted 3D structures covering ~70% of the Arabidopsis proteome, in the context of functional sites from the Conserved Domain Database or from Pfam, in addition to allow the exploration of other Arabidopsis data sets from the kilometer to nanometer scales. Pins along the sequence in the MoleculeView denoting non-synonymous SNP changes are scaled in size and colour according to their frequency of occurrence in the 1001 Proteomes data set. ePlant is also available as a "mega-app" on Araport. See URL: <https://goo.gl/L9aMe9>

(E) Deepen international cooperation and coordination

Future goals include:

- Undertaking a coordinated analysis of natural variation and comparative -omics with the international Brassicales Map Alignment Project (BMAP), Multinational Brassica Genome Project (MBGP), International Arabidopsis Informatics Consortium (IAIC), and Brassibase.
- Continuing BMAP workshops at international conferences to coordinate efforts, share expertise, and develop -omics standards and comparative ontologies.

(F) Subcommittee specific goals

Future goals include:

- Studying natural variation within Arabidopsis and comparative 'omic and systems biology investigations in related species is central to understanding plant biology and plant environment interactions.
- Coordinating gene naming conventions across the Brassica species, with planned discussions among the Arabidopsis and Brassica communities to coordinate various standards and ontologies, as well as conventions for annotation, pan-genomes, ancestral genomes, and other -omics efforts within and across species in the Brassicales.

### Tools and Resources

Pan-genomes: population genomics meets comparative genomics; network biology, systems biology, synthetic biology, and so forth.

1- Important resources from Detlef Weigel are AraPheno and AraGeno: <https://arapheno.1001genomes.org/> and <https://arageno.gmi.oeaw.ac.at>

2. Brassibase  
<http://brassibase.cos.uni-heidelberg.de/>

BrassiBase is continuously developed into a comprehensive Brassicaceae-knowledge-database system. During 2016/2017 the first family-wide species check-list has been created and launched with a new version of BrassiBase in March 2017 now comprising 52 tribes and nearly 4000 species. In total, more than 15,000 taxonomic entities ("names" of species, subspecies, etc., including synonyms) have been collected, checked and cross-referenced. We are now in the process to use this most actual and accurate species check-list as "backbone" for BrassiBase and will link given information whenever possible to this information.

Furthermore, morphological descriptions of characters of any genus are now finalized and implemented into an interactive key to the genera. The distribution of morphological variation can now be visualized using viewer functions implemented in BrassiBase. We hope that this will help to identify cultivated and/or collected wild material more easily, particularly if used in combination with the "Phylogenetic placement tool" implemented with BrassiBase, which has been also updated significantly.

We intend to release the third version of BrassiBase during 2016 and we invite and encourage the Arabidopsis community to register with BrassiBase (it's free) and help improving the system - by reporting and contributing with results and data and/or spotting problems and making suggestions for future releases.

BrassiBase workshop will be held in Heidelberg in October 2017. Detailed information is found on [www.ruhr-uni-bochum.de/dfg-spp1529](http://www.ruhr-uni-bochum.de/dfg-spp1529).

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## Phenomics

<http://Arabidopsisresearch.org/index.php/subcommittees/metabolomics>



Fabio Fiorani (chair) with contribution from subcommittee members and the wider Arabidopsis community.

### Conferences and Workshops

- 4th International Phenotyping Symposium. December 13-15, El Batan, Texcoco, Mexico

- 2nd Annual Conference of COST Action PhenomenALL, April 18-20 Copenhagen, Denmark

- PhenoHarmonis Workshop 9-13 May 2016 - Montpellier, France

- IPAP 2016, 2nd Integrated Plant and Algal Phenomics Meeting, 3-7 September, Prague, Czech Republic

- Phenome 2017, Tucson, AZ, US, Feb 2017

### Selected Publications

- Arend D, Lange M, Pape J-M, Weigelt-Fischer K, Arana-Ceballos F, Mücke I, Klukas C, Altmann T, Scholz U, Junker A (2016a) Quantitative monitoring of Arabidopsis growth and development using high-throughput plant phenotyping. *Scientific Data* 3, 160055. [dx.doi.org/10.1038/sdata.2016.55](https://doi.org/10.1038/sdata.2016.55)

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- Sánchez-López ÁM, Bahaji A, De Diego N, Baslam M, Li J, Muñoz FJ, Almagro G, García-Gómez P, Azmetoy del Amo K, Ricarte-Bermejo A, Li J, Novák O, Humplík JF, Spíchal L, Doležal K, Ciordia S, Mena MC, Navajas R, Baroja-Fernández E, Pozueta-Romero J. 2016. Arabidopsis Responds to *Alternaria alternata* Volatiles by Triggering Plastid Phosphoglucose Isomerase-Independent Mechanisms. *Plant Physiology* 172: 1989–2001

### Analysis and Recommendations

In 2016 there has been a continued development of automated platforms and methods including new software for non-invasive phenotyping of Arabidopsis and crop phenotyping increasing the capacity and the number of research centers that are engaged in large-scale phenomics research. There were significant examples of

comprehensive pipeline approaches to link genome to phenome and enable multi-trait analysis towards this goal.

Comprehensive efforts continued in 2016 within The International Plant Phenotyping Network (IPPN), the EU COST Action Phenotyping, and the implementation of national phenotyping networks.

### Future Goals of the Committee

Promote best practices in phenotyping experimentation. Coordinated efforts will be required across phenotyping centers regarding germplasm used for sequencing (e.g., 1001 genome project) and mutant collections would be desirable. Notable examples include to phenotype all re-sequenced Arabidopsis accessions under a series of defined challenging environments and phenotype the “no phenotype” T-DNA knock-out mutants by subjecting the collection of homozygous T-DNA k.o. mutants, or double mutants hitherto without a discernable mutant phenotype to deep phenotyping under a series of well-defined challenging environments.

Continue the development of methods for phenotyping across well-defined environmental conditions.

### Tools and Resources

Updates contributed by Roland Pieruschka (Forschungszentrum Jülich GmbH, IBG2 Plant Science), Minami Matsui, David Gifford (RIKEN, Japan), Astrid Junker and Thomas Altmann (IPK Gatersleben), Lukás Spíchal (Olomouc, Czech Republic),

*IBG2, Forschungszentrum Jülich, Germany*

- The International Plant Phenotyping Network (IPPN e. V.; <http://www.plant-phenotyping.org/>) is an academic non-profit association located at the Institute of Bio- and Geosciences, IBG-2: Plant Sciences at the Forschungszentrum Jülich represents the major plant phenotyping centers worldwide. The association aims to provide all relevant information about plant phenotyping. The goal is to increase the visibility and impact of plant phenotyping and enable cooperation by fostering communication between stakeholders in academia, industry, government, and the general public.

Specifically IPPN enables efforts to establish an interaction platform to link the expertise of diverse groups from platform scientists, diverse users groups, technology developers, and policy makers by i) integrating the plant phenotyping community in synergistic identification of phenotyping concepts and technologies, ii) addressing technology development and implementation, iii) enabling exchange of knowledge, information, and expertise between diverse stakeholders iv) integrating the regionally and globally fragmented activities in plant phenotyping, v) advising decision and policy makers on state-of-the art and future opportunities and limits.

The key instruments of IPPN is the organization of International Plant Phenotyping Symposia as well as addressing relevant topics in working groups. Additionally, the association has started a discussion with the industry to specify and foster the interaction between academia and industry in plant phenotyping.

- The European Strategy Forum for Research Infrastructure (ESFRI) has identified “Plant Phenotyping” as a priority for the European research area and the project EMPHASIS (<http://emphasis.plant-phenotyping.eu/>) has been listed on the ESFRI Roadmap as an infrastructure project to develop and implement a pan-European plant phenotyping infrastructure.

The EMPHASIS project (European Infrastructure for Multi-Scale Plant Phenotyping And Simulation for Food Security in a Changing Climate) coordinated by the Institute of Bio- and Geosciences, IBG-2: Plant Sciences at the Forschungszentrum Jülich has started a process that aims at long-term operation of a pan-European plant phenotyping infrastructure and specifically, to make it available and accessible to a wide user community in Europe.

To reach this goal EMPHASIS has started the preparatory phase with the final goal to elaborate a business plan and a legal entity for future operation of the project. Specifically, the preparatory phase of EMPHASIS will establish a transparent, open and inclusive process that will enable close interaction within the European plant phenotyping community and develop a business plan by addressing the four major steps: i) mapping of the infrastructure, funders, access procedure and models, stakeholder community, e-infrastructure, imaging approaches, legal and governance scenarios etc.; ii) analyzing the gaps and limitations based on the mapping activities; iii) developing strategies to address the gaps; iv) combining the strategies in a business plan for future operation of EMPHASIS within a corresponding legal framework.

*RIKEN and University of Tokyo*

- BioResource Center (BRC) Experimental Plant Division (<http://epd.brc.riken.jp/en/>) Phenotype database of natural accessions (<http://bit.ly/2mrkm9m>) Arabidopsis Seed, DNA, Cell line (<http://bit.ly/2mri7Tq>)

- RIPPS (RIKEN Plant Phenotyping System) (K. Shinozaki, Miki Fujita, Kaoru Urano, Takanari Tanabata) is an automated system for evaluating plant growth under environmental stress conditions developed by the Gene Discovery Research Group of CSRS. RIPPS provides high-throughput and accurate measurements of plant traits, facilitating understanding of gene function in a wide range of environmental conditions (<http://bit.ly/1sObBEE>). Ability to focus on water use efficiency, not just growth or leaf shape. (Kuromori *et al.*, 2016)

- RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) is an integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary, with both RIKEN RAPID and CSHL Trapper DB for Ac/Ds transposon tagged lines in Arabidopsis. (Akiyama *et al.*, 2014; Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki)(<http://rarge-v2.psc.riken.jp/>).

- The Chloroplast Function Database II is a comprehensive database analyzed by combining genotypic and phenotypic multiparametric analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins. The phenotype and segregation data of Arabidopsis Ds/Spm and T-DNA-tagged mutants of nuclear genes encoding chloroplast proteins includes more than 300 morphological mutants and 48 transmission electron microscopic images of mutant plastid (Fumiyoshi Myouga and Kazuo Shinozaki) (<http://rarge-v2.psc.riken.jp/chloroplast/>).

- PosMed Positional Medline (Y. Makita, *et al.* RIKEN Synthetic Genome Research Group) Semantic web association study (SWAS) search engine ranks resources including Arabidopsis genes and metabolites, using associations between user-specified phenotypic keywords and resources connected directly or inferentially via a semantic web of biological databases such as MEDLINE, OMIM, pathways, co-expressions, molecular interactions and ontology terms (<http://bit.ly/2qEPFuyvv>).

- For Genome to Phenome, location information of T-DNA in the genome is available for RIKEN Arabidopsis Activation Tagging lines (Minami Matsui collaboration with NEC Soft co Ltd.) ([http://metadb.riken.jp/metadb/db/SciNetS\\_ria37i](http://metadb.riken.jp/metadb/db/SciNetS_ria37i)) and around 10,000 Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA Over-eXpressing) lines is available (<http://ricefox.psc.riken.jp/>).

- The RIKEN MetaDatabase portal site is used to provide information on RIKEN's various life science databases. In this database phenotype information of Activation tagging lines, Ac/ Ds transposon lines and FOX lines are available (<http://metadb.riken.jp/>).

- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) selected about 4,000 transposon insertion lines which have the Ds transposon in gene coding region, and observed visible phenotypes systematically depending on growth stage. Phenotypic descriptions were classified into eight primary and fifty secondary categories, then all recorded images can be searched by the line number or the phenotype categories (<http://rarge-v2.psc.riken.jp/phenome/>).

*University of Tokyo*

- A phenotype analysis program was developed at the University of Tokyo to characterize the pattern of epidermal cells and guard cells of Arabidopsis leaves

and seedlings. Research is funded by JST Project (<http://bit.ly/22oyHC6>) for evaluation of morphological measurement. CARTA (clustering-aided rapid training agent) software was developed for auto learning system (Dr. Kutsuna, N. and Hasezawa, S., University of Tokyo; Higachi *et al.*, 2015)

IPK Gatersleben, Germany

- The whole-plant phenotyping infrastructure at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben, Germany) comprises three conveyor belt-based, automated, high throughput plant-to-sensor phenotyping facilities (Junker *et al.* 2015). The system for small plants such as Arabidopsis is situated inside a phytochamber and allows for growth and automated imaging as well as weighing/watering of up to 4608 plants in parallel under fully controlled environmental conditions. Imaging in the RGB and near-infrared wavelength ranges, imaging of static and kinetic fluorescence in combination with 3D surface scanning enables the quantification of a hundreds of plant features ranging from plant architectural traits (plant height and width, projected leaf area (top, side view), estimated volume, Klukas *et al.* 2014), through physiological traits (color-related traits, Klukas *et al.* 2014, CHL fluorescence-related such as Fv/Fm, Fv'/Fm', PhiPSII, relations to moisture content by NIR), to 3D related traits (leaf angles, 3D corrected projected areas).

A wireless sensor network enables the monitoring of environmental and soil conditions throughout the plant growth area and single pots, respectively. Upgrades for root phenotyping are under development which, will enable simultaneous HTP assessment of shoot and root properties. Experience cumulated since 2011 was used to establish appropriate experimental procedures and designs that support the detection of genotypic and environmental effects on plant growth, development, and performance (Junker *et al.* 2015). In a recent study a polymorphism in the Arabidopsis FUM2 gene was associated with plant growth / biomass accumulation as quantified by high throughput plant phenotyping (Riewe *et al.* 2016). In order to expand the options to assess the expression of developmental and physiological traits under controlled environmental variation, the automated Arabidopsis phenotyping phytochamber has been upgraded with a series of LED bars, which allow the precise simulation of fluctuation of light intensities in a homogeneous manner during the course of the day.

Current and future efforts include the phenotypic screening of Arabidopsis accession panels for responses in growth and photosynthetic performance elicited by light fluctuations, for natural variation in photosynthetic efficiency and the identification of the underlying genetic basis in respective mapping populations as well as the analysis of hybrids and segregating populations with respect to the genetic determination of growth, metabolism control and heterosis.

A first Arabidopsis high throughput phenomics dataset has been made available by Arend *et al.* (2016a) through the PGP repository (Arend *et al.* 2016b) using the underlying e!DAL data publication infrastructure (Arend *et al.* 2014) and comprises a comprehensive standardized metadata documentation compliant with the recently proposed Minimal Information About a Plant Phenotyping Experiment (MIAPPE, Cwiek-Kupczynska *et al.* 2016). The existing image analysis platform (IAP, Klukas *et al.* 2014) is currently being extended for the integrated / combinatorial analysis of the data (projected 2D images, 3D point clouds) derived from the various camera and scanning installations of the multi-sensor setup in order to retrieve novel information and to increase the precision (spatial resolution) of phenotypic trait extraction and data interpretation.

- IAP - Integrated Analysis Platform (<http://iapg2p.sourceforge.net/>). The Integrated Analysis Platform (IAP) has been designed and developed to support the analysis of large-scale image data sets of different camera systems. It aims at bridging various -omics domains and offers integrated approaches for image analysis up to data post-processing. (Klukas *et al.* 2014).

- MCCC - Image-based Multi Channel Classification and Clustering (<http://mcccs.sourceforge.net/>). The MCCC represents a generalized, script-based classification system to be used for the processing of image data derived from a variety of sensors (RGB to hyper/multispectral). The implemented machine learning approaches enable solving different segmentation, classification and clustering problems. (Pape and Klukas *et al.* 2015a and b).

- PGP - Plant Genomics and Phenomics Research Data Repository (<http://edal.ipk-gatersleben.de/repos/pgp/>).

- The e!DAL data publication pipeline as the basis of the PGP repository provides an infrastructure to publish plant research data, in particular cross-domain data sets and phenomics datasets and respective metadata information which are assigned with citable DOIs for access and reuse by the scientific community. (Arend *et al.* 2014 and 2016a).

*The Centre of Region Haná for Biotechnological and Agricultural Research (Palacký University in Olomouc & IEB ASCR & Crop Research Institute)*

- Our department is equipped with two phenotyping systems PlantScreen™ (PSI, Brno, Czech Republic) dedicated to integrative phenotyping of shoots of various plant species (Humplík *et al.* 2015). Phenotyping platform allows measurement of plant growth, chlorophyll fluorescence, leaf temperature and leaf reflectance in fully controlled environment. Experiments performed in the systems are mainly focused on the evaluation of effectivity of synthetic growth regulators or potential bio-stimulants (Bahaji *et al.* 2015), but the selection of mutants or cultivars can be also provided on a request. We are developing protocols for assessing impact of various abiotic stresses in different plant developmental stages.

One of our aims is selection of cold-tolerant cultivars of field pea (*Pisum sativum* L.) for which the optimized measuring protocol was developed (Humplík *et al.* 2015b). Another applied analysis deals with the problem of salinity in the early development of crop species. Recently we have developed crop seedling emergence software that reveals ability of seeds to germinate and of the seedlings to reach the light before the reserves are exhausted. This high-throughput bioassay (60 variants, 6600 seeds; in one run) automatically provides information about emergence rate as well as the total number of emerged seedlings. Further standardized protocols include *in vitro* screening of Arabidopsis growth by RGB camera in 24-well or 6-well plates (up to 11 000 seedlings) or complex phenotyping of Micro-Tom tomatoes and baby-lettuce grown in pots.

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## Proteomics

<http://Arabidopsisresearch.org/index.php/subcommittees/proteomics>

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

Joshua Heazlewood (chair)



E) Subcommittee members are involved with the initiative on Multi-Organism Proteomes (iMOP) as part of the Human Proteome Organization (HUPO) and are active members of the International Plant Proteomics Organization (INPPO). As well as many serving as members of their national plant societies.

F) The subcommittee website has been re-launched .  
<http://www.masc-proteomics.org/>

### Future Goals of the Subcommittee

(A) Maintain and develop new resources for Arabidopsis focusing on protein function and proteomics.

(B) Demonstrate applicability of 1001 proteome data to the research community. Update the data for the recently released accessions.

(C) Highlight projects that have demonstrated translational proteomic approaches on the re-launched website.

(D) Start to construct proteomic Apps for the Arabidopsis Information Portal, Araport.

(E) Ensure attendance and involvement in future INPPO and HUPO activities.

(F) Maintain an active Arabidopsis proteomics subcommittee (<http://www.masc-proteomics.org/>).

### Tools and Resources

Pep2Pro - proteo-genomic resource (<http://fgcz-pep2pro.uzh.ch/>) by Baerenfaller

ProMEX - mass spectral resource (<http://promex.pph.univie.ac.at/promex/>) by Wienkoop and Weckwerth

GelMap - 2-DE proteomic repository (<https://gelmap.de/projects-Arabidopsis/>) by Braun

APP - targeted proteomics (SRM) tool (<http://www.plantenergy.uwa.edu.au/APP/>) by Taylor and Millar

SUBA - subcellular database (<http://www.suba.bcs.uwa.edu.au/>) by Millar

PPDB - plant protein database (<http://ppdb.tc.cornell.edu/>) by van Wijk

AT\_CHLORO - plastid proteomic resource ([http://www.grenoble.prabi.fr/at\\_chloro/](http://www.grenoble.prabi.fr/at_chloro/)) by Rolland and Ferro

AraPerox - peroxisome proteomic database (<http://www3.uis.no/AraPeroxV1/>) by Reumann

PhosPhAt - phosphoproteome database (<http://phosphat.uni-hohenheim.de/>) by Schulze

P3DB - plant phosphoproteome database (<http://p3db.org/>) by Thelen

RIPP-DB - phosphoproteome database (<http://phosphoproteome.psc.database.riken.jp/>) by Nakagami

MASC Gator - proteomics aggregation portal (<http://gator.masc-proteomics.org/>) by MASC

1001 Proteomes - non-synonymous SNPs from natural variants (<http://1001proteomes.masc-proteomics.org/>) by Heazlewood

MRMaid - MRM design tool (<http://elvis.misc.cranfield.ac.uk/mrmaid/>) by Jones

### Selected Publications

Hooper CM, Castleden IR, Tanz SK, Aryamanesh N, Millar AH (2017) SUBA4: the interactive data analysis centre for Arabidopsis subcellular protein locations. *Nucleic Acids Res* 45: D1064-D1074

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### Analysis and Recommendations

#### Progress Towards Goals of the Subcommittee

A) The subcommittee members maintain an array of Arabidopsis specific proteomic repositories. These resources currently contribute to information in the Arabidopsis Information Portal (AIP).

B) The 1001 Proteomes portal provides pre-computed nsSNP data from the sequenced accessions.

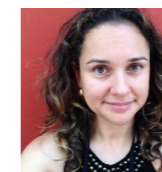
C) Members have ongoing interests in applying proteomic approaches in Arabidopsis to important crop species. A number of the on-line proteomic resources also provide proteomic datasets for agricultural relevant species.

D) Subcommittee members maintain extensive resources in the area of protein function in Arabidopsis, and it is expected that this information will be coordinated with the IAIC.

## Systems and Synthetic Biology

<http://Arabidopsisresearch.org/index.php/subcommittees/systems-biology>

Siobhan Brady (chair), Malcolm Bennett (co-chair) with contributions from Susannah Lydon, Leah Band, Gabriel Krouk, Pascal Falter-Braun, Rodrigo Gutierrez, Nicola Patron and Geraint Parry



### Conferences and Workshops

\*Plant Organ Growth Symposium 2017, Elche (Spain) March 15-17th 2017 <http://pogs2017.edu.umh.es>

\* Plant CRISPR Workshop CRISPR/Cas-mediated Plant Genome Editing: From Design to Analysis. Iowa State. May 10 & 11, 2016

\*NSF-RCN Workshop - "Arabidopsis Research and Training for the 21st century (ART-21)". Phoenix, Arizona, May 13-16, 2016. This group developed recommendations on the research and training approaches needed for Arabidopsis plant biologists to work effectively at the intersection of wet-lab and quantitative/computational biology for careers both inside and outside academia

\* Gordon Conference: Plant Molecular Biology - How Plants Sense, Process, Integrate and Store Information, Holderness School, Holderness, NH, June 12-17, 2016

\*Systems Biology Session, International Conference on Arabidopsis Research 2016, Gyeong Ju, Korea, July 1, 2016

\*New Biological Insights from Large Scale Biology, ASPB Annual Meeting, Austin Texas, July 11, 2016

\*Plant session at Synthetic Biology: Engineering, Evolution & Design (SEED), Chicago, IL. July 18-21, 2016

\*Emerging Genomics Techniques and the Future of Research using Arabidopsis Workshop, ICAR 2016, Gyeong Ju, Korea, June 30, 2016

\*Synthetic Biology Session and Introduction to CRISPR-Cas Workshop at GARNet2016: Innovation in the Plant Sciences. Cardiff University, UK. September 6th-7th 2016.

\*Genomics-enabled Accelerated Crop Breeding. Banbury Center, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY October 16-19, 2016

\*EMBO Conference: From Functional Genomics to Systems Biology. Heidelberg, Germany. November 12-15, 2016.

\*First International Plant Biology Course - Session on Systems Biology of Plant Nutrition, Nov. 25, Dec 5-6, 2016

\*Synthetic Biology Workshop, Puerto Natales, Chile, 2016

### Selected Publications

Mellor N, Band L R, Pencik A, Novakc O, Rashed A, Holman T, Wilson M H, Voß U, Bishopp A, King J R, Ljung K, Bennett M J and Owen M R (2016) Dynamic regulation of auxin oxidase and conjugating enzymes AtDAO1 and GH3 modulates auxin homeostasis *PNAS* 113 ,39 , 11022-11027

O'Malley RC, Huang SS, Song L, Lewsey MG, Bartlett A, Nery JR, Galli M, Gallavotti A, Ecker JR (2016) Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell* 165(5):1280-1292.

Ristova D, Carré C, Pervert M, Medici A, Kim GJ, Scalia D, Ruffel S, Birnbaum KD, Lacombe B, Busch W, Coruzzi GM, Krouk G. (2016) Combinatorial interaction network of transcriptomic and phenotypic responses to nitrogen and hormones in the Arabidopsis root. *Science Signaling* 9(451):rs13

Schaumberg KA, Antunes MS, Kassaw TK, Xu W, Zalewski CS, Medford JI & Prasad A (2016) Quantitative characterization of genetic parts and circuits for plant synthetic biology. *Nature Methods* 13, 94-100

Sparks EE, Drapek C, Gaudinier A, Li S, Ansariola M, Shen N, Hennacy JH, Zhang J, Turco G, Petricka JJ, Foret J, Hartemink AJ, Gordân R, Megraw M, Brady SM, Benfey PN. (2016) Establishment of Expression in the SHORTROOT-SCARECROW Transcriptional Cascade through Opposing Activities of Both Activators and Repressor Developmental Cell, 39(5):585-596

### Analysis and Recommendations

#### Progress Towards Goals of the Subcommittee

(A) - Biological systems are inherently complex, with multiple levels of regulation at wide ranges of spatial and temporal scales. Experimental biologists can alter an organism's genotype and quantify the resulting phenotype.

However, understanding how a genotype creates a phenotype requires knowledge of a complex network of interactions bridging multiple spatial and temporal scales and environmental inputs. Progress has recently been made developing multiscale plant organ models that integrate molecular scale regulatory pathways with cell and tissue geometries and mechanics,

The resulting predictive models provide powerful tools with which to probe complex processes such as organ patterning, growth and responses to environmental signals (e.g. Clark *et al.*, 2016; Fozard *et al.*, 2016).

Nevertheless, understanding complex multiscale biological systems is beyond the limits of current methods. Not only are there numerous regulatory steps at multiple spatial scales, but effects at each scale feed back on other scales resulting in a huge interconnected network of interactions. Examples of tools and applications to do this in microbial systems as an example are provided in Nunez *et al.*, 2016, ACS Synthetic Biology. Mathematical and computational models are essential to understand the behaviour of such complex multiscale systems; nevertheless, developing techniques and strategies to model a virtual organism remains a major challenge.

OpenPlant established the “PhytoBrick” standard for Plant Synthetic Biology, a common genetic syntax for exchange of DNA parts for plants. OpenPlant is a joint initiative for plant synthetic biology between the University of Cambridge, John Innes Centre and the Earlham Institute, funded by the BBSRC and EPSRC UK Research Councils. Open Plant is developing new tools and methods for plant synthetic biology; providing mechanisms for open sharing of standardized resources, applying these tools to world-leading projects in trait development, and facilitating interdisciplinary exchange, outreach and international development.

(B) Systematic mapping of the Arabidopsis protein interaction network is continuing (Braun lab) and an expanded map covering a 12k x 12k search space (expected 12k interactions) as well as map of the phytohormone signaling network is progressing - the data will be disseminated through existing channels, including the IntAct and BioGrid databases and TAIR. Data analysis will include investigation how natural variation affects protein interactions and should lead to insights on the mechanisms of network evolution.?

(C) The Ionomics Hub provides such a knowledge pipeline – linking Arabidopsis with crops like rice and *vica versa*. Training activities to facilitate knowledge exchange were also discussed in the NSF-RCN workshop held in Phoenix Arizona and which are summarized in a white paper to be published for the community in 2017.

(D) No progress to report.

(E) The International Genetically Engineered Machine (iGEM) synthetic biology competition, established a Plant Committee and introduced a special award for ‘Best Advancement in Plant Synthetic Biology’. In 2016 5,600 participants from across 42 countries took part in iGEM.

Members of the subcommittee are in the process of raising funds to organize the first International Plant Systems Biology (iPSB) meeting. The iPSB organizing committee includes S. Brady (USA), P. Falter-Braun (DE), G. Coruzzi

(US), R. Gutierrez (CH), G. Krouk (FR). Help to raise funds is also kindly provided by the co-organizers M. Gifford (UK) and R. Bastow (UK). The meeting is planned to be held in France. The dates and location of the 1st iPSB will depend on the success of diverse grant applications. (A, E) Members of the subcommittee are organizing a European Network Conference in Heidelberg from April 15-17, 2018. The focus of this conference will be on new experimental and bioinformatic approaches to transfer network-level information into mechanistic insights, which then serve as a foundation for quantitative models in both Plants and Animals. The organizing committee consists of Pascal Falter-Braun (Helmholtz München), Sorina Popescu (Michigan State U.), Sandra Orchard (IntAct - EBI) and Luis Serrano (CRG - Barcelona).

(A,E) G. Krouk and the G. Coruzzi have been awarded a International Associated Lab (LIA-CoopNet) supported by the CNRS (FR). We expect a substantial leverage effect on ongoing common grant application supporting systems biology investigations.

### Future Goals of the Subcommittee

A, B, C, D: The Institute of Network Biology together with the German Plant Phenotyping Network (DPPN), in particular the outpost at the Helmholtz Zentrum Munich, it is planning to embark on a network-driven deep-phenotyping of mutants for which the connectivity in the Arabidopsis protein interaction network is known. This is expected to deepen the understanding of how different type of network components affect different plant phenotypes and how connectivity relates to pleiotropy and specific phenotypes respectively. The initial studies with null alleles will serve as a baseline for future studies using interaction-deficient (edgetic) alleles. Funding for this project needs to be secured.

### Tools and Resources

Fozard J A, Bennett M J, King J R, Jensen O E (2016) Hybrid vertex-midline modelling of elongated plant organs Interface Focus doi: [10.1098/rsfs.2016.0043](https://doi.org/10.1098/rsfs.2016.0043)

### References

Clark NM, Hinde E, Winter CM, Fisher AP, Crosti G, Blilou I, Gratton E, Benfey PN, Sozzani R. (2016) Tracking transcription factor mobility and interaction in Arabidopsis roots with fluorescence correlation spectroscopy. *Elife*. 2016 Jun 11;5. pii: e14770. doi: [10.7554/eLife.14770](https://doi.org/10.7554/eLife.14770).

Fozard JA, Bennett MJ, King JR, Jensen OE. (2016) Hybrid vertex-midline modelling of elongated plant organs. *Interface Focus*. 2016 Oct 6;6(5):20160043.

Nuñez I, Matute T, Del Valle I, Kan A, Choksi A, Endy D, Haseloff J, Rudge TJ, Federici F. (2016) Artificial Symmetry-Breaking for Morphogenetic Engineering Bacterial Colonies. *ACS Synth Biol*. 2017 Feb 17;6(2):256-265. doi: [10.1021/acssynbio.6b00149](https://doi.org/10.1021/acssynbio.6b00149).

# Arabidopsis Community Projects and Resources

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

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

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

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

In order to provide a flexible platform to enable open sharing of the vast amount of data generated by today's omics approaches, the International Arabidopsis Informatics Consortium (IAIC) founded the Arabidopsis Information Portal, Araport, in 2013 (page 29). Araport is now beginning to interact with both other Arabidopsis resources such as BAR (page 32) and those from other organisms. This will begin to provide a one-stop analysis pipeline for researchers who aim to move their work from Arabidopsis into other model or crop species.

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

### Resource and Stock Centers

Arabidopsis Biological Resource Center (ABRC) (page 28)

Nottingham Arabidopsis Stock Center (uNASc) (page 28)

RIKEN BioResource Center (BRC) (page 29)

Arabidopsis Information Portal (Araport) (page 29)

The Arabidopsis Information Resource (TAIR) (page 30)

### Plant Projects and Resources with Strong Participation of the Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR) (page 32)

Gramene (page 33)

Work undertaken by BrassiBase (<https://brassibase.cos.uni-heidelberg.de/>) and by the EMPHASIS phenotyping program (<https://emphasis.plant-phenotyping.eu/>) have been included in the Natural Variation (page 17) and Phenomics (page 20) sub-committee reports respectively.

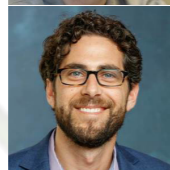
Besides the above listed projects and resources, there are many other international and multinational initiatives with major contributions from Arabidopsis researchers, e.g. the 1001 Arabidopsis Genomes Project ([www.1001genomes.org](http://www.1001genomes.org)), the Epigenomics of Plants International Consortium (EPIC; [www.plant-epigenome.org](http://www.plant-epigenome.org)), the Plant and Microbial Metabolomics Resource (<http://metnetdb.org/PMR/>) and the International Plant Phenotyping Network (<http://www.plant-phenotyping.org/>).

## Resource and Stock Centers

### The Arabidopsis Biological Resource Center (ABRC)

[www.abrc.osu.edu](http://www.abrc.osu.edu)

Erich Grotewold (Director)  
R. Keith Slotkin (Co-Director)  
Jelena Brkljacic (Associate Director)



#### Activities

Located at The Ohio State University, the ABRC is a community-driven clone and seed stock center.

The ABRC continues to provide incentives for its donors, including the Stocks for Stocks rewards program and a paid shipping option for donations. As a result, the number of donors and individual stock donations have increased three-fold in the past year. The ABRC has added popular genome editing resources, represented by a number of CRISPR/Cas9 vectors for monocots and dicots, as well as the pGreenII-derived pViridis vector and MW906 E.coli host strain designed to solve cloning rearrangements caused by the pGreenII backbone. The SALK Institute completed their collection of homozygous T-DNA lines by donating a total of 51,530 lines, representing 24,858 loci. The ABRC has also started soliciting, curating and distributing donations of resources for multiple non-Arabidopsis plant species. The focus is on clones and clone sets, as well as on the seeds of closely related species. Funds have been obtained to propagate and/or distribute several bioenergy crop resources as well.

The ABRC's education and outreach has included hands-on programs for students both on-campus and in schools, professional development for teachers, as well as participation in science education conferences. In 2016, the ABRC's outreach program reached more than 1,500 teachers and approximately 500 students. A manuscript "Life in Bloom: Using Arabidopsis Mutants to Study Plant Development" is being revised by the Course Source online teaching resource. A second manuscript entitled "Following Phenotypes: An Exploration of Mendelian Genetics" has been accepted for publication in the American Biology Teacher journal.

#### Current News

In collaboration with the technology team of The Ohio State University's College of Arts and Sciences, we have started building a stock-specific database for searching and ordering ABRC stocks. We expect to deliver a fully functional user interface by the end of 2017.

In addition to storing and distributing high quality Arabidopsis resources, ABRC continues to push forward to be at the cutting edge of the community needs in terms of the quality control. We continue to increase community-driven quality controls of clone and seed stocks, and are planning to start including the whole genome sequencing into our QC pipeline.

We are grateful to our current director, Dr. Erich Grotewold, for eight years of great service to the community. Dr. Grotewold will become the chair of the Department of Biochemistry and Molecular Biology at Michigan State University in August 2017. We are happy to announce that Dr. R. Keith Slotkin, a distinguished OSU researcher, has accepted the directorship of ABRC upon Dr. Grotewold's departure. In the meantime, Dr. Slotkin will be co-directing the activities of the Center.

#### Conferences, Workshops, Social Media

International Conference on Arabidopsis Research (ICAR 2017), June 19-23, St. Louis, MO: ABRC will have a booth and participate in the bioinformatics resources workshop

Plant Biology (ASPB 2017), June 24-28, Honolulu, HI: ABRC will have a booth at this meeting.



### The Nottingham Arabidopsis Stock Centre (uNASC)

<http://www.Arabidopsis.info>

Sean May, Director  
Marcos Castellanos-Urbe, Operations Manager.



We are very pleased to announce that our application for another four year extension of funding for NASC has been approved by the Bioinformatics and Biological Resources Fund (BBRF) of the UK BBSRC funding body. This ensures that NASC will continue to run (at least) from Nov 2017 - Oct 2021.

To prevent (some) confusion in the way we have previously reported distribution statistics - from Jan 1st 2017 our 'accounting year' has been synchronised with the calendar. Our statistics for this report will therefore overlap slightly with last year but still accounts for a full year of distribution.

Once again stock numbers sent to users have increased (the 11th consecutive year) - we sent over 180,000 tubes

of seed in 2016 to 56 countries. A little more than 40% of these were distributed as sets (rather than as individual stocks) showing the importance of these micro-structured (and cheaper per stock) resources.

In terms of geographic demand, over the last three years 6% of orders went to France, 14% Germany, and 19% to the UK, welcoming China as our biggest user served (33%) - for the second year running. In addition, we distribute to several countries on the DAC list of ODA recipients including Least Developed & Lower Middle Income: Bangladesh, India, Pakistan, and Ukraine. Total=2,037 stocks; and Upper Middle Income: Argentina, Brazil, Chile, Colombia, Iran, Iraq, Libya, Malaysia, South Africa, Thailand, and Turkey. Total = 2,704 stocks. As a final rather crude measure of interest in stock information our catalogue sees around 5,000 unique visits per month.

Several important new donations of seed this year show that the Arabidopsis community continues to flourish and expand with outstanding cooperative zeal and a genuine dependence on the kindness of strangers. For up-to-date details on stock donations, please visit the site for comprehensive information on new materials and perhaps take a look at [@NascArabidopsis](https://twitter.com/NascArabidopsis)

Please do remember that we (NASC and ABRC) can save you time, effort and promote your research impact by distributing seed on your behalf to the wider plant community - our joint effectiveness as a model organism network has been built on many years of reciprocal altruism.



See you in St Louis!

### RIKEN BioResource Center (RIKEN BRC)

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

Masatomo Kobayashi  
(RIKEN coordinator)



#### Activities

Since established in 2001, RIKEN BioResource Center (RIKEN BRC) has provided resources of plant, animal, human and microorganisms to the international research community. Our aim is the promotion of life sciences to contribute food, health and environment problems that are urgent global issues for human being



Since 2002, we join with the National BioResource Project (NBRP) funded by the Japanese Government (<http://www.nbrp.jp/index.jsp>). The fourth term of NBRP launched in this April. The Experimental Plant Division has been selected as the Core Facility of Arabidopsis/ Cultured plant cells and genes from NBRP, and is responsible for distributing plant resources from RIKEN BRC. Approximately, 840,000 materials are preserved, and they have been distributed to ca. 2,000 laboratories and research groups in 45 countries.

We focus our efforts to collect, preserve and distribute Arabidopsis resources that have been established by Japanese researchers, such as RIKEN Transposon-tagged Mutant (RATM) lines, activation(T-DNA)-tagged lines, FOX hunting lines, RIKEN Arabidopsis full-length cDNA (RAFL) clones, transcription factor (TF) clones and the genomic clones in the transformation-competent bacterial artificial chromosome vector (TAC). We also provide the seed lines of natural accessions and related species, individual mutant and transgenic lines, and Arabidopsis cultured cell lines (T87 and At wt).

In order to establish and support the pipeline "from bench to bountiful harvests", RIKEN BRC provides model plant resources such as Tobacco BY-2 cells, Rice Oc cells, and full-length cDNA clones of various plant species including Brachypodium distachyon, an experimental plant of monocot.

Quality control is an important issue for resource projects. Before shipment, end-sequence of every DNA material is obtained and compared with the data on our database. Insertion site of Ds transposable element in the RATM line is examined by PCR for confirmation. The results are provided to the recipients before or at the time of shipment. Other information necessary to utilize the resources are provided via website and/or e-mail.

### Arabidopsis Informatics and Data Sharing Resources

#### The Arabidopsis Information Portal (Araport)

[www.araport.org](http://www.araport.org)

Chris Town (PI) and Agnes Chan (co-PI)



#### Activities

Usage of Araport continues to increase. During the eleven month period between April 2016 and February 2017, over 40,000 visitors visited Araport.org. On average, there were over 3,700 visitors per month, and the number of visitors has increased over two years with a peak usage of over 5,000

visitors per month immediately following the GARNet Workshop at Cardiff (Wales) held in September 2016.

Users who register at [Araport.org](http://Araport.org) will have privileges to save work sessions, post comments, and access Science Apps. The number of registered users at [Araport.org](http://Araport.org) exceeds 1,600 as of February 2017, including a sharp increase of over 170 new users immediately following the Cardiff Workshop.

Araport's main features, ThaleMine and JBrowse have now been joined by a locally hosted instance of Nick Provart's ePlant, which users should certainly visit. ThaleMine provides functional gene annotations including the latest gene model updates from Araport11, gene-centric publications, GeneRIFs, and GO annotations, gene expression including RNA-seq and Affymetrix array data across tissues/organs and treatments, eFP visualization from BAR, protein interaction from IntAct and BioGrid; protein homology and orthology from Panther and Phytozome; germplasm and stock data from ABRC, pathway data from KEGG, TDNA-Seq insertions, and more.

Users can access ThaleMine via the Gene Report page, the Gene List Enrichment analysis tool, or a sophisticated Query Builder for cross-data-type analysis. Significantly, all InterMines have built-in web services for programmatic access of all the InterMine warehoused data where often none existed before.

The Araport JBrowse instance has been populated and extended to host close to 100 genome-wide data tracks. Federated data provided via third-party web services include epigenetics (CoGe), cross-species (VISTA) alignments and 1001 genomes variant data.

### News

The Araport project was officially approved for 5 years, with funding initially allocated for the first two years. The Araport team are actively working with the IAIC, our Scientific Advisory Board, community members and NSF to develop a work plan/proposal for the next three years that should be complete by the time this report is published. Prominent among future plans are simplified ways for community users to submit and share biological data sets for hosting by Araport and cloud-based tools both for app development and web service deployment.

### Conferences, Workshops, Social Media

Project PIs attended the 27th ICAR in Gyeong Ju, Korea in at the end of June 2016 and gave a talk in the Genome Editing session. We attended the ASPB meeting in Austin, July 2016, presented a talk in the "Bioinformatics Resources for Plant Biology Research" and also staffed a booth in the Exhibitor area together with colleagues from other resources.

PI Town gave an invited talk at GARNet2016: Innovation in the Plant Sciences" meeting in Wales in September 2016. Together with Software Engineer Sergio Contrino from the Cambridge InterMine group PI Town presented a 90-minute hands-on workshop that was attended by ~30 people and was deemed highly successful both by the attendees and the conference.

We co-organized the IAIC/Araport workshop at PAG, San Diego in January 2017 that included presentations from project personnel and community members.

This year we plan presences at the 28th ICAR in St Louis and ASPB 2017 in Hawaii.

### Additional Information

Araport11 annotation is described in Plant J, 2017; 89: 789–804. ThaleMine is described in more detail in Plant Cell Physiol 2017; 58 (1): e4.



## The Arabidopsis Information Resource (TAIR)

[www.Arabidopsis.org](http://www.Arabidopsis.org)

Leonore Reiser (TAIR curator)  
Eva Huala (Director)



### Activities

The Arabidopsis Information Resource (TAIR) is a continuously updated, manually curated, online database of genetic and molecular biology data for the model plant Arabidopsis. TAIR's biocurators extract, organize, and interconnect experimental data with computational predictions, community submissions, and high throughput datasets to provide a 'gold standard' annotation for this important reference genome. TAIR provides tools to visualize and analyze data and enables online ordering of seed and DNA stocks, protein chips and other experimental resources from the Arabidopsis Biological Resource Consortium (ABRC).

### Gene Family Integration

A major focus area for plant biologists is translational plant biology, which aims to transfer knowledge gained from lab experiments into the field to improve agriculture. In 2016 we solicited feedback from our community to help prioritize new data integration and visualization in TAIR.

We found there was a clear preference for the addition of gene family/orthology data to facilitate comparison and inference of gene function across species. In response to this feedback we have integrated gene family data and resources into the TAIR locus pages.

This work included three components: 1) import and display of plant homologs from the PANTHER database; 2) addition of links directly to the PANTHER Tree Viewer where researchers can view phylogenetic relationships spanning many taxonomic groups; and 3) addition and reorganization of links to gene family datasets at Ensembl Plants, Phytozome, PLAZA and PANTHER to improve visibility. We hope these new TAIR locus page features will make it easier to find orthologs, view phylogenetic trees and infer gene function for species lacking experimental data.

### Curation

TAIR continues to mine published data to provide researchers with continuously updated information about Arabidopsis gene function, expression and mutant phenotypes. To produce a gold standard annotated genome, we manually extract information about gene function from experimental results reported in the literature. Additional information flows into TAIR from authors who curate their own publications, thereby bringing increased visibility to their work. We capture this experimentally derived knowledge in the form of Gene Ontology (GO) and Plant Ontology (PO) annotations, individually composed gene summaries and phenotype descriptions, and new links between articles and genes, which are added to TAIR on a weekly basis. Although our NIH funding to support our ontology annotation work has come to an end as of March 1 2017, we will continue annotating Arabidopsis gene function using GO terms and releasing the annotations to the GO consortium and on our website. Public releases of bulk data to GO and via the TAIR website will occur on a quarterly basis.

Between March 2016 and February 2017, we added 627 new gene symbols to TAIR and added or updated 696 new gene summaries. We also added 8890 new GO and PO annotations, generated by TAIR curators, TAIR community, UniProt and the GO consortium, to 4883 loci, incorporating experiment-based data from 1542 research articles. We linked 2572 articles to 3808 loci, and we added 243 new alleles and 213 new phenotypes to TAIR from the literature. Phenotype curation has focused primarily on adding value to the extensive library of Arabidopsis T-DNA insertion stocks by associating phenotypes and publications where available. To ensure that TAIR is up to date, we are completing integration of the Araport11 genome annotation into TAIR database and tools (i.e. GBrowse, SeqViewer, BLAST and bulk downloads).

### Subscriptions and Free Access

TAIR is financially supported by contributions from

individual researchers, academic institutions and consortia, companies and country-level subscriptions that together represent 29 countries. As of February 2017, subscribers included: 2 countries (China which renewed for another 3 year term, and Switzerland), 4 academic consortia, 189 academic institutions (list at <http://bit.ly/1RPlaue>), and approximately 479 individuals. Corporate subscribers include 8 major agricultural companies and 7 smaller companies.

From March 2016 to February 2017 we provided free teaching subscriptions for students in 53 courses. Of these, 39 courses were granted free access after August 2016 when we launched a campaign to publicize our complimentary access to academics using TAIR for coursework.

### Data Releases

In accordance with our data sharing policy, TAIR continued to publish quarterly data releases ([http://www.Arabidopsis.org/download/index-auto.jsp?dir=/download\\_files/Public\\_Data\\_Releases](http://www.Arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases)). There have been nine releases that have included all Gene Ontology and Plant Ontology annotations, gene symbols and names, links between genes and publications, and updated gene descriptions added to TAIR through 12/31/2015. Access to quarterly release files does not require a subscription and we do not impose any restrictions on reuse or redistribution of data contained in these year-old data releases. Subscribers have immediate access to all new information in TAIR through the website, which is updated on a weekly basis, and through quarterly releases of current data ([http://www.Arabidopsis.org/download/index-auto.jsp?dir=/download\\_files/Subscriber\\_Data\\_Releases](http://www.Arabidopsis.org/download/index-auto.jsp?dir=/download_files/Subscriber_Data_Releases)). Subscribers may also request custom data sets via our helpdesk ([curator@Arabidopsis.org](mailto:curator@Arabidopsis.org)).

### Conferences, Workshops, Social Media

TAIR staff manned exhibit booths at the following meetings: ICAR 2016 (Seoul, S. Korea), ASPB 2016 (Austin, TX), Biocuration 2016 (Geneva, CH) and PAG 2017 (San Diego, CA). TAIR curators will attend ICAR 2017 in St. Louis, MO and ASPB 2017 in Honolulu, HI to present our continuing efforts to provide up-to-date literature-based functional annotation and analysis tools, and solicit feedback from the community to inform future developments.

TAIR curators are also available to assist the community through our HelpDesk ([curator@Arabidopsis.org](mailto:curator@Arabidopsis.org)), and through social media on Facebook (<https://www.facebook.com/tairnews>), Twitter ([https://twitter.com/tair\\_news](https://twitter.com/tair_news)), and YouTube (<https://www.youtube.com/user/TAIRinfo>).

### Thanks to our supportive community

Once again we wish to express our gratitude to the worldwide Arabidopsis and plant research community.





## Plant Projects and Resources with Strong Participation of Arabidopsis Community

### Bio-Analytic Resource for Plant Biology (BAR)



Nicholas Provart (Director)  
<http://bar.utoronto.ca>

#### Activities

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

- \* 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser.
- \* 70,944 predicted protein-protein interactions plus 36,352 documented PPIs (rice interologs also available!).
- \* 29,180 predicted protein tertiary structures and 402 experimentally-determined structures.
- \* Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee’s site at 1001proteomes.masc-proteomics.org.
- \* Documented subcellular localizations for 9.3k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

#### News

The BAR server was upgraded in March 2017 to provide faster service. Work was completed on a final module for [Araport.org](http://Araport.org), ePlant (Waese *et al.*, 2017, in revision). ePlant is a zoomable user interface for exploring data across 12 orders of magnitude, from the kilometre scale down to the nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested, open source tool. ePlant is accessible from [Araport.org](http://Araport.org) and from the Bio-Analytic Resource at <http://bar.utoronto.ca/eplant>.

Two further papers describing useful Arabidopsis bioinformatic tools at the BAR were published by the in 2016 by Austin *et al.* and Waese *et al.* The first describes a new version of Expression Angler for identifying sets of coexpressed genes according to a user-defined pattern, and Cistome for exploring potential cis-regulatory elements in the promoters of such sets of genes. The

second, Gene Slider, allows easy exploration of conserved regions in 9 species of the Brassicaceae (Haudry *et al.*, 2013; doi: [10.1038/ng.2684](https://doi.org/10.1038/ng.2684)), with the ability to visualize whether known cis-elements occur in conserved regions of Arabidopsis promoters.

New Lateral Root Initiation data sets from the Gifford, Muday and Bennett groups were added to our eFP Browser, to the Lateral Root Initiation Data Source, along with stomatal lineage cell-type-specific expression profiling data from the Bergmann Lab at Stanford. For RNA-seq data, we released our “eFP-Seq Browser” for exploring 113 RNA-seq data sets used to reannotate the Arabidopsis genome for the Araport11 release. [http://bar.utoronto.ca/~dev/eFP-Seq\\_Browser/](http://bar.utoronto.ca/~dev/eFP-Seq_Browser/).

For translational researchers, we’ve added a couple of other new eFP Browser views: a Developmental Map for Brachypodium distachyon from Marek Mutwil and colleagues ([http://bar.utoronto.ca/efp\\_brachypodium/](http://bar.utoronto.ca/efp_brachypodium/)), and a Maize Root view, part of the Maize eFP Browser, from Stefan Hey and colleagues ([http://bar.utoronto.ca/efp\\_maize/cgi-bin/efpWeb.cgi](http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi)). Check out an eFP Browser for peanut (Arachis hypogaea), put together by Josh Clevenger from Peggy Ozias-Akins’ lab at UGA, too!

#### BAR Publications

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- Waese J, Pasha A, Wang TT, van Weringh A, Guttman DS, Provart NJ (2016) Gene Slider: sequence logo interactive data-visualization for education and research. Bioinformatics 32: 3670-3672. doi: [10.1093/bioinformatics/btw525](https://doi.org/10.1093/bioinformatics/btw525).
- Waese J, Fan J, Pasha A, Yu H, Fucile G, Shi R, Kelley L, Sternberg M, Krishnakumar V, Ferlanti E, Miller J, Town C, Stuerzlinger W, Provart NJ (in revision) ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology.

#### Conferences, Workshops, Social Media

The BAR participated in the International Plant Growth Substances Association (IPGSA) Conference in Toronto in 2016; the 2016 American Society of Plant Biology (ASPB) Plant Biology conference in Austin, Texas, as part of the Plant Genome Resource Outreach booth; and Plant and Animal Genomes (PAG) XXV in San Diego, California.

#### Additional Information

A book chapter and a mini-review describing BAR tools came out in 2016, both by Jamie Waese and Nicholas Provart, one in a Methods in Molecular Biology volume on Plant Genomics Databases ([http://dx.doi.org/10.1007/978-1-4939-6658-5\\_6](http://dx.doi.org/10.1007/978-1-4939-6658-5_6)) and the other in Current Plant Biology (<http://dx.doi.org/10.1016/j.cpb.2016.12.001>).

## Gramene: A comparative genomics and pathways resource for plants

Marcela Karey Tello-Ruiz (Project Manager)  
 Doreen Ware (PI)  
<http://www.gramene.org>



#### Activities

The Gramene database is an integrated resource for comparative genome and functional analysis in plants. The database provides the Arabidopsis community, agricultural researchers, and plant breeders access to reference genomes, comparative resources including whole-genome DNA alignment (WGA) and protein-based gene trees, curated and projected gene pathways for 44 crops and model species including Arabidopsis, A. lyrata, Brassicas, sugar beet, Solanaceae, cereals, and fruits, and pathways for 67 plant species, thus enabling powerful cross-species comparisons.

The Gramene project has had four data releases since January 2016. Of significance for the Arabidopsis community are three new dicot genomes: Brassica napus (oilseed rape), sugar beet, and red clover, as well as two red algae genomes. We also released significant updates to two major crops, two maize (RefGen\_V4) and bread wheat (TGACv1) genome assemblies. In addition, since November 2016, we adopted the AraPort11 gene model annotation for *A. thaliana*. Our phylogenetic gene trees classifying orthologous and paralogous relationships, provide evolutionary history and insights into speciation and duplication events. These gene trees provide the basis that informs synteny maps, which enable inter-species browsing across ancestral regions. In addition to the protein-based gene trees, our WGA mappings provide a valuable resource to characterize non-coding conservation. The analyses for multiple species can be viewed simultaneously with links showing homologous genes and WGA mappings. Our existing WGA collection was built against *A. thaliana* (dicot model crop; 26 alignments) and *Oryza sativa Japonica* (monocot staple food crop; 36 alignments). Our synteny collection includes synteny maps for *A. thaliana* against four species: *A. lyrata*, *O. sativa japonica*, poplar and grape. SNP and structural diversity data, including individual genotypes, are available for *A. thaliana*, and another 11 species. The SNPs are displayed in the context of gene annotation and protein domain structure, along with predicted functional consequences (e.g. missense variant).

Gramene hosts several of the Arabidopsis community variation resources including: 1,179 strains from the 2012 study by Horton and collaborators using the Affymetrix 250k Arabidopsis SNP chip, and an updated data set produced through a BBSRC funded multi-institutional

collaboration involving resequencing 18 Arabidopsis lines published by Clark *et al* in 2007, and 392 strains from the 1001 Genomes Project (80 strains from the Cao pilot study; 132 strains from a study by the Salk Institute; and 180 strains from a study by the Nordborg group at GMI). Phenotype data from a GWAS study of 107 phenotypes in 95 inbred lines carried out by Atwell *et al* (2010) is also available. Under the Fort Lauderdale agreement, the 1001 Arabidopsis Genomes project freely released data from the Salk Institute, WTCHG, MPI, and GMI in a pre-publication format. During the past year, we added new rice variants (*O. sativa Japonica* and *O. glumaepatula*) as well as EMS-derived mutation data for sorghum.

In collaboration with the Expression Atlas project (EMBL-EBI), we are now providing experimental baseline gene expression data for 14 plant species including Arabidopsis, through our Ensembl genome browser and Plant Reactome pathways interfaces. In addition, we provide direct links to differential gene expression from 493 experiments in *A. thaliana* as well as from another 15 species on the Atlas website. Through Gramene’s Plant Reactome, we continue to offer ~240 curated rice pathways, as well as orthology-based pathway projections to 66 plant species including both, *A. thaliana* and *A. lyrata*.

In the past year, our integrated search database and modern user interface (<http://search.gramene.org>) were greatly enhanced to leverage the diverse annotations above described to facilitate finding genes through selecting auto-suggested filters with interactive views of the results. We now offer detailed views for search results featuring genomic location, gene trees and homologs lists, gene expression, and cross-references, while a pathways view is in development. Our Blast and BioMart interfaces enable complex queries of sequence, annotation, homology, and variation data. The genomes portal of the Gramene project is developed on the Ensembl infrastructure and in collaboration with the Ensembl Genomes project (EMBL-EBI). The pathways portal of the project is the Plant Reactome (<http://plantreactome.gramene.org>). The project supports application programming interfaces to access the data, in addition to the graphical users interface, which support visual displays, and download of the data in standardized formats for the genome and pathway data, as well as as high-resolution, publication-ready, image files.

As we aim to reach out to a larger audience, we continue our monthly webinar series and invite the [arab-gen@net.bio.net](mailto:arab-gen@net.bio.net) mailing list whenever topics most relevant to the Arabidopsis community are covered. Recorded webinars are available for public view from Gramene’s YouTube channel.

#### Conferences and Workshops

During 2016, Gramene staff attended 3 international and 7 domestic conferences with a total of 13 oral presentations and 8 posters. Project workshops with

live demos were presented at the Plant & Animal Genome (PAG), Maize Genetic Conference, and CSHL Cereal Genomics Course. At the PAG conferences, we co-sponsored a community outreach booth with the participation of bioinformatics resources including Arabidopsis resources like BAR & NASC.

At Oregon State University, we held a Summer Camp for High school students and K-12 educators, and at Cold Spring Harbor Laboratory, we organized educational events with local K-6 students and faculty to celebrate Plants Fascination Day. The project published 7 peer-reviewed articles and 5 book chapters. Delivered eight monthly webinars between February 2016 & February 2017, that are available on the Gramene YouTube channel. We continue to foster ~55 international collaborations. Between CSHL & OSU, we trained five post-doctorates, two graduate students, two undergraduate students (one as part of CSHL's Undergraduate Research Program), one high-school student & one visiting scholar from Huazhong Agricultural University in China.

**Gramene Publications 2016**

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 - Tello-Ruiz MK, Stein J, Wei S, Preece J, Olson A, Naithani S, Amarasinghe V, Dharmawardhana P, Jiao Y, Mulvaney J, Kumari S, Chougule K, Elser J, Wang B, Thomason J, Bolser DM, Kerhornou A, Walts B, Fonseca NA, Huerta L, Keays M, Tang YA, Parkinson H, Fabregat A, McKay S, Weiser J, D'Eustachio P, Stein L, Petryszak R, Kersey PJ, Jaiswal P, Ware D. (2016) Gramene: comparative plant genomics and pathway resources. *Nucleic Acids Res*. 2016 Jan 4;44(D1):D1133-40. doi: 10.1093/nar/gkv1179.  
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**Gramene Books**  
 - Jaiswal P, Usadel B (2016). Plant Pathway databases. *Plant Bioinformatics: Methods in Molecular Biology* 2nd. David Edwards. Humana Press. doi: 10.1007/978-1-4939-3. ISBN: 978-1-4939-3167-5. PMID: 26519401  
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 - Naithani S, Nonogaki H, Jaiswal P (2016). Exploring crossroads between seed development and stress-response. *Mechanism of Plant Hormone Signaling under Stress* 1st. Girdhar K. Pandey. Wiley.  
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# Arabidopsis Basic and Translational Research

## Research Outlook 2016/17

Arabidopsis continues to be the most commonly mentioned plant in the publications listed on NCBI Pubmed (Figure 3). The overall number of papers has plateaued over the past three years but after a small decrease in 2015, these numbers rose again in 2016. Whilst the number of papers that include rice/oryza or corn/maize continue to rise we feel that it is fair to conclude that Arabidopsis remains the most popular organism for global plant science research.

Maintaining the numbers of published Arabidopsis research papers is supported by a continued rise in outputs from China. Although it is gratifying to observe that the overall number of Arabidopsis outputs from 'Western' countries remains largely consistent, it is Chinese labs that are continuing to see a significant increase in outputs. As stated in the Country Report from China (page 55), funding levels for Arabidopsis research remains strong so we can expect to see a continued rise in these outputs over the coming years.

There is little doubt that basic research into fundamental biological questions will underpin the agricultural development that is necessary in efforts to support global food security. This is arguably most clearly demonstrated

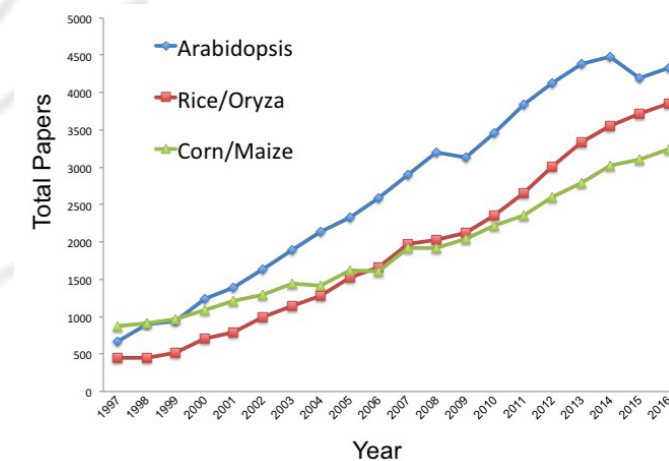


Figure 3. Papers published globally with Arabidopsis, rice/oryza or corn/maize in the Title/Abstract.

in the identification of genes that play a role a plants response to a changing environment or in the interaction with novel pathogens.

It is challenging to track how discoveries in Arabidopsis directly relate to research conducted using other organisms. Figure 5 shows the number of publications that contain keywords 'Arabidopsis' and/or 'rice/oryza' or 'corn/maize' and shows that the number of papers has not increased over the past few years.

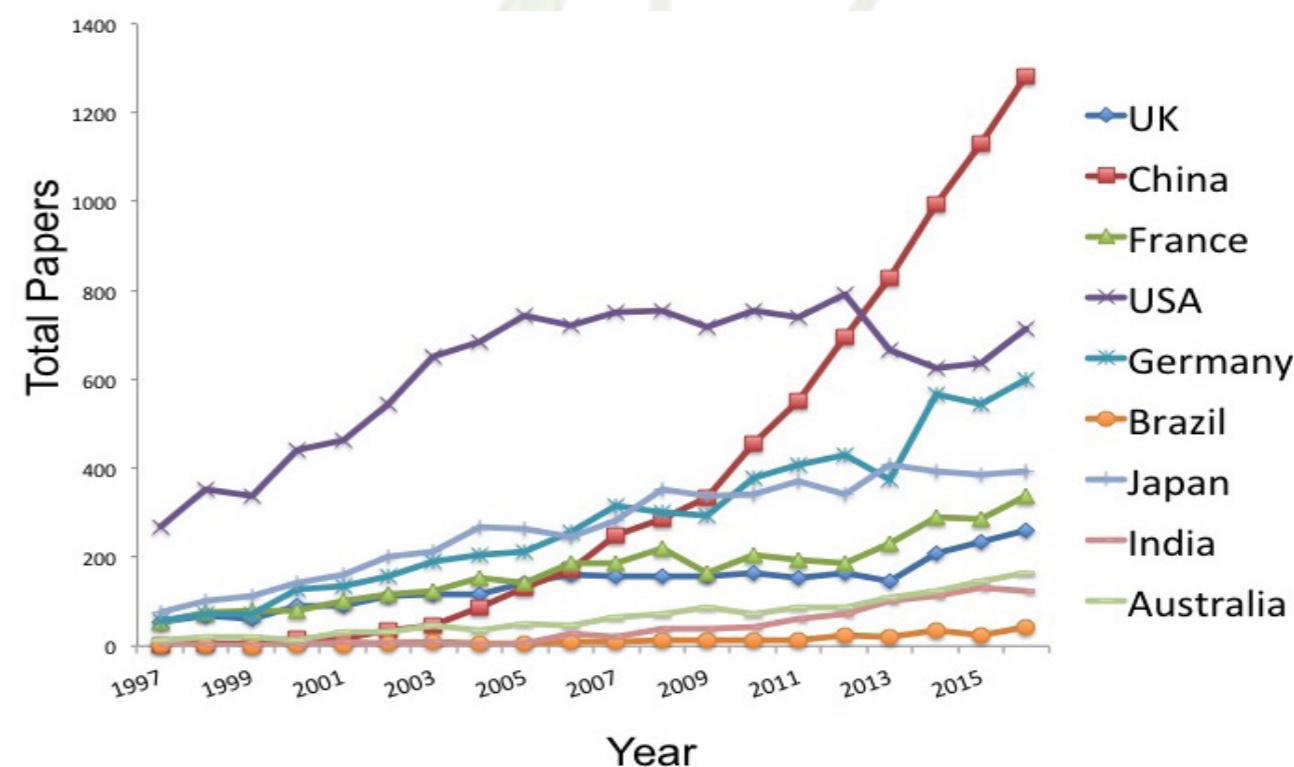
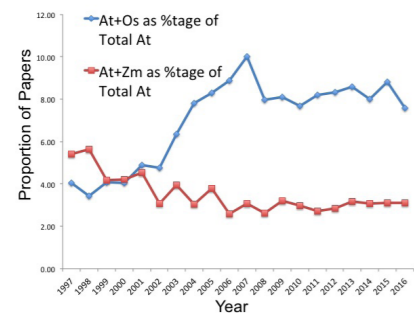


Figure 4. The number of Arabidopsis papers published in selected countries over the past twenty years

However this might not be the best mechanism of measuring 'translation' as it is more likely that researchers will take information from Arabidopsis and then use it in subsequent research without concurrently conducting publishable research from two or more organisms.

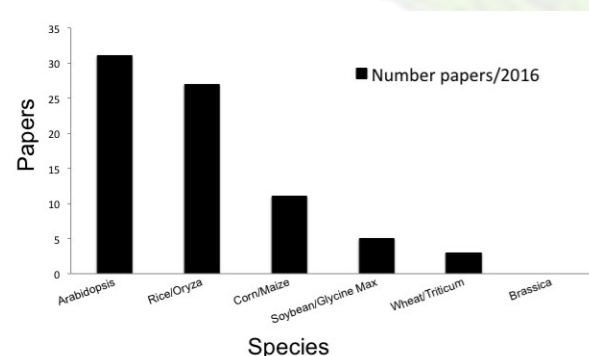


**Figure 5.** Proportion of papers featuring Arabidopsis (At) and Rice (Os) or Maize (Zm) as a proportion of total Arabidopsis papers.

As outlined the 2015 Tansley Review entitled '50 years of Arabidopsis research: highlights and future directions', many research 'firsts' in plant science have been discovered using Arabidopsis as a model organism. However measuring how this information is directly translated to other organisms is less straightforward.

One mechanism to measure that Arabidopsis remains relevant for work in crop species is to assess the amount of research that is occurring that has great potential for future crop improvement. It has clear that genome and gene-editing represents game-changing technology for the precise alteration of plant growth in response to changing environmental conditions. Arguably the most promising of these technologies involves CRISPR-Cas9 gene-editing. We looked at the number of papers published in 2016 that feature the terms 'CRISPR' and 'Cas9' alongside a range of plant species. Although Figure 6 shows that there aren't an large number of papers on this topic, Arabidopsis remains the most commonly used organism.

This small example highlights the continued importance of Arabidopsis as a model for the development of experimental techniques that have broad relevance for other plant species. In this example the development of CRISPR-Cas9 in Arabidopsis will allow the more facile transfer of this technology into crop species, ready to face the challenges of food insecurity, population growth and adaptations to climate change.



**Figure 6.** Number of 2016 papers featuring 'CRISPR' or 'Cas9' with different plant species

## Research Highlights

Over the coming pages we feature a selection of outstanding Arabidopsis work that has been conducted by the global community of researchers. These manuscripts include those that reveal fundamentally important discoveries that have altered our understanding of plant growth as well as those that demonstrate the power of Arabidopsis as a starting point for translational research.

Importantly each of these papers are **Open Access**.

The phytohormone auxin plays a fundamental role in the control of plant development and over the past decade the mechanism of auxin signaling has been well elucidated. However work from Simonini *et al* (2016) has characterised a novel mechanism of auxin signaling that is separate from the canonical TIR1/AFB-Aux/IAA interaction. In this new method the ARF3/ETTIN module directly responds to the auxin signal through interactions with different transcription factors.

Light is perhaps the most important external cue that controls growth and plants have the ability to differentially respond to different wavelengths of light. Pedmale *et al* (2016) have determined the mechanisms by which plants perceive reduced levels of blue light such that might occur under a canopy. They show that blue-light sensing cryptochrome proteins interact with two bHLH transcription factors, PIF4 and PIF5, in a response that is distinct from their involvement during the response to red/far red light.

The power of Arabidopsis genomic research is highlighted by a manuscript from The 1001 Genomes Consortium (2016). In this paper they present a detailed map of variation in over 1100 fully resequenced accessions.

A genome-wide study from Stuart *et al* (2016) identifies an increasingly important role for transposons in the control of gene expression and epigenetic regulation.

Senkler *et al* (2016) perform a proteomic analysis of the protein complexes that reside within Arabidopsis mitochondria, identifying several components not previously known in plants.

Adam *et al* (2016) show that Arabidopsis can be used as a model for studying potential future phytoaccumulation strategies. They performed a chemical biology screen to identify compounds that function in plants to sequester caesium.

CRISPR-Cas9 will be key technology in future attempts to genetically modify both model organisms and crop plants. Ryder *et al* (2017) demonstrate that this technology can be used in Arabidopsis to create null mutants even in tetraploid plants.

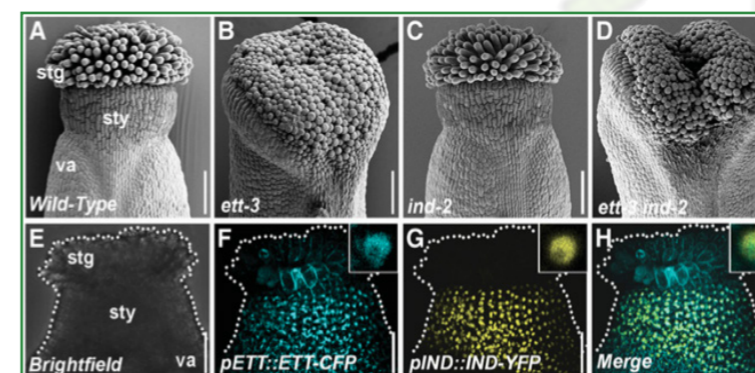
Automated phenotyping platforms will be key in the development of novel crop varieties. Toward that end Arend *et al* (2017) have produced an experimental workflow that measures a range of growth parameters in Arabidopsis.

Finally Groen *et al* (2016) show Arabidopsis can be used in unusual experiments that have translational relevance, in their case looking at the effect of viral infection on the production of insect-attracting volatiles.

## A noncanonical auxin-sensing mechanism is required for organ morphogenesis in Arabidopsis.

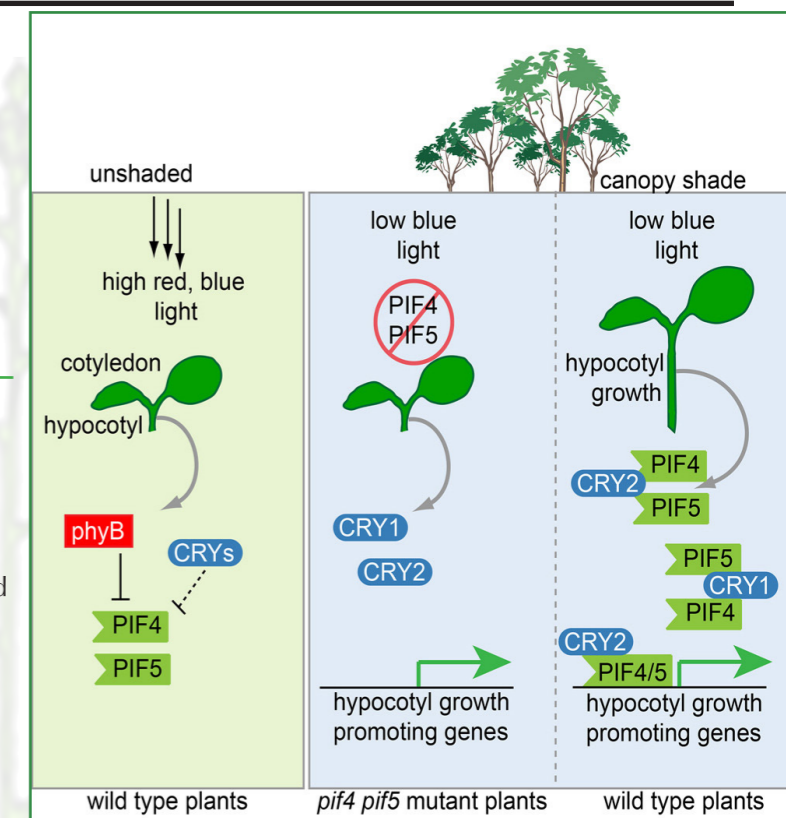
Simonini S, Deb J, Moubayidin L, Stephenson P, Valluru M, Freire-Rios A, Sorefan K, Weijers D, Friml J, Østergaard L (2016) *Genes Dev.* 30(20):2286-2296 <http://dx.doi.org/10.1101/gad.285361.116>

Tissue patterning in multicellular organisms is the output of precise spatio-temporal regulation of gene expression coupled with changes in hormone dynamics. In plants, the hormone auxin regulates growth and development at every stage of a plant's life cycle. Auxin signaling occurs through binding of the auxin molecule to a TIR1/AFB F-box ubiquitin ligase, allowing interaction with Aux/IAA transcriptional repressor proteins. These are subsequently ubiquitinated and degraded via the 26S proteasome, leading to derepression of auxin response factors (ARFs). How auxin is able to elicit such a diverse range of developmental responses through a single signaling module has not yet been resolved.



**Figure 7.** ETT and IND genetically interact to regulate gynoecium development. <http://dx.doi.org/10.1101/gad.285361.116>

This paper presents an alternative auxin-sensing mechanism in which the ARF ARF3/ETTIN controls gene expression through interactions with process-specific transcription factors. This noncanonical hormone-sensing mechanism exhibits strong preference for the naturally occurring auxin indole 3-acetic acid (IAA) and is important for coordinating growth and patterning in diverse developmental contexts such as gynoecium morphogenesis, lateral root emergence, ovule development, and primary branch formation. Disrupting



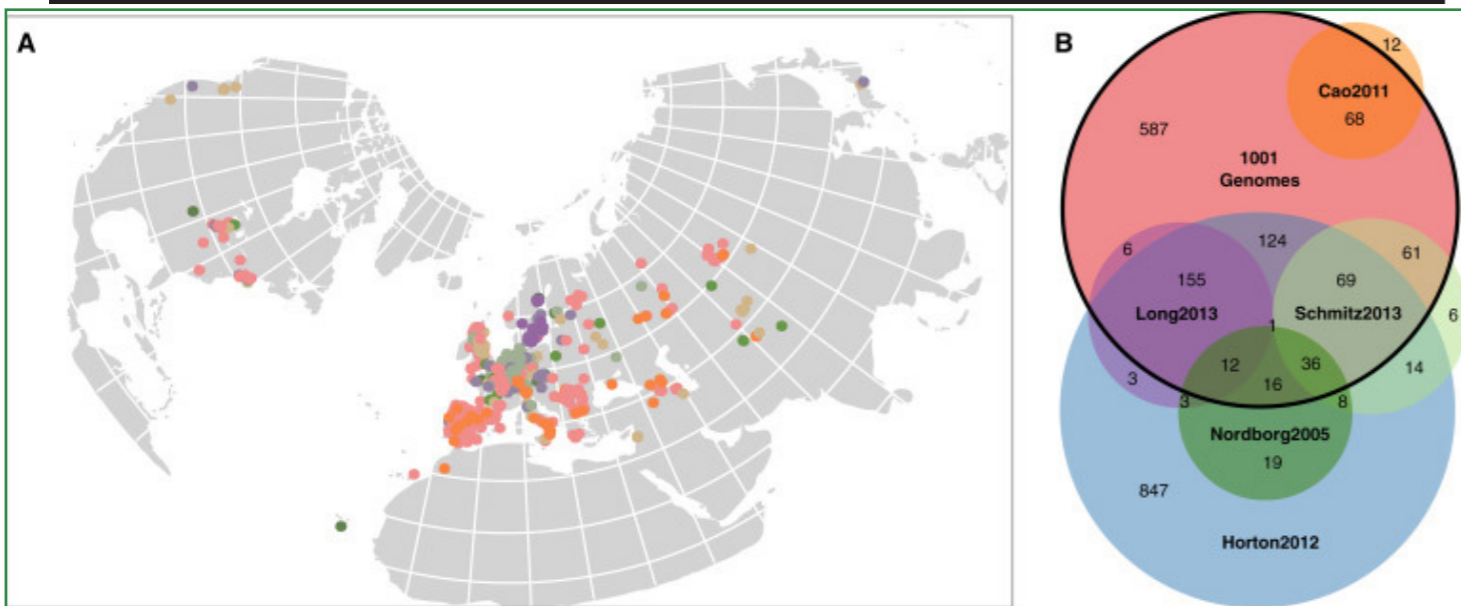
**Figure 8.** Model describing the plant response to blue light <http://dx.doi.org/10.1016/j.cell.2015.12.018>

this IAA-sensing ability induces morphological aberrations with consequences for plant fitness. Therefore, these findings introduce a novel transcription factor-based mechanism of hormone perception in plants.

## Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light.

Pedmale UV, Huang SSC, Zander M, Cole BJ, Hetzel J, Ljung K, Reis PAB, Sridevi P, Nito K, Nery JR, Ecker JR, Chory J (2016) *Cell* 164: 233-245.

Sun-loving plants have the ability to detect and avoid shading through sensing of both blue and red light wavelengths. Higher plant cryptochromes (CRYs) control how plants modulate growth in response to changes in blue light. For growth under a canopy, where blue light is diminished, CRY1 and CRY2 perceive this change and respond by directly contacting two bHLH transcription factors, PIF4 and PIF5. These factors are also known to be controlled by phytochromes, the red/far-red photoreceptors; however, transcriptome analyses indicate that the gene regulatory programs induced by the different light wavelengths are distinct. Our results indicate that CRYs signal by modulating PIF activity genome wide and that these factors integrate binding of different plant photoreceptors to facilitate growth changes under different light conditions.



**Figure 9.** Origins of the 1001 Genomes Accessions  
<http://dx.doi.org/10.1016/j.cell.2016.05.063>

**Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis**

The 1001 Genomes Consortium (2016) 1,135 Cell  
<http://dx.doi.org/10.1016/j.cell.2016.05.063>

Arabidopsis serves as a model organism for the study of fundamental physiological, cellular, and molecular processes. It has also greatly advanced our understanding of intraspecific genome variation. This paper presents a detailed map of variation in 1,135 high-quality re-sequenced natural inbred lines representing the native Eurasian and North African range and recently colonized North America.

The authors identify relict populations that continue to inhabit ancestral habitats, primarily in the Iberian Peninsula. They have mixed with a lineage that has spread to northern latitudes from an unknown glacial refugium and is now found in a much broader spectrum of habitats.

Insights into the history of the species and the fine-scale distribution of genetic diversity provide the basis for full exploitation of *A. thaliana* natural variation through integration of genomes and epigenomes with molecular and non-molecular phenotypes.

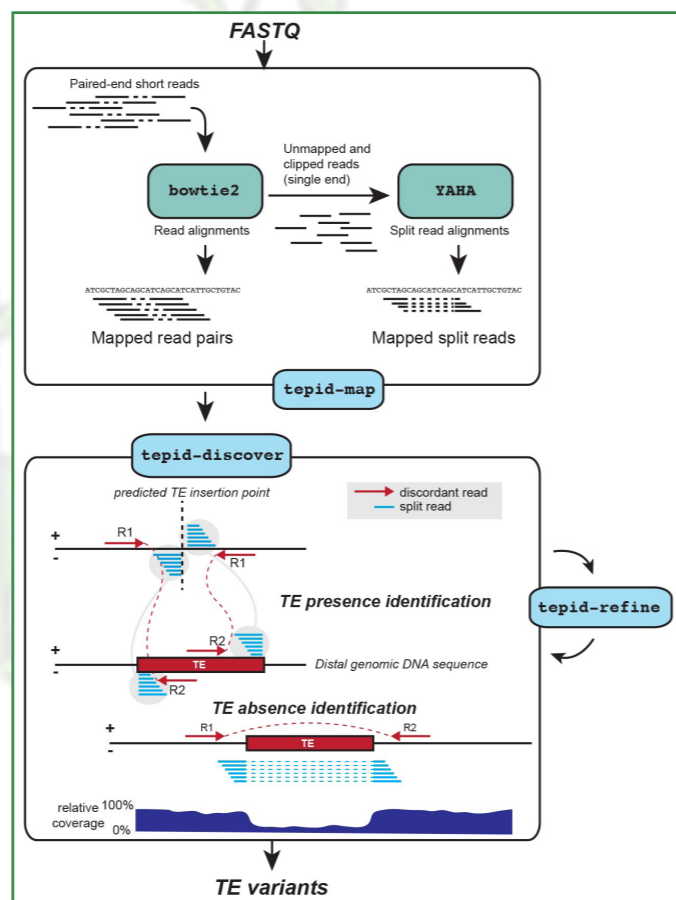
**Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation.**

Stuart T, Eichten SR, Cahn J, Karpievitch YV, Borevitz JO, Lister R (2016) Elife.  
<http://dx.doi.org/10.7554/eLife.20777>

Variation in the presence or absence of transposable elements (TEs) is a major source of genetic variation between individuals. This paper identified 23,095 TE presence/absence variants between 216 Arabidopsis

accessions. Most TE variants were rare, and we find these rare variants associated with local extremes of gene expression and DNA methylation levels within the population. Of the common alleles identified, two thirds were not in linkage disequilibrium with nearby SNPs, implicating these variants as a source of novel genetic diversity.

Many common TE variants were associated with significantly altered expression of nearby genes, and a major fraction of inter-accession DNA methylation



**Figure 10.** TE variant discovery pipeline from  
<http://dx.doi.org/10.7554/eLife.20777>

differences were associated with nearby TE insertions. Overall, this demonstrates that TE variants are a rich source of genetic diversity that likely plays an important role in facilitating epigenomic and transcriptional differences between individuals, and indicates a strong genetic basis for epigenetic variation.

**The Mitochondrial Complexome of Arabidopsis**

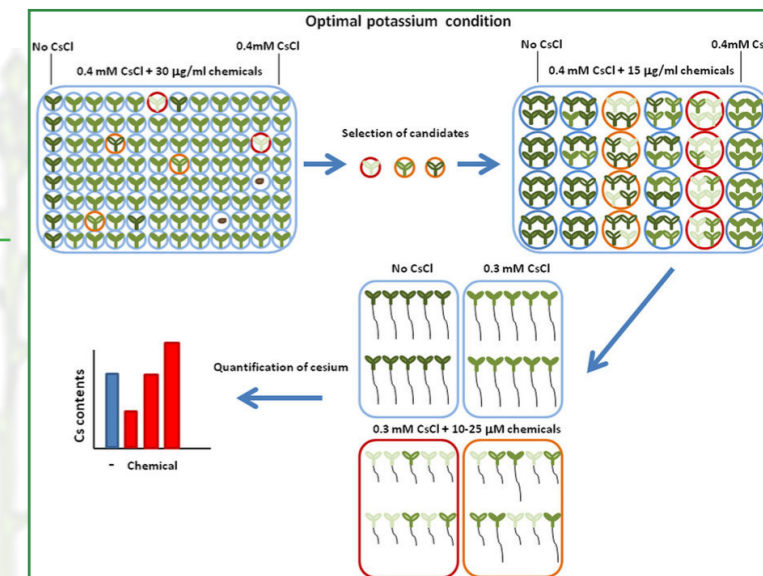
Senkler J, Senkler M, Eubel H, Hildebrandt T, Lengwenus C, Schertl P, Schwarzlander M, Wagner S, Wittig I, Braun HP (2017) Plant J 89: 1079-1092  
<http://dx.doi.org/10.1111/tpj.13448>

Mitochondria are central to cellular metabolism and energy conversion. In plants they also enable photosynthesis through additional components and functional flexibility. A majority of those processes relies on the assembly of individual proteins to larger protein complexes, some of which operate as large molecular machines. There has been a strong interest in the makeup and function of mitochondrial protein complexes and protein-protein interactions in plants, but the experimental approaches used typically suffer from selectivity or bias. Here, we present a complexome profiling analysis for leaf mitochondria of the model plant Arabidopsis for the systematic characterization of protein assemblies. Purified organelle extracts were separated by 1D Blue native (BN) PAGE, a resulting gel lane was dissected into 70 slices (complexome fractions) and proteins in each slice were identified by label free quantitative shotgun proteomics. Overall, 1359 unique proteins were identified, which were, on average, present in 17 complexome fractions each. Quantitative profiles of proteins along the BN gel lane were aligned by similarity, allowing us to visualize protein assemblies. The data allow re-annotating the subunit compositions of OXPHOS complexes, identifying assembly intermediates of OXPHOS complexes and assemblies of alternative respiratory oxidoreductases. Several protein complexes were discovered that have not yet been reported in plants, such as a 530 kDa Tat complex, 460 and 1000 kDa SAM complexes, a calcium ion uniporter complex (150 kDa) and several PPR protein complexes. We have set up a tailored online resource ([https://complexomemap.de/at\\_mito\\_leaves](https://complexomemap.de/at_mito_leaves)) to deposit the data and to allow straightforward access and custom data analyses.

**A Novel Role for Methyl Cysteinate, a Cysteine Derivative, in Cesium Accumulation in Arabidopsis.**

Adams E, Miyazaki T, Hayaishi-Satoh A, Han M, Kusano M, Khandelja H, Saito K & Shin R. (2017) Scientific Reports 7 doi: [10.1038/srep43170c](https://doi.org/10.1038/srep43170c)

Phytoaccumulation is a technique to extract metals from soil utilising ability of plants. Cesium is a valuable metal



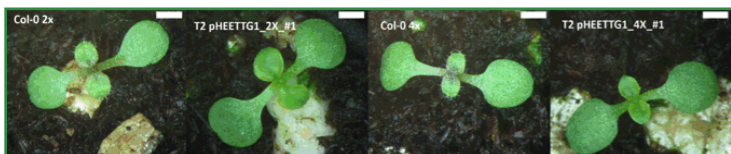
**Figure 11.** Schematic representation of chemical library screening.  
<http://dx.doi.org/10.1038/srep43170>

while radioactive isotopes of cesium can be hazardous. In order to establish a more efficient phytoaccumulation system, small molecules which promote plants to accumulate cesium were investigated. Through chemical library screening, 14 chemicals were isolated as ‘cesium accumulators’ in Arabidopsis. Of those, methyl cysteinate, a derivative of cysteine, was found to function within the plant to accumulate externally supplemented cesium. Moreover, metabolite profiling demonstrated that cesium treatment increased cysteine levels in Arabidopsis. The cesium accumulation effect was not observed for other cysteine derivatives or amino acids on the cysteine metabolic pathway tested. Our results suggest that methyl cysteinate, potentially metabolised from cysteine, binds with cesium on the surface of the roots or inside plant cells and improve phytoaccumulation.

**Generation of stable nulliplex autopolyploid lines of Arabidopsis using CRISPR/Cas9 genome editing.**

Ryder P, McHale M, Fort A, Spillane C (2017) Plant Cell Rep. doi: [10.1007/s00299-017-2125-0](https://doi.org/10.1007/s00299-017-2125-0)

RNA-guided endonuclease-mediated targeted mutagenesis using the clustered regularly interspersed short palindromic repeats (CRISPR)/Cas9 system has been successful at targeting specific loci for modification in plants. While polyploidy is an evolutionary mechanism enabling plant adaptation, the analysis of gene function in polyploid plants has been limited due to challenges associated with generating polyploid knockout mutants for all gene copies in polyploid plant lines. This study investigates whether CRISPR/Cas9 mediated targeted mutagenesis can generate nulliplex tetraploid mutant lines in Arabidopsis, while also comparing the relative efficiency of targeted mutagenesis in tetraploid (4x) versus diploid (2x) backgrounds. Using CRISPR/Cas9 genome editing to generate knockout alleles of the TTG1 gene,

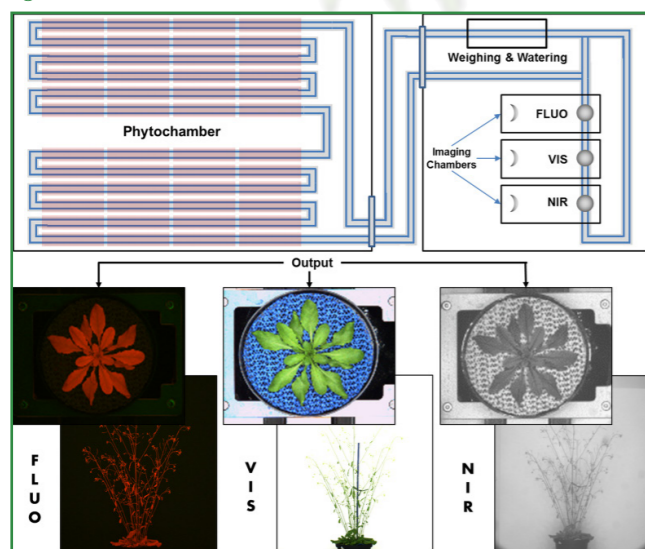


**Figure 12.** CRISPR-Cas9 gene-edited diploid and tetraploid seedlings. <http://dx.doi.org/10.1007/s00299-017-2125-0>

we demonstrate that homozygous nulliplex mutants can be directly generated in tetraploid Arabidopsis plants. CRISPR/Cas9 genome editing now provides a route to more efficient generation of polyploid mutants for improving understanding of genome dosage effects in plants.

### Quantitative monitoring of Arabidopsis growth and development using high-throughput plant phenotyping.

Arend D, Lange M, Pape J-M, Weigelt-Fischer K, Arana-Ceballos F, Mücke I, Klukas C, Altmann T, Scholz U, Junker A (2016) Scientific Data 3, 160055. [dx.doi.org/10.1038/sdata.2016.55](https://doi.org/10.1038/sdata.2016.55)



**Figure 13.** Automated phenotyping platform for Arabidopsis <http://dx.doi.org/10.1038/sdata.2016.55>

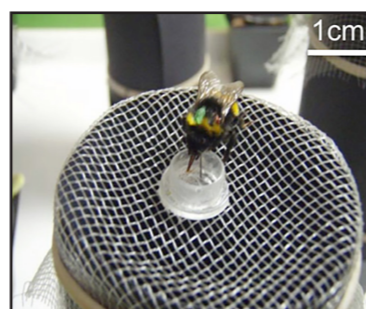
With the implementation of novel automated, high throughput methods and facilities in the last years, plant phenomics has developed into a highly interdisciplinary research domain integrating biology, engineering and bioinformatics. This paper presents a dataset of a non-invasive high throughput plant phenotyping experiment, which uses image- and image analysis- based approaches to monitor the growth and development of 484 Arabidopsis plants. The result is a comprehensive dataset of images and extracted phenotypical features. Such datasets require detailed documentation, standardized description of experimental metadata as well as sustainable data storage and publication in order to ensure the reproducibility of experiments, data reuse and comparability among the scientific community. Therefore the here presented dataset has been annotated using the standardized ISA-Tab format and considering the recently

published recommendations for the semantical description of plant phenotyping experiments.

### Virus Infection of Plants Alters Pollinator Preference: A Payback for Susceptible Hosts?

Groen SC, Jiang S, Murphy AM, Cunniffe NJ, Westwood JH, Davey MP, Bruce TJ, Caulfield JC, Furzer OJ, Reed A, Robinson SI, Miller E, Davis CN, Pickett JA, Whitney HM, Glover BJ, Carr JP (2016) PLoS Pathog. 12(8):e1005790

Plant volatiles play important roles in attraction of certain pollinators and in host location by herbivorous insects. Virus infection induces changes in plant volatile emission profiles, and this can make plants more attractive to insect herbivores, such as aphids, that act as viral vectors. However, it is unknown if virus-induced alterations in volatile production affect plant-pollinator interactions. We found that volatiles emitted by cucumber mosaic virus (CMV)-infected tomato (*Solanum lycopersicum*) and Arabidopsis plants altered the foraging behaviour of bumblebees (*Bombus terrestris*). Virus-induced quantitative and qualitative changes in blends of volatile organic compounds emitted by tomato plants were identified by gas chromatography-coupled mass spectrometry. Experiments with a CMV mutant unable to express the 2b RNA silencing suppressor protein and with Arabidopsis silencing mutants implicate microRNAs in regulating emission of pollinator-perceivable volatiles. In tomato, CMV infection made plants emit volatiles attractive to bumblebees.



**Figure 14.** Experimental bumblebee! <https://doi.org/10.1371/journal.ppat.1005790>

Bumblebees pollinate tomato by ‘buzzing’ (sonicating) the flowers, which releases pollen and enhances self-fertilization and seed production as well as pollen export. Without buzz-pollination, CMV infection decreased seed yield, but when flowers of mock-inoculated and CMV-infected plants were buzz-pollinated, the increased seed yield for CMV-infected plants was similar to that for mock-inoculated plants. Increased pollinator preference can potentially increase plant reproductive success in two ways: i) as female parents, by increasing the probability that ovules are fertilized; ii) as male parents, by increasing pollen export. Mathematical modeling suggested that over a wide range of conditions in the wild, these increases to the number of offspring of infected susceptible plants resulting from increased pollinator preference could outweigh underlying strong selection pressures favoring pathogen resistance, allowing genes for disease susceptibility to persist in plant populations. We speculate that enhanced pollinator service for infected individuals in wild plant populations might provide mutual benefits to the virus and its susceptible hosts.

# Country Reports of the International Arabidopsis Community

## Country Highlights

### Argentina

> Legris *et al* (2016): Phytochrome B acts as a thermoreceptor in addition to its well established role as a photoreceptor. Legris M, Klose C, Burgie ES, Rojas CC, Neme M, Hiltbrunner A, Wigge PA, Schäfer E, Vierstra RD, Casal JJ. Phytochrome B integrates light and temperature signals in Arabidopsis. Science. 2016 Nov 18;354(6314):897-900.

### Australia

> In 2015 and 2016 Ian David Small and Geoff Fincher become Fellows of the Australian Academy of Science. Several Australian researchers working with Arabidopsis were listed in the Thomson Reuters High Cited Researcher for 2016: James Whelan, Steven Smith, Harvey Millar, Ian Small, Christine Beveridge, Steffan Persson, John Manners, Kemal Kazan, and Peter Dodds.  
> The ARC Centre of Excellence, Plant Energy Biology received \$26 million from the Australian Research Council and \$14 million from partner universities and companies to fund the Centre until 2020.

### Austria

> Magnus Nordberg (Gregor Mendel Institute, Vienna) as co-corresponding author for the 1001 genomes manuscript that investigated global Arabidopsis Natural Variation. The 1001 Genomes Consortium (2016) **1,135** Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis. Cell 166(2):481-91.  
> Nine holders of current ERC Starting and Consolidator grants

### Belgium

> New ERC Starting and Consolidator Grants obtained by Bert De Rybel for work on vascular development in Arabidopsis embryos and roots (2017-2022) and Daniel Van Damme for work on cell division control in Arabidopsis roots (2016- 2021).

### Canada

> Nicolas Provart (University of Toronto) continues to develop outstanding tools for visualisation of gene expression with the BAR resource. <http://bar.utoronto.ca/>

### Chile

> The Chilean Society for Plant Biologists was founded. Rodrigo A. Gutiérrez is the first elected president.  
> Our Chilean Society for Plant Biologist is part of The Global Plant Council coalition being represented by Ariel Orellana.

### China

> Yao *et al.* (2016) A non-canonical hormone receptor for strigolactone. Nature. 536, 469–473  
doi: [10.1038/nature19073](https://doi.org/10.1038/nature19073)  
> Cui *et al.* (2016) REF6 recognizes a specific DNA sequence to demethylate H3K27me3. Nature Genetics. 8(6):694-9. doi: [10.1038/ng.3556](https://doi.org/10.1038/ng.3556)

### Czech Republic

> EPSO plant biology meeting “Plant Biology Europe EPSO/FESPB 2016 Congress” was organized by the Czech plant researchers (lead by prof. Jana Albrechtova) in Prague between June 26-30 2016. <http://europlantbiology-2016.webnode.cz/>

### Denmark

> Olsen LI, Hansen TH, Larue C, Østerberg JT, Hoffmann RD, Liesche J, Krämer U, Surblé S, Cadarsi S, Samson VA, Grolimund D, Husted S, Palmgren M (2016) Mother-plant-mediated pumping of zinc into the developing seed. Nature Plants 2(5):16036. doi: [10.1038/nplants.2016.36](https://doi.org/10.1038/nplants.2016.36)

### Finland

> Plant Biology Scandinavia 2017 will be held in Naantali, Finland from August 15-18 2017.  
> Finland will host the 29<sup>th</sup> ICAR from June 25-29 2018 in Turku and is organized by researchers from the Universities of Helsinki, Turku and Oulu

### France

> Continued development of outstanding shared resources at Saclay Plant Sciences Centre: [http://www6.inra.fr/saclay-plant-sciences\\_eng/Infrastructures](http://www6.inra.fr/saclay-plant-sciences_eng/Infrastructures)

### Germany

> Newly designed and updated AFGN website is online at <http://www.dbg-afgn.de/>.  
> Detlef Weigel as co-corresponding author for The 1001 Genomes Consortium. The 1001 Genomes Consortium (2016) **1,135** Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis. Cell 166(2):481-91.

**India**

> Prof Utpal Nath's lab at IISc, Bengaluru has shown that miR319-regulated transcription factor TCP4, directly activate YUCCA5 transcription and connects the auxin response to a brassinosteroid-dependent process that promotes hypocotyl elongation in Arabidopsis.  
 > Prof. Sudip Chattopadhyay's group confirmed the model that At Calmodulin7 interacts with Z-box DNA with high affinity and Arg-127 determines its DNA-binding ability.

**Ireland**

> Fort, A., Ryder, P., McKeown, P.C., Wijnen, C., Aarts, M.G., Sulpice, R. and Spillane, C., 2016. Disaggregating polyploidy, parental genome dosage and hybridity contributions to heterosis in Arabidopsis. *New Phytologist*, 209(2), pp.590-599. doi: [10.1111/nph.13650](https://doi.org/10.1111/nph.13650)  
 > de Marchi R, Sorel M, Mooney B, Fudal I, Goslin K, Kwasniewska K, Ryan PT, Pfalz M, Kroymann J, Pollmann S, Feechan A, Wellmer F, Rivas S, Graciet E., 2016. The N-end rule pathway regulates pathogen responses in plants. *Scientific reports*, 6, 26020 doi: [10.1038/srep26020](https://doi.org/10.1038/srep26020)

**Israel**

> Strong support for fundamental research at Israeli Centers of Research Excellence (I-CORE)  
 > About 60 research articles employing Arabidopsis were published since the beginning of 2016 and until March 2017.

**Italy**

> Cecchetti V, Celebrin D, Napoli N, Ghelli R, Brunetti P, Costantino P, and Cardarelli M. (2017) An auxin maximum in the middle layer is necessary for stamen and pollen maturation in Arabidopsis *New Phytologist* Feb; 213(3):1194-1207. doi: [10.1111/nph.14207](https://doi.org/10.1111/nph.14207)  
 > Ezquer I, Mizzotti C, Nguema-Ona E, Gotté M, Beauzamy L, Viana VE, Dubrulle N, Costa de Oliveira A, Caporali E, Koroney AS, Boudaoud A, Driouch A, Colombo L. The Developmental Regulator SEEDSTICK Controls Structural and Mechanical Properties of the Arabidopsis Seed Coat. *Plant Cell*. 2016 Oct;28(10):2478-2492 doi: [10.1105/tpc.16.00454](https://doi.org/10.1105/tpc.16.00454)

**Japan**

> Among 75 scientists selected as Highly Cited Researchers 2016 (Clarivate Analytics) in Japan, 30 are plant scientists, revealing the strength of plant science in Japan. <http://hcr.stateofinnovation.com>

**Netherlands**

> The significant number of newly funded projects indicates that funding of Arabidopsis research in the Netherlands remains good!

**New Zealand**

> Peters B, Casey J, Aidley J, Zohrab S, Borg M, Twell D and Brownfield L. (2017). A conserved cis-regulatory module determines germline fate through activation of the transcription factor DUO1 promoter. *Plant Physiology* 173: 280-293. doi: [10.1104/pp.16.01192](https://doi.org/10.1104/pp.16.01192).

**Spain**

> Martín G, Leivar P, Ludevid D, Tepperman JM, Quail PH and Monte E (2016) Phytochrome and retrograde signalling pathways converge to antagonistically regulate a light-induced transcriptional network. *Nature Communications* 7: 11431. doi: [10.1038/ncomms11431](https://doi.org/10.1038/ncomms11431)

**South Korea**

> Establishment of the 'Systems & Synthetic Agrobiotech Center' (~\$9M/yr for 10 years by Rural Development Administration).  
 > Welcomed 1000 delegates to the ICAR2016 meeting hosted in Gyeongju, Korea.

**Sweden**

> Gruel *et al.* (2016) An epidermis-driven mechanism positions and scales stem cell niches in plants. *Science Advances*. doi: [10.1126/sciadv.1500989](https://doi.org/10.1126/sciadv.1500989)  
 > Porco *et al.* (2016) Dioxygenase-encoding AtDAO1 gene controls IAA oxidation and homeostasis in Arabidopsis. *Proc Natl Acad Sci U S A*. doi: [10.1073/pnas.1604375113](https://doi.org/10.1073/pnas.1604375113)

**Switzerland**

> Switzerland has had regularly a high-quality publications (e.g. Doblas *et al.*, *Science* 2017, Zürcher *et al.*, *Science* 2016).  
 > A 5.5-year joint project for Japan and Switzerland on polyploid Arabidopsis and crop species was funded by Japan Science and Technology Agency (JST) (PI, Kentaro Shimizu).

**United Kingdom**

> GARNet brought together world-leading experts on 'Natural Variation in Gene Discovery and Crop Improvement', University of Cambridge, Dec 2016 <http://garnetnatvar2016.weebly.com/>  
 > The GARNet YouTube channel features interviews about important papers from Arabidopsis researchers: <https://www.youtube.com/channel/UC89b0H0Mvu5SRbgFNhf2rfQ>

**United States**

> United States hosts the 28th International Conference on Arabidopsis Research (ICAR) in St. Louis, June 19-23, 2017.  
 > Five US Arabidopsis researchers were selected as Howard Hughes Medical Institute (HHMI) or HHMI-Simons Foundation Faculty Scholars: 5 year awards to early-career scientists deemed to have great potential to make unique contributions to their field.

**Argentina**

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 Fundación Instituto Leloir, CONICET,  
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**General Activities**

**Research Facilities**

There are more than 30 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.

**Arabidopsis Projects**

The research topics and research groups include, among others, water transport (Gabriela Amodeo), responses to water deficit (Raquel Chan, Norberto Iusem), light signaling and photomorphogenesis (Jorge Casal, Carlos Ballaré, Javier Botto), responses to UV-B light (Paula Casati, Carlos Ballaré), oxidative stress (Nestor Carrillo, Daniel Gonzalez, Estela Valle, Diego Gomez Casati), leaf growth and development (Javier Palatnik, Ramiro Rodriguez), circadian rhythms (Marcelo Yanovsky), flowering time (Pablo Cerdán), flower development (Jorge Muschietti, Gabriela Pagnussat, Eduardo Zabaleta, Ariel Goldraj), hormone biology (Lorenzo Lamatina, Ana Laxalt, Carlos García Mata, Santiago Mora García, Ruben Bottini), carbohydrate metabolism (Graciela Salerno, Fernando Carrari), root growth and development (José Estevez) biotic stress responses (Sebastián Azurmendi, Mariana del Vas, María Elena Alvarez), gene expression, micro RNAs, alternative splicing (Pablo Manavella, Javier Palatnik, Marcelo Yanovsky, Ezequiel Petrillo, Alberto Kornblihtt).

**Road Map Related Activities**

**Conference and Workshops**

A Plant Functional Genomics Symposium will be held in Rosario, Argentina, from May 17 to May 19. The Symposium will cover topics such as Functional Genomics and NGS, Agrobiotechnology, Gene expression regulatory mechanisms involved in the control of plant development and environmental

responses, Non coding RNAs and Plant-Microbe interactions. The symposium will include the participation of Arabidopsis researchers from Argentina, Chile, Spain, France and Switzerland.

**Selected Publications**

Di Giorgio JA, Bienert GP, Ayub ND, Yaneff A, Barberini ML, Mecchia MA, Amodeo G, Soto GC, Muschietti JP (2016) Pollen-Specific Aquaporins NIP4;1 and NIP4;2 Are Required for Pollen Development and Pollination in Arabidopsis. *Plant Cell* 28(5):1053-77.

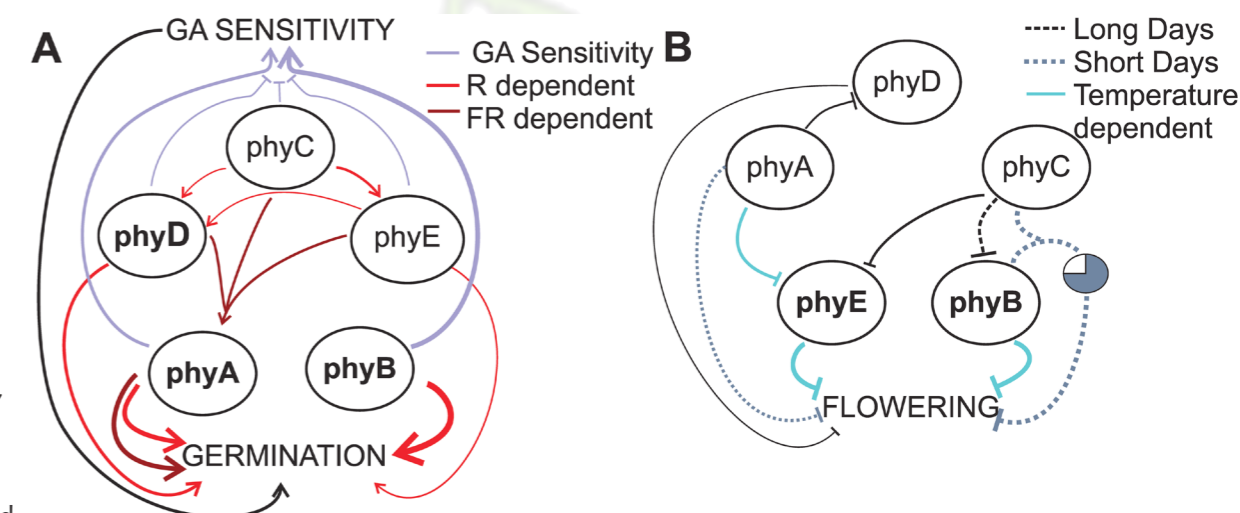
Legris M, Klose C, Burgie ES, Rojas CC, Neme M, Hiltbrunner A, Wigge PA, Schäfer E, Vierstra RD, Casal JJ (2016) Phytochrome B integrates light and temperature signals in Arabidopsis. *Science* 18;354(6314):897-900.

Sánchez-Lamas M, Lorenzo CD, Cerdán PD (2016) Bottom-up Assembly of the Phytochrome Network. *PLoS Genetics* 7;12(11):e1006413.

Distéfano AM, Martin MV, Córdoba JP, Bellido AM, D'Ippólito S, Colman SL, Soto D, Roldán JA, Bartoli CG, Zabaleta EJ, Fiol DF, Stockwell BR, Dixon SJ, Pagnussat GC (2017) Heat stress induces ferroptosis-like cell death in plants. *J Cell Biol* ;216(2):463-476.

**Major Funding Sources**

Argentinean National Research Council (CONICET) and Agencia Nacional de Promoción Científica y Tecnológica (ANPCyT).



**Figure 15.** Summary of the roles of phytochromes and the interactions between them during germination (A) and flowering (B). Positive interactions are depicted by arrows and negative interactions by lines. The thickness of each line indicates the strength of the action. <https://doi.org/10.1371/journal.pgen.1006413>

## Australia

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



Currently funded Centres of Excellence:  
 Plant Energy Biology 2014-2020: Energy metabolism, Gatekeeper cells and Specialisation, Gene Variants and Epigenetics.

Plant Cell Walls 2011-2017: Synthesis and assembly, Molecular and cellular mechanisms, Cell wall interactions.

Translational Photosynthesis 2014-2020: Improving leaf carbon dioxide capture efficiency and maximising light interception by the leaf.

Selected examples of individual ARC funded research projects are listed below:  
 Bostjan Kobe, Plant immune receptors. 2016-2019 ARC Discovery Project.  
 John Bowman, Development and evolution of land plant shoots. 2016-2019 ARC Discovery Project.  
 Bernard Carroll, Systemic gene silencing in Arabidopsis. 2015-2018 ARC Discovery Project.  
 Monika Murcha, tRNA mitochondrial import. 2015-2018 ARC Discovery Project.

### Outlook

Arabidopsis research remains a strong focus for many researchers for the core understanding of many cellular processes, plant microbe interactions and establishing technologies and platforms. Researchers are striving to ensure that their discoveries in Arabidopsis is relevant to applied research.

### Road Map Related Activities

### Arabidopsis Tools and Resources

Online Resources:  
 • SUBA4: The SubCellular Proteomic Database (SUBA) houses large scale proteomic and GFP localisation sets from cellular compartments of Arabidopsis. <http://suba.plantenergy.uwa.edu.au/>  
 • RICE DB: Rice DB facilitates and integrates direct comparison of rice annotations to Arabidopsis allowing parallel comparison between these two model species within one database. <http://ricedb.plantenergy.uwa.edu.au/>  
 • Epigenome data sets including Arabidopsis transposon variation, Arabidopsis stress and root cell methylomes. <http://listerlab.org/browsers.html>  
 • MASC Gator: a proteomics aggregation utility that displays information from a variety of online Arabidopsis proteomic resources.  
 • 1001 Proteomes: Arabidopsis non-synonymous SNP browser created from data made available as part of the 1001 Genomes consortium.

Facilities and Platform technologies:  
 • Australian Plant Phenomics Facility. The APPF provides a suite of analytical tools to support high-throughput phenotyping and deep phenotyping. <http://www.plantphenomics.org.au/>

### General Activities

### Research Facilities

Arabidopsis research encompasses a large number of research groups spanning the country, with a diverse range of research topics. Arabidopsis research is carried out at most universities and at the Commonwealth Scientific and Industrial Research Organisation (CSIRO). Three large collaborative research centres, funded by the Australian Research Council and partner universities are dedicated to plant science and currently carry out Arabidopsis functional genomic research.

Australian Research Council Centres of Excellence:  
 • Plant Cell Walls (<http://www.plantcellwalls.org.au/>)  
 • Plant Energy Biology (<http://www.plantenergy.uwa.edu.au/>)  
 • Translational Photosynthesis (<http://photosynthesis.org.au/>)

Selected examples of Arabidopsis research topics:  
 • Chloroplast development and function, oxidative stress (Barry Pogson)  
 • Mitochondrial Respiration (Kathleen Soole)  
 • Transcriptional networks and DNA methylation (Mathew Lewsey)  
 • Mitochondrial biogenesis, phosphate use efficiency (James Whelan)  
 • Flowering time (Anthony Gendall)  
 • Epigenetics (Ryan Lister)  
 • Plant defence (Karam Singh)  
 • PPR proteins (Ian Small)  
 • Protein turnover (Harvey Millar)  
 • Gene silencing and RNAi (Peter Waterhouse)  
 • Plant cell wall synthesis (Josh Heazelwood)  
 • Adaptation to environmental stress (Alexandre-Fournier-Level)  
 • Transcriptional regulators that control cell differentiation (John Goltz)  
 • Salinity, membrane transport (Matthew Gilliam)  
 • Parasitic interactions (Peer Schenk)  
 • Population genetics (Justin Borevitz)

### Arabidopsis Projects

Arabidopsis research is mainly funded through the Australian Research Council as Centres of Excellence, Discovery projects and fellowships ([www.arc.gov.au](http://www.arc.gov.au)) with a diverse range of topics.

• Comprehensive Microarray Polymer Profiling (CoMPP)-n high-throughput screening technique for characterising the polysaccharide composition of cell walls

### Outreach Activities

The Australian plant research environment strongly supports applied plant research and industry collaborations with several research groups and Centre's linking to industry. Australian Research Council Linkage programs and the Grains Research and Development Corporation (GRDC) have supported translational research in Australia:

Australian Centres and Universities are very active in communicating their research to the general public and in particular to the next generation of plant scientists. Several examples of outreach programs are listed below:  
 • Bio-Bounce, An inflatable 11m x 13m plant cell allowing for an immersive educational experience (<http://www.plantenergy.uwa.edu.au/education/eto.html>).

• The Virtual Plant Cell (VPC) allows users to become immersed in, and interact with, a plant cell to learn about the complex processes that various topics of research ([https://www.youtube.com/watch?v=ZUPBtpm\\_XXI](https://www.youtube.com/watch?v=ZUPBtpm_XXI)).

### Conference and Workshops

Combined Biological Societies Annual Conference (<https://www.asbmb.org.au>). Annual national scientific conference that includes several symposia dedicated to plant research and incorporating the annual meeting of the Australian Society of Plant Biologists.

- ComBio 2016, Brisbane Convention Centre 3-7 Oct 2016  
 - ComBio 2017, Adelaide Convention Centre 2-5 Oct 2017

### Selected Publications

Australian researchers have been involved in 194 publications since Jan 2016-March 2017, using Pubmed search of Arabidopsis (keyword) and Australia (affiliation). Highlighted publications are listed below:



**Figure 16.** Representative phenotypes (cohorts) of plants transformed with a hairpin construct specifically targeting GFT1 expression compared with control plants (plants transformed with the empty vector). <https://doi.org/10.1038/ncomms12119>

Chan KX, Mabbitt PD, Phua SY, Mueller JW, Nisar N, Gigolashvili T, Stroehrer E, Grassl J, Arlt W, Estavillo GM, Jackson CJ, Pogson BJ (2016) Sensing and signaling of oxidative stress in chloroplasts by inactivation of the SAL1 phosphoadenosine phosphatase. *Proc Natl Acad Sci U S A.* 113(31):E4567-76

Greaves IK, Eichten SR, Groszmann M, Wang A, Ying H, Peacock WJ, Dennis ES (2016) Twenty-four-nucleotide siRNAs produce heritable trans-chromosomal methylation in F1 Arabidopsis hybrids. *Proc Natl Acad Sci U S A.* 113(44):E6895-E6902.

Rautengarten C, Ebert B, Liu L, Stonebloom S, Smith-Moritz AM, Pauly M, Orellana A, Scheller HV, Heazlewood JL (2016) The Arabidopsis Golgi-localized GDP-L-fucose transporter is required for plant development. *Nat Commun* 7:12119. doi: 10.1038/ncomms12119.

Stuart T, Eichten SR, Cahn J, Karpievitch YV, Borevitz JO, Lister R. (2016) Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. *Elife.* 2;5.

Sureshkumar S, Dent C, Seleznev A, Tasset C, Balasubramanian S (2016) Nonsense-mediated mRNA decay modulates FLM-dependent thermosensory flowering response in Arabidopsis. *Nat Plants* 2(5):16055.

### Major Funding Sources

Basic research is funded by the Australian Research Council ([www.arc.gov.au](http://www.arc.gov.au)). Translational research is funded by the Grains Research and Development Corporation (GRDC) (<https://grdc.com.au/>).

## Austria



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 University of Natural Resources and Life Sciences BOKU, Vienna

### General Activities

#### Locations

University of Natural Resources & Life Science Vienna (BOKU), Department of Applied Genetics & Cell Biology (DAGZ) ([www.dagz.boku.ac.at/en/](http://www.dagz.boku.ac.at/en/))  
 Gregor Mendel Institute of Molecular Plant Biology (GMI) ([www.gmi.oeaw.ac.at/](http://www.gmi.oeaw.ac.at/))  
 Max F. Perutz Laboratories (MFPL) ([www.mfpl.ac.at/](http://www.mfpl.ac.at/))  
 Institute of Science and Technology, Austria (IST Austria) ([ist.ac.at/en/](http://ist.ac.at/en/))  
 AIT Austrian Institute of Technology ([www.ait.ac.at/themen/improvement-of-plant-quality-vigor/](http://www.ait.ac.at/themen/improvement-of-plant-quality-vigor/))  
 University of Salzburg, Division of Plant Physiology ([www.uni-salzburg.at/index.php?id=32701&L=1](http://www.uni-salzburg.at/index.php?id=32701&L=1))  
 University of Vienna, Ecogenomics and Systems Biology ([www.univie.ac.at/mosys](http://www.univie.ac.at/mosys))  
 VBCF ProTech facility ([www.vbcf.ac.at/facilities/protein-technologies/](http://www.vbcf.ac.at/facilities/protein-technologies/))  
 VBCF PlantsS facility ([www.vbcf.ac.at/facilities/plant-sciences/](http://www.vbcf.ac.at/facilities/plant-sciences/))

#### Subject Areas

**Population Genetics**  
 - Magnus Nordborg ([www.gmi.oeaw.ac.at/research-groups/magnus-nordborg/](http://www.gmi.oeaw.ac.at/research-groups/magnus-nordborg/)): Scientific Director of the GMI Molecular Biology and Signaling;  
 - Andreas Bachmair ([www.mfpl.ac.at/mfpl-group/group/bachmair.html](http://www.mfpl.ac.at/mfpl-group/group/bachmair.html)): Stress response pathways, posttranslational modification by Ubiquitin and by SUMO  
 - Claudia Jonak ([www.ait.ac.at/themen/improvement-of-plant-quality-vigor/](http://www.ait.ac.at/themen/improvement-of-plant-quality-vigor/)): Stress signal transduction towards metabolic and chromatin adjustments  
 - Markus Teige ([www.univie.ac.at/mosys/markus\\_teige\\_cv.html](http://www.univie.ac.at/mosys/markus_teige_cv.html)): signaling in acclimation to stress, organellar signaling,

#### Chromosome Biology

- Peter Schlögelhofer (<http://www.mfpl.ac.at/mfpl-group/group/schloegelhofer.html>): meiotic recombination

#### Epigenetics

- Frederic Berger ([www.gmi.oeaw.ac.at/research-groups/frederic-berger/](http://www.gmi.oeaw.ac.at/research-groups/frederic-berger/)): Chromatin architecture and function.  
 - Ortrun Mittelsten Scheid ([www.gmi.oeaw.ac.at/research-groups/ortrun-mittelsten-scheid/](http://www.gmi.oeaw.ac.at/research-groups/ortrun-mittelsten-scheid/)): Epigenetic changes in plants  
 - Claude Becker ([www.gmi.oeaw.ac.at/research-groups/claude-becker/](http://www.gmi.oeaw.ac.at/research-groups/claude-becker/)): Genetics & Epigenetics of Allelopathy

**Development, Molecular Genetics & Cell Biology**  
 - Wolfgang Busch ([www.gmi.oeaw.ac.at/research-groups/wolfgang-busch/](http://www.gmi.oeaw.ac.at/research-groups/wolfgang-busch/)): Systems Genetics of Root Growth  
 - Michael Nodine ([www.gmi.oeaw.ac.at/research-groups/michael-nodine/](http://www.gmi.oeaw.ac.at/research-groups/michael-nodine/)): Small RNA functions in plant embryos.  
 - Eva Benkova ([ist.ac.at/en/research/research-groups/benkova-group/](http://ist.ac.at/en/research/research-groups/benkova-group/)): Hormonal regulation of plant development  
 - Jiri Friml ([ist.ac.at/research/research-groups/friml-group/](http://ist.ac.at/research/research-groups/friml-group/)): Auxin transport and signaling, cell polarity, endocytic trafficking, evolution of auxin transport  
 - Marie-Theres Hauser ([www.dagz.boku.ac.at/en/pgz/hauser/](http://www.dagz.boku.ac.at/en/pgz/hauser/)): development and abiotic stress responses  
 - Jürgen Kleine Vehn ([www.dagz.boku.ac.at/arbeitsgruppen/team-kleine-vehn/](http://www.dagz.boku.ac.at/arbeitsgruppen/team-kleine-vehn/)): phytohormonal crosstalk, differential growth regulation  
 - Barbara Korbei ([www.dagz.boku.ac.at/pgz/korbei/](http://www.dagz.boku.ac.at/pgz/korbei/)): Elucidating the role of TOL proteins in post-Golgi trafficking  
 - Yasin Dagdas ([www.gmi.oeaw.ac.at/research-groups/yasin-dagdas/](http://www.gmi.oeaw.ac.at/research-groups/yasin-dagdas/)): Autophagy in Plant Development & Stress Tolerance

#### Glycobiology

- Richard Strasser ([www.dagz.boku.ac.at/en/mzg/strasser/](http://www.dagz.boku.ac.at/en/mzg/strasser/)): Function of N-glycans  
 - Doris Lucyshyn ([www.dagz.boku.ac.at/pgz/abas/lucyshyn/](http://www.dagz.boku.ac.at/pgz/abas/lucyshyn/)): O-GlcNAcylation  
 - Raimund Tenhaken ([www.uni-salzburg.at/index.php?id=32790&L=1](http://www.uni-salzburg.at/index.php?id=32790&L=1)): Nucleotide sugars biosynthesis and function

#### RNA metabolism

- Maria Kalyna ([www.dagz.boku.ac.at/en/pgz/hauser/kalyna/](http://www.dagz.boku.ac.at/en/pgz/hauser/kalyna/)): Alternative splicing  
 - Andrea Barta ([www.mfpl.ac.at/groups/mfpl-group/group-info/barta.html](http://www.mfpl.ac.at/groups/mfpl-group/group-info/barta.html)): Post-transcriptional regulation of gene expression in plants

#### Plant pathogen interaction

- Youssef Belkhadir ([www.gmi.oeaw.ac.at/research-groups/youssef-belkhadir/](http://www.gmi.oeaw.ac.at/research-groups/youssef-belkhadir/)): Defense/Growth Decision Making  
 - Armin Djamei ([www.gmi.oeaw.ac.at/research-groups/armin-djamei/](http://www.gmi.oeaw.ac.at/research-groups/armin-djamei/)): Plant Fungal Effectors

#### Current Arabidopsis Projects

##### Doctoral programmes financed by the FWF

- 2012-2019 “Chromosome Dynamics” ([www.chromosome-dynamics.at](http://www.chromosome-dynamics.at))
- 2010-2018 “Population Genetics” ([www.popgen-vienna.at](http://www.popgen-vienna.at))
- 2007-2019 „RNA Biology“ ([www.mfpl.ac.at/rna-biology/doctoral-program/](http://www.mfpl.ac.at/rna-biology/doctoral-program/))

##### ITN (international training network)

2013-2017 “CALIPSO - Calcium and Light Signals in Photosynthetic Organisms” ([itn-calipso.univie.ac.at/](http://itn-calipso.univie.ac.at/))

2013–2017 “COMREC: Control of Meiotic Recombination: Arabidopsis to Crops” ([www.birmingham.ac.uk/comrec](http://www.birmingham.ac.uk/comrec))  
**ERC**  
 • 2012-2017 Polarity and subcellular dynamics in plants, J. Friml  
 • 2014-2019 EFFECTOMICS- elucidating the toolbox of biotrophic pathogens, A. Djamei  
 • 2015-2020 Small RNA regulation of the body plan and epigenome in Arabidopsis embryos (sRNA-EMB), M. Nodine  
 • 2015-2020 AuxinER: Mechanism of Auxin-dependent Signaling in the Endoplasmic Reticulum, J Kleine-Vehn ERA-CAPS projects ([www.ercaps.org/](http://www.ercaps.org/))  
 • 2014-2017 “Dimorphic fruits, seed and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments (SeedAdapt)”  
 • 2014-2017 “EURO-PEC - European Plant Embryology Consortium”  
 • 2014-2017 “The role of the N-end rule pathway in controlling plant response to the environment (N-vironment)”  
 • 2014-2017 “Delineating the crossover control networks in plant (DeCOP)”  
 • 2015-2018 “Evolution of sexual reproduction in plants (EVOREPRO)”

##### WWTF projects

- 2011-2018 “Plant Cell and Molecular Biology”
- 2014-2018 “Quantitative Live Imaging to Determine the Regulatory Impact of Chromatin Dynamics”

##### APART fellowship of the Austrian Academie of Sciences

- 2014-2018 “O-GlcNAc Modification of Plant Proteins”, D. Lucyshyn
- FFG project**  
 2016 “Mysteries of plant gravitropism” E. Benkova

##### EMBO Fellow project

“Molecular mechanism of auxin-driven formative divisions delineating lateral root organogenesis in plants”

##### FWF projects

- 2008-2019 “Chromosome Dynamics” SFB 34
- 2014-2017 “Impact of a new histone H2A variant on chromatin structure and dynamics”
- 2014-2017 “N-vironment - The role of the N-end rule in plant response to the environment”
- 2014-2017 “In vivo Protein Interaction during Cell Signaling”
- 2014-2018 “Pectin signaling in responses to heavy metals and pathogens” (bilateral project with France)
- 2014-2019 “TOL Proteins in post-Golgi Trafficking in Plants”
- 2014-2019 “DNA damage and alternative splicing in plants”
- 2015-2017 “Root growth Control and Epistasis”
- 2015-2017 “Elucidating Salicylic Acid Sensing in Biotrophic Smut Fungi”

- 2015-2017 “Hormone cross-talk drives nutrient-dependent root development” (bilateral project with France)
  - 2015-2017 “Pectin signaling in responses to heavy metals and pathogens”
  - 2015-2018 “Dissecting the glycan-dependent ERAD pathway in plants”
  - 2015-2018 “Characterization of an essential virulence factor in the maize pathogen Ustilago maydis”
  - 2015-2018 “EXO70 exocyst subunits in morphogenesis and adaptation”
  - 2015-2019 “Small RNA directed reprogramming of lineage-specific epigenomes in plant embryos”
  - 2015-2020 “Signaling Salt Stress to the chromatin”
  - 2016-2017 “The histone variant H2A.W: a novel component that structures chromatin domains”
  - 2016-2018 “CESP” (Cross-talk of Calcium- and Energy Signalling in Plants)
  - 2016-2018 “Evolution of the chromatin organization in plants”
  - 2016-2018 “The role of PLD zeta1 in iron dependent root growth regulation”
  - 2016-2019 “Importance of Lewis A Epitopes for Pseudomonas syringae Infection of Arabidopsis”
  - 2017-2019 “Sweet Immunity (bilateral project with Belgium)”
  - 2017-2020 “Host Jump Enabling Factors in a Fungal/ Grass Pathosystem”
  - 2017-2021 “Plant Salt Stress Tolerance and Oxidative Signalling”
  - 2017-2021 “DNA double strand break repair in the context of chromatin” (bilateral project with France)
- DFG**  
 2011-2017 “Evolutionary plant solutions to ecological challenges: Molecular mechanisms underlying adaptive traits in the Brassicaceae s.l. (Adaptomics)”

#### Road Map Related Activities

##### Arabidopsis Tools and Resources

- Root chip tracking system: Platform for specific cell ablation combined with real-time imaging in plants
- Light sheet (SPIM) microscope for Arabidopsis roots, lateral roots, apical hook (von Wangenheim *et al.*, 2017)
- Vertical confocal microscope allowing automatic tracking of the root growth (not published)
- Microfluidic-like device - “root chip” for simultaneous root treatments and confocal visualization.
- AraPheno - database for Arabidopsis phenotypes
- GWA-Portal - web-based interface for performing Arabidopsis GWAS



- AraGeno - web-based interface for identifying Arabidopsis accessions and performing sequence based genotyping

- VBCF Plants facility: offering state of the art growth chambers and greenhouse space along with automated phenotyping

- VBCF ProTech facility: offering made-to-order CRISPR/Cas9 transgenics ([www.vbcf.ac.at/facilities/protein-technologies/](http://www.vbcf.ac.at/facilities/protein-technologies/))

- Novel pipeline with stringent filters and quality control measures for generating high quality non-redundant transcriptomes for improved accuracy of RNA-seq analyses.

- Reference Transcript Dataset for Arabidopsis (AtRTD2) containing 82,190 non-redundant transcripts from 34,212 genes

- Modified version of AtRTD2, AtRTD2-QUASI, Reference Transcript Dataset for Arabidopsis for Quantification of Alternatively Spliced Isoforms

- Novel algorithm for translating alternatively spliced isoforms into polypeptides

- New Arabidopsis peptide database based on AtRTD2 protein isoforms for proteomic analyses

### Outreach Activities

Open campus day IST Austria presenting, June 5, 2016

### Conferences and Workshops

EMBO Workshop: New model systems for early land plant evolution 22-24 June, 2016, Vienna

10th Tri-National Arabidopsis Meeting 14-16 Sep, 2016, Vienna

### Selected Publications

Rabe F, Bosch J, Stirnberg A, Guse T, Bauer L, Seitner D, Rabanal FA, Czedik-Eysenberg A, Uhse S, Bindics J, Genencher B, Navarrete F, Kellner R, Ekker H, Kumlehn J, Vogel JP, Gordon SP, Marcel TC, Münsterkötter M, Walter MC, Sieber CM, Mannhaupt G, Güldener U, Kahmann R, Djamei A (2016) A complete toolset for the study of Ustilago bromivora and Brachypodium sp. as a fungal-temperate grass pathosystem. *eLife* 5:e20522

The 1001 Genomes Consortium (2016) 1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis. *Cell* 166(2):481-91.

Novikova PY, Hohmann N, Nizhynska V, Tsuchimatsu T, Ali J, Muir G, Guggisberg A, Paape T, Schmid K, Fedorenko OM, Holm S, Säll T, Schlötterer C, Marhold K, Widmer A, Sese J, Shimizu KK, Weigel D, Krämer U,

Koch MA, Nordborg M (2016) Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. *Nat Genet* 48(9):1077-82.

Elsayad K, Werner S, Gallemí M, Kong J, Sánchez Guajardo ER, Zhang L, Jaillais Y, Greb T, Belkhadir Y (2016) Mapping the subcellular mechanical properties of live cells in tissues with fluorescence emission-Brillouin imaging. *Sci Signal* 9(435):rs5.

Rakusová H, Abbas M, Han H, Song S, Robert HS, Friml J. (2016) Termination of Shoot Gravitropic Responses by Auxin Feedback on PIN3 Polarity. *Curr Biol.* 26(22):3026-3032.

Fendrych M, Leung J, Friml J. (2016) TIR1/AFB-Aux/IAA auxin perception mediates rapid cell wall acidification and growth of Arabidopsis hypocotyls. *eLife.* 5:e1904

Nukarinen E, Nägele T, Pedrotti L, Wurzinger B, Mair A, Landgraf R, Börnke F, Hanson J, Teige M, Baena-Gonzalez E, Dröge-Laser W, Weckwerth W (2016) Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. *Sci Rep.* 6:31697.

Marhavý P, Montesinos JC, Abuzeineh A, Van Damme D, Vermeer JE, Duclercq J, Rakusová H, Nováková P, Friml J, Geldner N, Benková E. (2016): Targeted cell elimination reveals an auxin-guided biphasic mode of lateral root initiation. *Genes Dev.* 30(4):471-83.

### Major Funding Sources

Austrian Science Fund (FWF)

[www.fwf.ac.at/en/](http://www.fwf.ac.at/en/)

OeAD

[www.oead.at/projects\\_cooperations/EN/](http://www.oead.at/projects_cooperations/EN/)

Austrian Academy of Sciences (ÖAW)

[www.oeaw.ac.at/en/fellowship-funding/stipendien-preise/nachwuchsfoerderung-der-oeaw/](http://www.oeaw.ac.at/en/fellowship-funding/stipendien-preise/nachwuchsfoerderung-der-oeaw/)

Vienna Science and Technology Fund (WWTF)

[wwtf.at/index.php?lang=EN](http://wwtf.at/index.php?lang=EN)

Austrian Research Promotion Agency (FFG)

[www.ffg.at/en](http://www.ffg.at/en)

European Research Council (ERC)

[erc.europa.eu/](http://erc.europa.eu/)

Marie Skłodowska-Curie actions

<http://ec.europa.eu/research/mariecurieactions/>

ERA CAPS

[www.ercaps.org/](http://www.ercaps.org/)

DFG

[www.dfg.de/en/](http://www.dfg.de/en/)

EMBO Long-Term Fellowships

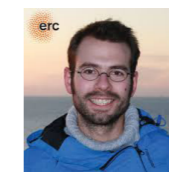
[www.embo.org/funding-awards/fellowships](http://www.embo.org/funding-awards/fellowships)

## Belgium

Moritz K. Nowack

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VIB-UGent Center for Plant Systems Biology, Ghent, Belgium



### General Activities

### Research Facilities

Arabidopsis Research Centers in Belgium:

VIB-UGent Center for Plant Systems Biology, <https://www.psb.ugent.be/>

University of Ghent <https://www.ugent.be/en>

University of Leuven <https://www.kuleuven.be/english>

University of Antwerpen <https://www.uantwerpen.be/en/>

University of Hasselt <http://www.uhasselt.be/en>

Universite catholique de Louvain <https://uclouvain.be/fr/index.html>

University of Liege [https://www.ulg.ac.be/cms/c\\_5000/en/home](https://www.ulg.ac.be/cms/c_5000/en/home)

Arabidopsis research topics in Belgium include cell cycle regulation (D. Inzé, L. De Veylder), root and leaf growth and development (D. Inzé, T. Beeckman, M. Nowack, G. Beemster, M. Van Lijsebettens, K. Vissenberg, B. De Rybel), oxidative stress and cell death (F. Van Breusegem, M. Nowack, P. Motte, H. Asard), genome annotation and evolution (S. Maere, Y. Van de Peer, K. Vandepoele), proteomics (G. De Jaeger, I. De Smet), tree biotechnology and bioenergy (W. Boerjan, B. Vanholme), cell biology (D. Geelen, D. Van Damme), hormone biology (D. Van Der Straeten, J. Russinova E., Prinsen, A. Goossens), carbohydrates (E. Van Damme, P. Van Dijck; F. Roland), membrane proteins (M. Boutry), abiotic stress (N. Verbruggen; C. Hermans, Y. Guisez; M. Hanikenne), flowering (C. Périlleux; P. Tocquin) and plant pathogen interaction (G. Angenon, B. Cammue, L. Gheysen; P. du Jardin, J. Vanderleyden, P. Delaplace, J. Dommès).

### Arabidopsis Projects

Belgian Arabidopsis projects are funded by university-, regional-, federal-, or European-level grants, but not within calls specifically targeting this model plant species or plants.

A Belgian national research project (IAP), coordinated by D. Inzé, focuses on how root and shoot influence each other and how this interaction contributes to the development of the plant.

This program also involves T. Beeckman, F. Van Breusegem G. Beemster, L. De Veylder, M. Boutry, X. Draye, N. F. Chaumont, and C. Périlleux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project. For more information, see <http://www.iuap-mars.be/>.

FWO (Research Foundation – Flanders) research grants were appointed to L. De Veylder to study DNA damage checkpoint control (in collaboration with I. De Smet), to F. Roland to study energy signalling, to F. Van Breusegem to study redox control of proteins, to E. Van Damme to study lectin-carbohydrate interactions, to Moritz Nowack to study programmed cell death in plant reproduction, and to D. Van Der Straeten to study mitochondrial editing factors. An F.R.S.-FNRS grant was appointed to C. Hermans to study mineral influences on root architecture.

An ERC Starting Grant was obtained by Moritz Nowack for work on developmental programmed cell death in Arabidopsis roots (2015- 2020).

An ERC Starting Grant was obtained by Bert De Rybel for work on vascular development in Arabidopsis embryos and roots (2017-2022).

An ERC Consolidator Grant was obtained by Daniel Van Damme for work on cell division control in Arabidopsis roots (2016- 2021).

An Odysseus Group II grant was obtained by Bert De Rybel, to work on cellular patterning in Arabidopsis embryogenesis <http://www.fwo.be/en/fellowships-funding/research-projects/odysseusprogramme/>

### Outlook

There is a gradual move to other model species besides Arabidopsis, particularly crop species. Arabidopsis may remain the species of choice to pioneer new molecular genetics approaches due to its strengths as a small plant with short generation time that is easily transformable. Limitation however in applicability and possibilities to use when larger sample sizes are required (e.g. metabolomics, proteomics, biochemistry approaches are pretty much limited to whole plant level).

New impulses come from CRISPR-based genome editing. After initial difficulties, genome editing with high frequencies is now achieved in Arabidopsis. For now mostly targeted knock-out of genes and gene families is achieved, but in future also more sophisticated editing operations including gene- or tag- knock-ins, alteration of the methylome etc, will open up new possibilities in Arabidopsis research.

### Road Map Related Activities

### Arabidopsis Tools and Resources

The Department of Plant Systems Biology (PSB) continuously develops and disseminates an exhaustive collection of destination vectors, designed for the functional analysis of genes in plant cells and compatible with the recombinational cloning Gateway technology ([www.psb.ugent.be/gateway/](http://www.psb.ugent.be/gateway/)).

The Yield Booster website provides the scientific community with information on genes and molecular mechanisms that govern plant growth and productivity. Data on model plants (including Arabidopsis) as well as crops are presented ([www.yieldbooster.org/](http://www.yieldbooster.org/)).

PLAZA is an access point for plant comparative genomics centralizing genomic data produced by different genome sequencing initiatives. It integrates plant sequence data and comparative genomics methods and provides an online platform to perform evolutionary analyses and data mining within the green plant lineage (<http://bioinformatics.psb.ugent.be/plaza/>).

Other developed resources include:

- Platform for semi-automated kinematic analysis of growth in Arabidopsis root tips and leaves
- Phenotyping platforms
- Metabolomics and Enzyme activity assays for antioxidant system.
- VLeaf modelling platform based simulation models of Arabidopsis root tip and leaf growth.
- A collection of adventitious rooting mutants
- Marker lines for cell cycle, DNA stress, and meiosis specific events
- Marker lines for developmental cell death

### Outreach Activities

- International Plant Biotechnology Outreach (IPBO) <http://www.vib.be/en/research/scientists/Pages/IPBO.aspx>
- Day of Science <http://www.dagvandewetenschap.be/>
- Day of Biotechnology <http://flandersbio.be/events/dag-van-de-biotechnologie/>

### Conference and Workshops

- Plant Omics and Biotechnology for Human Health, 21-24 November 2016, Ghent, Belgium <https://www.psb.ugent.be/PSE/>
- At the Forefront of Plant Research, 15-16 June 2017, Ghent, Belgium, <http://www.vibconferences.be/event/at-the-forefront-of-plant-research>
- Genome Engineering and Synthetic Biology, 28-29 January 2016, Ghent, Belgium, <http://www.vibconferences.be/event/genome-engineering-and-synthetic-biology-tools-and-technologies>
- CRISPR-based Genome Engineering, 27 October 2016, Leuven, Belgium <https://goo.gl/rygKMI>

### Selected Publications

Clauw P, Coppens F, Korte A, Herman D, Slabbinck B, Dhondt S, Van Daele T, De Milde L, Vermeersch M, Maleux K, Maere S, Gonzalez N, Inzé D (2016) Leaf Growth Response to Mild Drought: Natural Variation in Arabidopsis Sheds Light on Trait Architecture. *Plant Cell* 28(10):2417-2434.

Hu Z, Vanderhaeghen R, Cools T, Wang Y, De Clercq I, Leroux O, Nguyen L, Belt K, Millar AH, Audenaert D, Hilson P, Small ID, Mouille G, Vernhettes S, Van Breusegem F, Whelan J, Höfte H, De Veylder L (2016) Mitochondrial Defects Confer Tolerance against Cellulose Deficiency. *Plant Cell* pii: tpc.00540.2016.

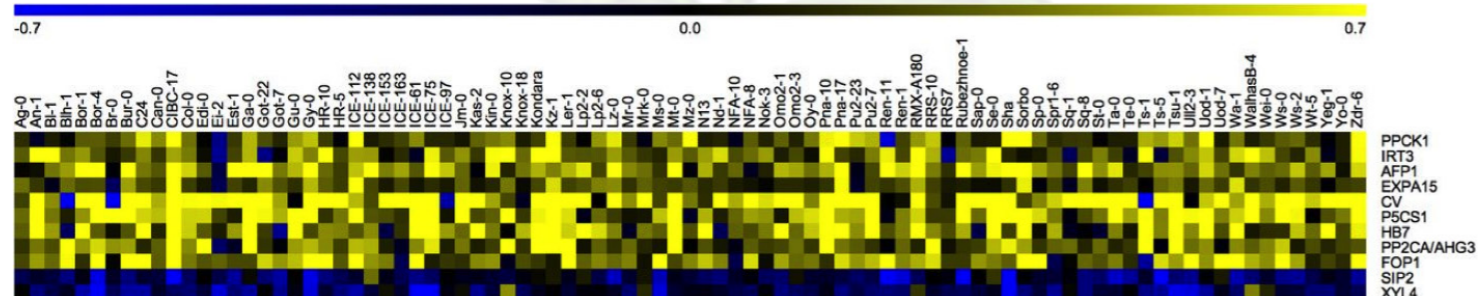
Karampelias M, Neyt P, De Groeve S, Aesaert S, Coussens G, Rolík J, Bruno L, De Winne N, Van Minnebruggen A, Van Montagu M, Ponce MR, Micol JL, Friml J, De Jaeger G, Van Lijsebettens M (2016) Proc Natl Acad Sci U S A 113(10):2768-73.

Orman-Ligeza B, Parizot B, de Rycke R, Fernandez A, Himschoot E, Van Breusegem F, Bennett MJ, Périlleux C, Beeckman T, Draye X (2016) RBOH-mediated ROS production facilitates lateral root emergence in Arabidopsis. *Development* 143(18):3328-39.

Ortiz-Morea FA, Savatin DV, Dejonghe W, Kumar R, Luo Y, Adamowski M, Van den Begin J, Dressano K, Pereira de Oliveira G, Zhao X, Lu Q, Maddar A, Friml J, Scherer de Moura D, Russinova E (2016) Danger-associated peptide signaling in Arabidopsis requires clathrin. *Proc Natl Acad Sci U S A* 113(39):11028-33.

### Major Funding Sources

- Flanders Institute for Biotechnology (VIB; [www.vib.be](http://www.vib.be))
- European Union Framework ([cordis.europa.eu/](http://cordis.europa.eu/))
- Belgian Federal Science Policy Office ([www.belspo.be](http://www.belspo.be))
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; [www.iwt.be](http://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/>)



**Figure 17.** Differential Expression of Eleven “Signature” Genes in 89 Accessions. The genes displayed show similar fold changes upon mild drought stress in at least 80 accessions <http://dx.doi.org/10.1105/tpc.16.00483>

## Canada

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### General Activities

#### Research Facilities

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

#### Arabidopsis Projects

The Provart Lab finished up work on a final module for [Araport.org](http://Araport.org), ePlant (Waese *et al.*, 2017, in revision). ePlant is a zoomable user interface for exploring data across 12 orders of magnitude, from the kilometre scale down to the nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested, open source tool. ePlant is accessible from the [Araport.org](http://Araport.org) homepage, and from the Bio-Analytic Resource: <http://bar.utoronto.ca/eplant>.

Two further papers describing useful Arabidopsis bioinformatic tools were published by the Provart Lab in 2016 by Austin *et al.* and Waese *et al.* The first describes a new version of Expression Angler for identifying sets of coexpressed genes according to a user-defined pattern, and Cistome for exploring potential cis-regulatory elements in the promoters of such sets of genes. The second, Gene Slider, allows easy exploration of conserved regions in 9 species of the Brassicaceae (Haudry *et al.*, 2013; doi: [doi:10.1038/ng.2684](https://doi.org/10.1038/ng.2684)), with the ability to visualize whether known cis-elements occur in conserved regions of Arabidopsis promoters.

J Waese, A Pasha, TT Wang, A van Weringh, DS Guttman, NJ Provart. (2016) Gene Slider: sequence logo interactive data-visualization for education and research *Bioinformatics* 32: 3670-3672. doi: [10.1093/bioinformatics/btw525](https://doi.org/10.1093/bioinformatics/btw525)

Jamie Waese, Jim Fan, Asher Pasha, Hans Yu, Geoff Fucile, Ruian Shi, Lawrence Kelley, Michael Sternberg, Vivek Krishnakumar, Erik Ferlanti, Jason Miller, Chris Town, Wolfgang Stuerzlinger and Nicholas J. Provart (2017) ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology  
In revision *The Plant Cell*

### Outlook

Funding for Arabidopsis research is largely from NSERC, one of the three federal funding agencies in Canada. Statistics reflecting money received or future investment in plant biology are not yet available.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

The BAR is funded in part by Centre for the Analysis of Genome Evolution and Function, grants from the Canada Foundation for Innovation to NJP, and from Genome Canada to the Arabidopsis Research Group at the Department of Cell and Systems Biology, University of Toronto.

Centre for the Analysis of Genome Evolution and Function (CAGEF) <http://bar.utoronto.ca>

### Selected Publications

Holbrook-Smith D, Toh S, Tsuchiya Y, McCourt P. (2016) Small-molecule antagonists of germination of the parasitic plant *Striga hermonthica*. *Nat Chem Biol.* 12(9):724-9.

Laflamme B, Middleton M, Lo T, Desveaux D, Guttman DS. (2016) Image-Based Quantification of Plant Immunity and Disease. *Mol Plant Microbe Interact.* 29(12):919-924.

Ryan S Austin, Shu Hiu, Jamie Waese, Matthew Ierullo, Asher Pasha, Ting Ting Wang, Jim Fan, Curtis Foong, Robert Breit, Darrell Desveaux, Alan Moses, Nicholas J Provart (2016) New BAR tools for mining expression data and exploring Cis-elements in Arabidopsis. *Plant J* 88: 490-504.

Yan D, Easwaran V, Chau V, Okamoto M, Ierullo M, Kimura M, Endo A, Yano R, Pasha A, Gong Y, Bi YM, Provart N, Guttman D, Krapp A, Rothstein SJ, Nambara E. (2016) NIN-like protein 8 is a master regulator of nitrate-promoted seed germination in Arabidopsis. *Nat Commun.* 7:13179.

### Major Funding Sources

National Science and Engineering Research Council (NSERC) (<http://www.nserc-crsng.gc.ca>)  
Genome Canada (<http://www.genomecanada.ca/en/>)



**Figure 18.** An example output from the BAR interface <http://dx.doi.org/10.1111/tbj.13261>

## Chile

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### General Activities

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

Francisca Blanco's laboratory studies signaling pathways involved in plant responses to pathogen infections and how the pathogen manipulates the host to its own benefits. Using system biology approaches to integrate the omics data into genome-scale metabolic models of both *Arabidopsis* and *Pseudomonas syringae*, to better understand the underlying mechanisms governing plant immunity and growth responses that finally leads to the pathogen success and plant sickness.

Paulo Canessa's Using RNAseq of plants infected with *Botrytis cinerea* and after data analysis and integration, we expect to determine the global transcriptional impact of light on *B. cinerea* when infecting plant tissue, but also to generate information related to the genome-wide expression profile of *A. thaliana* upon light stimulation when the wild-type fungus, or one that is sensing the environment in an altered manner ( $\Delta$ bcwcl1) are interacting with the plant tissue.

Ariel Orellana's laboratory studies regulation of polysaccharides biosynthesis in the Golgi Apparatus. Nucleotide sugar transporters (NSTs), proteins necessary for the translocation of nucleotide-sugars from cytosol,

place where they are synthesized, to the lumen of the Golgi apparatus, where polysaccharide biosynthesis takes place. They could identify some *Arabidopsis* proteins which share molecular characteristics with NSTs from other organisms, transporting GDP sugars. Their research is focused on determining the substrate specificity of these NSTs using their transient expression in plants, stable over-expression in *Arabidopsis* and insertional mutant lines.

Susana Saéz-Aguayo's laboratory studies the role of PMEs and PMEIs (cell wall remodeling enzymes) and to understand the different role of these proteins in the Homogalacturonan structuration (the main polysaccharide of pectins) in seed coat mucilage.

Michael Handford's lab is interested in the study of *Arabidopsis* sugar alcohol metabolism. Sugar alcohols (polyols) like sorbitol and mannitol perform various roles in vivo. In plants, they are a means of long-distance phloem carbon transport, of redistributing boron and act as compatible solutes in abiotic stress. *Arabidopsis* possesses low basal levels of sorbitol and other sugar alcohols, in addition to low-specificity sugar alcohol transporters. By reverse genetics, we identified AtSDH in this species which oxidizes sorbitol, and atsdh- mutants are more resistant to drought stress.

Lorena Norambuena's laboratory studies are focused on endocytosis. Using chemical biology, they have described an *Arabidopsis* lateral root formation mechanism induced by endocytic trafficking through late endosome towards the vacuole, a mechanism distinctive from auxin-driven promotion of lateral root formation.

Patricio Arce's laboratory is interested in viral spread and the effect of viral infections on plants. They use the model plant *Arabidopsis* and the most important fruit plant in Chile, *Vitis vinifera* for these studies. Using methods of functional genetics, they could identify several genes affected by the infection, and at present they are looking for the key regulators of the plant response

Loreto Holuigue's lab research goal is to contribute to understanding plant defense mechanism in response to stress. They study the mechanism of Salicylic Acid (SA) function using *Arabidopsis*. They could identify and perform functional characterization of SA induced defense genes and study the mechanism how SA induce their expression.

Rodrigo Gutierrez' lab goal is to understand how nitrogen signaling intersects with other signaling networks to control plant growth and development. This is essential to improving nitrogen use efficiency in plants or the amino acid content of seeds, important issues for health, agriculture and human nutrition.

Xavier Jordana's lab studies mitochondrial RNA editing. In *Arabidopsis* there are 400 editing sites in mitochondria. Mitochondrial editing is essential for the synthesis of

functional components of the respiratory chain and mitochondrial ribosomes. The specificity is controlled by nuclear factors (PPR proteins) encoded by a very large gene family. This laboratory contributes to the characterization of these genes by isolation mutant plants and analysis of editing defects in those mutants.

Pablo Figueroa's lab research goal is to contribute to understanding the connection between Jasmonate and abiotic stress such as high salinity. Jasmonate (JA) is an essential hormone involved in plant defense against herbivory and in responses to abiotic stress. However, the relationship between the salt stress response and the JA pathway in *Arabidopsis* is not well understood at a molecular and cellular level. In this work, we investigated the activation of JA signaling by NaCl and its effect on primary root growth. We found that JA-responsive JAZ genes were upregulated by salt stress in a COI1-dependent manner in the roots.

Javier Canales's laboratory focusses on research on the molecular mechanisms underlying the response of plants to nutrients, specifically, on the complex interactions between nutrients in metabolic pathways. Plant growth is limited by the availability of nutrients in the soil, particularly by nitrogen and sulfur, which are required in large amounts for plant growth.

Elena Vidal's laboratory studies temporal expression of root-expressed sRNAs during plant development, the gene regulatory networks they control and how these sRNA-controlled networks influence root phenotypical, molecular and physiological response to external cues such as nutrient availability over the plant life cycle.

### Current Arabidopsis Projects

Francisca Blanco. Title. "System-level analysis of *Arabidopsis* –*Pseudomonas syringae* interaction: dual assessment of the transcriptomic and metabolomic responses to unravel bacterial effects leading to resistance or susceptibility through the regulatory node WRKY7/11/17". Funded by Conicyt FONDECYT #1170259, funding period 2017-2020.

Paulo Canessa. Title. "Digging into the light-dependent regulation of a pathogen/host molecular system: understanding the effects of light modulating *Botrytis cinerea* pathogenesis on *Arabidopsis*". Funded by Conicyt FONDECYT #11140678, funding period 2015-2017.

Ariel Orellana. Title: "The role of the UDP-rhamnose transporters in the biosynthesis of rhamnagalacturonan -I and -II in *Arabidopsis*". FONDECYT #1151335. Funded by Conicyt funding period 2014-2018.

Susana Saéz-Aguayo. Title: "Characterization of Pectin Methylesterases (PMEs) and Inhibitor of Pectin Methylesterases (PMEIs) acting on homogalacturonan methylesterification in *Arabidopsis* seed coat mucilage".

FONDECYT #11160787. Funded by Conicyt funding period 2016-2018.  
Michael Handford. Title: "Sorbitol synthesis and its role in abiotic stress tolerance in non-Rosaceae species". Sponsored by Fondecyt 1140527, Anillo ACT-1110, funding period 2014-2018.

Rodrigo Gutiérrez. Howard Hughes Medical Institute International Early Career Scientist. Fondecyt grant Funded by Conicyt, funding period 2014-2017. Science Cloud: An informatic platform for collaborative interdisciplinary research. Funded by middle-size scientific and technological equipment program, FONDEQUIP, Chile. EvoNet. A phylogenomic and systems biology approach to identify genes underlying plant survival in marginal, low-N soils. In collaboration with Gloria Coruzzi (New York University). Funded by Department of Energy, USA 2015-2020. FONDAP Center for Genome Regulation (<http://www.genomacrg.cl/>). Funded by Conicyt, funding period 2016-2020. Millennium Nucleus Center for Plant Systems and Synthetic Biology ([www.genomicavegetal.cl](http://www.genomicavegetal.cl/)), Funded by ICM period 2015-2017.

Loreto Holuigue. Title: "Study Of The Mechanisms That Regulate Salicylic Acid Levels And Functions In The Redox Modulation Of Defense Responses Against Biotic And Abiotic Stress In *Arabidopsis*". Funded by Conicyt FONDECYT #1141202, funding period 2014-2018.

Xavier Jordana. Title: "Mitochondrial Biogenesis and Function In Plants: Insights Into The Role Of Respiratory Complex Ii, Sirtuins And Pentatricopeptide Repeat Proteins". Funded by Conicyt FONDECYT #1141197, funding period 2014-2018.

Hannetz Roschtardt. Title: "Insights into iron homeostasis in *Arabidopsis* seed production". Funded by Conicyt FONDECYT 1160334, funding period 2016-2019.  
Javier Canales. Title: "Uncovering gene regulatory networks involved in the crosstalk between sulfur and nitrogen nutrition in *Arabidopsis*". FONDECYT n°11150070. Funded by Conicyt funding period 2015-2019.

Elena Vidal. Title: "Identification of endogenous root small RNA-controlled regulatory networks expressed during *Arabidopsis* vegetative development". FONDECYT. Funded by Conicyt funding period 2017-2020.

### Outlook for Arabidopsis Research

Our research community is very small as can be easily deduced from the previous section. However, the few groups are very active in research and training. The main research focus is on metabolism and responses to environmental cues (abiotic and biotic). In many instances, there are close ties to the Chilean industry and research groups use *Arabidopsis* and some other plant model systems that are of interest to the local economy (e.g. grapes, tomatoes, fruit trees). We believe this will

continue to be the case in coming years with not much space to grow in terms of number of independent groups or topics.

Chile is also suffering major changes in the way Science and Technology is conducted at the government level, which introduces uncertainties. It is difficult to foresee how research will change in the upcoming years because of these changes. For example, the President recently approved creation of the Ministry for Science and Technology. How this will impact science research direction and funding possibilities is unknown at this stage, but we certainly all hope it will be for the best.

### Road Map Related Activities

#### Tools and Resources

Summary: GENIUS is a user-friendly web server that uses a novel machine learning algorithm to infer functional gene networks focused on specific genes and experimental conditions that are relevant to biological functions of interest. These functions may have different levels of complexity, from specific biological processes to complex traits that involve several interacting processes. GENIUS also enriches the network with new genes related to the biological function of interest, with accuracies comparable to highly discriminative Support Vector Machine methods. Availability and Implementation: GENIUS currently supports eight model organisms and is freely available for public use: <http://networks.bio.puc.cl/genius>. Contact: [genius.psbl@gmail.com](mailto:genius.psbl@gmail.com)

Puelma T, Araus V, Canales J, Vidal EA, Cabello JM, Soto A, Gutiérrez RA (2016) GENIUS: web server to predict local gene networks and key genes for biological functions. *Bioinformatics*.19. pii: btw702.

#### Outreach Activities

December 10th, 2016- "Mitochondrial metabolism in the regulation of growth and abiotic stress tolerance" Guest: Dr. Wagner L. Araújo (Universidade Federal de Vicosa, Minas Gerais, Brazil). Organizers: Dr. Andrea Miyasaka (Universidad Andres Bello). Workshop "International Plant Biology Course 2016". November 25th, 2016- Plant Nutrition  
December 5th, 2016- Plant Development  
December 6th, 2016- Environmental impact of genetically engineered crops.

#### Conferences and Workshops

November 28th to December 1st, 2016- Second Meeting of the Chilean Society of Plant Biologist (XI Chilean Plant Biology Meeting)

As it is now a tradition, the last year conference consisting of sessions ranging across plant sciences: Plant Genome Regulation, Cell and Developmental Biology, Metabolism and Natural Products, Biotic/Abiotic Stress, Genetic Resources and Plant Breeding. Attendees at our conference

are primarily students, young scientists and faculty from major Universities and research institutes in Chile. The last year, the XI ReBiVe, have around 220 attendees.

The scientific program featured a list of 6 speakers (one opening lecture, 5 plenary lectures, 20 invited, as well as another 13 selected speakers for concurrent sessions), covering almost all the disciplines of plant biology research. Nearly 250 abstracts have been submitted to the Meeting. Nearly 180 research M.Sc. or Ph.D. students are among the participants who with their great enthusiasm and hard work will be the future world leaders of our research field. Organizers: Chilean Society of Plant Biologist

#### Selected Publications

Araus V, Vidal EA, Puelma T, Alamos S, Mieulet D, Guiderdoni E, Gutiérrez RA. Members of BTB Gene Family of Scaffold Proteins Suppress Nitrate Uptake and Nitrogen Use Efficiency. *Plant Physiol.* 2016 Jun;171(2):1523-32. doi: [10.1104/pp.15.01731](https://doi.org/10.1104/pp.15.01731).

Rodríguez-Furlán C, Salinas-Grenet H, Sandoval O, Arraño-Salinas P, Soto-Alvear S, Orellana A, Blanco-Herrera F. The root hair specific SYP123 regulates the localization of cell Wall components and contributes to rhizobacterial priming of induced systemic resistance. *Front Plant Sci.* 2016 Jul 26;7:1081. doi: [10.3389/fpls.2016.01081](https://doi.org/10.3389/fpls.2016.01081).

Saez-Aguayo S, Rautengarten C, Temple H, Sanhueza D, Ejsmentewicz T, Sandoval-Ibañez O, Doñas D, Parra-Rojas JP, Ebert B, Lehner A, Mollet JC, Dupree P, Scheller HV, Heazlewood JL, Reyes FC, Orellana A. UUAT1 Is a Golgi-Localized UDP-Uronic Acid Transporter That Modulates the Polysaccharide Composition of Arabidopsis Seed Mucilage. *Plant Cell.* 2017 Jan; 29(1):129-143. doi: [10.1105/tpc.16.00465](https://doi.org/10.1105/tpc.16.00465).

Timmermann T, Armijo G, Donoso RA, Seguel A, Holuigue L, Gonzalez B. Paraburkholderia phytofirmans PsJN protects Arabidopsis against a virulent strain of Pseudomonas syringae through the activation of induced resistance. *Mol Plant Microbe Interact.* 2017 Jan 24. doi: [10.1094/MPMI-09-16-0192-R](https://doi.org/10.1094/MPMI-09-16-0192-R).

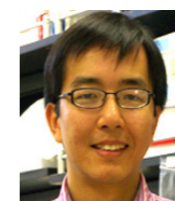
Valenzuela CE, Acevedo-Acevedo O, Miranda GS, Vergara-Barros P, Holuigue L, Figueroa CR, Figueroa PM. Salt stress response triggers activation of the jasmonate signaling pathway leading to inhibition of cell elongation in Arabidopsis primary roots. *J Exp Bot.* 2016 Jul; 67(14):4209-20. doi: [10.1093/jxb/erw202](https://doi.org/10.1093/jxb/erw202).

#### Major Funding Sources

<http://www.conicyt.cl>  
<http://www.iniciativamilenio.cl/>  
<http://www.corfo.cl>  
<http://www.fia.cl>

## China

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#### General Activities

Arabidopsis research in China is conducted throughout the country. Most Arabidopsis research occurs in Universities, Chinese Academy of Sciences (CAS) Institutes, and Chinese Academy of Agricultural Sciences Institutes. There are a significant number of labs mainly work on Arabidopsis, and use it as a model for discovery. However, more labs use Arabidopsis as a supplement to crop species, i.e. as a proxy to translational research. As a consequence, Arabidopsis research in China encompasses a vast array of topics.

#### Current Arabidopsis Projects

The majority of Chinese Arabidopsis grants are awarded to individual research groups through the National Natural Science Foundation of China (NSFC). In addition, the Ministry of Science and Technology (MOST) funds a number of consortium grants that include Arabidopsis research.

#### Outlook for Arabidopsis Research

NSFC will continue to provide support to research using Arabidopsis as a model for discovery. MOST will further shift its focus toward applied research using crop species. Thus, continuing but limited grant support will be provided to Arabidopsis research in China in the coming years.

#### Road Map Related Activities

#### Tools and Resources

- AHD2.0: Arabidopsis hormone database 2.0 (<http://ahd.cbi.pku.edu.cn/>)  
- PlantGSEA: a gene set enrichment analysis toolkit for plant community (<http://structuralbiology.cau.edu.cn/PlantGSEA/>)  
- PlantLoc: An accurate web server for predicting plant protein subcellular localization by substantiality motif (<http://cal.tongji.edu.cn/PlantLoc/>)  
- PlantTFDB: Plant transcription factor database (<http://planttfdb.cbi.pku.edu.cn/link.php>)  
- PsRobot: Plant small RNA analysis toolbox (<http://omicslab.genetics.ac.cn/psRobot/>)  
- Shoot cell type-specific expression ebrowser (<http://jiaolab.genetics.ac.cn/sa>)

#### Outreach Activities

Arabidopsis research in China is often conducted in labs focusing on crops, making applied plant research often highly connected to Arabidopsis research. Nevertheless,

this is also a reflection of funding focus on crop research. In 2016, CAS and the John Innes Centre of the UK jointly launched the CAS-JIC Centre of Excellence for Plant and Microbial Science (CEPAMS) that brings together three institutes in China and the UK to tackle the global challenges of food security. Research in CEPAMS centers on Arabidopsis research in addition to food crops.

#### Conferences and Workshops

- 1st International Conference on Plant Meristem Biology (Meristem 2016), Tai'an, Shandong, 8-11, June 2016 ([www.meristem2016.org](http://www.meristem2016.org))
- 4th International Conference on Plant Vascular Biology (PVB2016), Shenzhen, Guangdong, 19-23, July 2016 (<http://pvb2016.org/>)
- 2nd Molecular Plant International Symposium: From Genes to Networks, Beijing, 11-14, August 2016 (<http://www.mplant.org/2016symposium/>)
- 2016 National Congress of Plant Biology, Wuhan, Hubei, 9-12, October 2016 (<http://www.ncpb.net/2016/>)
- 5th International Conference on Auxin Research (Auxin 2016), Sanya, Hainan, 20-25, October 2016
- 6th International Conference on Plant Cell Wall Biology (PCWB2017), Dalian, Shenyang, 16-20, 2017 (<http://www.cspb.org.cn/2017/pcwb.asp>)
- 19th International Botanical Congress (IBC2017), Shenzhen, China, July 23 - 29, 2017 (<http://www.ibc2017.cn/>)

#### Selected Publications

- Chen Q, Zhong Y, Wu Y, Liu L, Wang P, Liu R, Cui F, Li Q, Yang X, Fang S, Xie Q (2016) HRD1-mediated ERAD tuning of ER-bound E2 is conserved between plants and mammals. *Nat Plants.* 2:16094.
- Cui X, Lu F, Qiu Q, Zhou B, Gu L, Zhang S, Kang Y, Cui X, Ma X, Yao Q, Ma J, Zhang X, Cao X (2016) REF6 recognizes a specific DNA sequence to demethylate H3K27me3 and regulate organ boundary formation in Arabidopsis. *Nat Genet.* 48(6):694-9.
- Shi H, Shen X, Liu R, Xue C, Wei N, Deng XW, Zhong S (2016) The red light receptor phytochrome B directly enhances substrate-E3 ligase interactions to attenuate ethylene responses. *Dev Cell.* 39(5):597-610.
- Wang T, Liang L, Xue Y, Jia PF, Chen W, Zhang MX, Wang YC, Li HJ, Yang WC (2016) A receptor heteromer mediates the male perception of female attractants in plants. *Nature* 531(7593):241-4.
- Yao R, Ming Z, Yan L, Li S, Wang F, Ma S, Yu C, Yang M, Chen L, Chen L, Li Y, Yan C, Miao D, Sun Z, Yan J, Sun Y, Wang L, Chu J, Fan S, He W, Deng H, Nan F, Li J, Rao Z, Lou Z, Xie D (2016) DWARF14 is a non-canonical hormone receptor for strigolactone. *Nature* 536(7617):469-73.

#### Major Funding Sources

National Natural Science Foundation (NSFC). (<http://www.nsf.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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biology, Charles University" project supported by Ministry of Education of the Czech republic using Arabidopsis as a main model).

CSF projects deal with plant telomere dynamics, cytoskeletal and endomembrane regulators (katanins, formins, gamma tubulin, exocyst) and whole plant physiological context - cytokinin-ethylene cross talk, interaction of light and phytohormonal regulations. Ministry of Education supports work on functions of strigolactones in context of other phytohormones, NRT1.1 function in nutrient sensing and structure of Arabidopsis rDNA loci.

### Outlook

Plant research infrastructure development was funded by the EU funds over the last several years and Arabidopsis driven research is well established and important in the Czech republic, supported both by CSF and Ministry of Education. In coming years Arabidopsis research in Czech republic will be further stably well supported mostly on the individual projects basis.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

BRNO - CEITEC - Central European Institute of Technology Proteomics Core Facility  
<http://www.ceitec.eu/ceitec-mu/proteomics-core-facility/z8>

The Core Facility is part of Czech National Affiliated Centre of INSTRUCT. All CEITEC core facilities are available to external users (academia and companies). Czech and international researchers from universities and research institutes interested in accessing core facilities can benefit from support of CEITEC – open access project funded by the Ministry of Education, Youth and Sports of the Czech Republic.

#### Outreach Activities

OLOMOUC - "Centre of the Region Hana for Biotechnological and Agricultural Research" using Arabidopsis as a fundamental research model also includes The Department of Genetic Resources for Vegetables, Medicinal and Special Plants CRI and keeps a broad collections of genetic resources of vegetables (9,245 accessions), medicinal, aromatic and culinary plants (MAPs, 828 accessions) traditionally grown in the Central Europe and a collection of fungi (mainly morel).  
<http://www.cr-hana.eu/en/research-and-development/research-programs/genetic-resources-of-vegetables-and-special-crops/>

#### Conference and Workshops

Major European plant biology meeting "Plant Biology Europe EPSO/FESPB 2016 Congress" was organized by the Czech plant biology researchers (lead by prof. Jana Albrechtova) in Prague between June 26-30.

### General Activities

#### Research Facilities

In the Czech republic Arabidopsis research is focused mostly on the three major areas - cell biology, plant physiology - esp.plant growth regulators biology, developmental biology and cytogenetics/genome biology. Traditional centers of experimental plant research exist at the universities and institutes of the Academy of Sciences of the Czech republic.

In Brno:  
Masaryk University - <https://www.muni.cz/sci/314010>  
Mendel University - <http://ubfr.af.mendelu.cz/en/?lang=en>  
Institute of Biophysics - <http://www.ibp.cz/en/>  
"Central European Institute of Technology (CEITEC)" (<http://www.ceitec.eu/>) in Brno includes big units devoted to genomics and proteomics of plant systems used for studies in cell and developmental biology and cytogenomics.

In Olomouc:  
Palacky university in Olomouc - <http://www.prf.upol.cz/en/menu/departments/>  
Institute of Experimental Botany - <http://www.ueb.cas.cz/en>  
"Centre of the Region Hana for Biotechnological and Agricultural Research" (<http://www.cr-hana.eu/en/index.html>) in Olomouc combines researchers from Palacky University, Crop Research Institute (VURV) and Institute of Experimental Botany ASCR with many links with the commercial sphere.

In České Budejovice  
Institute of Plant Molecular Biology - <http://www.umbr.cas.cz/>  
In Prague  
Institute of Experimental Botany - <http://www.ueb.cas.cz/en>  
Charles University in Prague - <http://kfrserver.natur.cuni.cz/english/index.html>

#### Arabidopsis Projects

Arabidopsis research in the Czech republic is funded mostly on the individual grants basis. In the year 2016 about 15 projects using Arabidopsis as a driving model were supported - 10 by the Czech Science Foundation (GACR) and 5 by the Ministry of Education (in 2014 Department of Experimental plant biology at the Charles University was granted a "Centre of plant experimental

## Denmark

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University of Copenhagen, Department of  
Plant and Environmental Sciences



### General Activities

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) is a new initiative at University of Copenhagen scheduled to be inaugurated in 2017. CPSC will be rooted in the Department of Plant and Environmental Sciences and will include up-to-date facilities for Arabidopsis research.

### Current Arabidopsis Projects

There are no dedicated Arabidopsis consortia or centers in Denmark, but Arabidopsis is commonly used by plant biologists as a model organism. The Danish National Research Foundation funds a number of major Centers of Excellence. In one such center Arabidopsis is employed as a model organism: Center for Dynamic Molecular Interactions (Dynamo; directed by Prof. Barbara Ann Halkier).

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.

### Road Map Related Activities

#### Selected Publications

Arribas-Hernández L, Kielbinski LJ, Brodersen P (2016) mRNA Decay of Most Arabidopsis miRNA Targets Requires Slicer Activity of AGO1. *Plant Physiol* 171(4):2620-32.  
Hoffmann RD, Palmgren M (2016) Purifying selection acts on coding and non-coding sequences of paralogous genes in Arabidopsis. *BMC Genomics* 17:456.

Arribas-Hernández L, Marchais A, Poulsen C, Haase B, Hauptmann J, Benes V, Meister G, Brodersen P (2016) The slicer activity of ARGONAUTE1 is required specifically for the phasing, not production, of trans-acting short interfering RNAs in Arabidopsis. *Plant Cell* 28(7):1563-80.

Persson DP, Chen A, Aarts MG, Salt DE, Schjoerring JK, Husted S (2016) Multi-element bioimaging of Arabidopsis roots. *Plant Physiol.* 172(2):835-847.

Olsen LI, Hansen TH, Larue C, Østerberg JT, Hoffmann RD, Liesche J, Krämer U, Surblé S, Cadarsi S, Samson VA, Grolimund D, Husted S, Palmgren M (2016) Mother-plant-mediated pumping of zinc into the developing seed. *Nat Plants* 2(5):16036.

### Selected Publications

Balla, Jozef; Medved'ova, Zuzana; Kalousek, Petr; *et al* (2016) Auxin flow-mediated competition between axillary buds to restore apical dominance *SCIENTIFIC REPORTS* Volume: 6 Article Number: 35955 doi: [10.1038/srep35955](https://doi.org/10.1038/srep35955)

Bloch, Daria; Pleskot, Roman; Pejchar, Premysl (2016) *et al*. Exocyst SEC3 and Phosphoinositides Define Sites of Exocytosis in Pollen Tube Initiation and Growth. *PLANT PHYSIOLOGY* Volume: 172 Issue: 2 Pages: 980-1002 doi: [10.1104/pp.16.00690](https://doi.org/10.1104/pp.16.00690)

Matyasek, Roman; Dobesova, Eva; Huska, Dalibor; *et al*. (2016) Interpopulation hybridization generates meiotically stable rDNA epigenetic variants in allotetraploid *Tragopogon mirus* *PLANT JOURNAL* Volume: 85 Issue: 3 Pages: 362-377 doi: [10.1111/tbj.13110](https://doi.org/10.1111/tbj.13110)

Pavlistova, Veronika; Dvorackova, Martina; Jez, Michal; *et al* (2016) Phenotypic reversion in fas mutants of Arabidopsis by reintroduction of FAS genes: variable recovery of telomeres with major spatial rearrangements and transcriptional reprogramming of 45S rDNA genes *PLANT JOURNAL* Volume: 88 Issue: 3 Pages: 411-424 doi: [10.1111/tbj.13257](https://doi.org/10.1111/tbj.13257)

Pernisova, Marketa; Prat, Tomas; Grones, Peter; *et al*. (2016) Cytokinins influence root gravitropism via differential regulation of auxin transporter expression and localization in Arabidopsis. *NEW PHYTOLOGIST* Volume: 212 Issue: 2 Pages: 497-509. doi: [10.1111/nph.14049](https://doi.org/10.1111/nph.14049)

### 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.

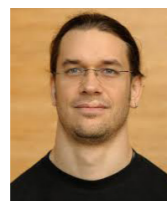
1. Czech Science Foundation/GACR, Prague (<http://www.gacr.cz>)
2. Ministry of Education, Youth and Sports of Czech Republic, Prague (<http://www.msmt.cz/research-and-development-1>)

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 (<https://goo.gl/JPGv1O>)

## Finland

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### General Activities

Research concentrating on Arabidopsis is carried out at several universities in Finland with two main centres at the Universities of Helsinki and Turku. Research at the University of Helsinki focuses on plant stress responses and plant development. Research projects address the role of reactive oxygen species (ROS) as signaling molecules in plants, the role of transcription factors in the stress response, receptor and receptor-like kinase signaling, plant stem cell maintenance, root development, plant-pathogen interactions, as well as the role of the proteasome in the regulation of flowering. A saturating mutant screen is being carried out with the goal to identify components in early stomatal signaling down-stream of apoplast. Causative mutations are being identified by next-generation sequencing techniques.

Groups in Helsinki are also exploiting natural variation of Arabidopsis to identify new regulators of stress tolerance. The flower-related ubiquitin proteasome system project is currently characterizing a collection of about 100 Arabidopsis T-DNA mutants using the new phenotyping facility (<http://blogs.helsinki.fi/nappi-blog/>). Finnish researchers have curated the Arabidopsis RING domain proteins and established the new number to 509 (50 new ones and 31 removed). Researchers in Helsinki use genetics to understand the evolution of crossing barriers between Arabidopsis species. The receptor-ligand signaling group is aiming to integrate plant biochemistry and physiology with evolutionary analysis to facilitate translational research using Arabidopsis as a tool to provide insights into complex gene families for subsequent application in crops.

Research at the University of Turku is centered on stress signaling and photosynthesis. Projects address the role of protein kinases and protein phosphatases as well as the regulation of photosynthesis and the integration of the chloroplastic light harvesting machinery into cell- and plant-wide signaling networks. The Centre of Excellence (CoE) "Molecular Biology of Primary Producers" (2014-2019) funded by the Academy of Finland brings together groups from Turku and Helsinki in order to combine expertise on plant development, stress signaling and photosynthesis. While several plant species and also cyanobacteria are being used Arabidopsis continues to be the most important model for the fundamental research carried out within the Centre of Excellence.

### Current Arabidopsis Projects

Academy of Finland Centre of Excellence "Molecular Biology of Primary Producers" (2014-2019) directed by Prof. Eva-Mari Aro (University of Turku) as chair and Prof. Jaakko Kangasjärvi (University of Helsinki) as vice-chair.

Dr. Ari Pekka Mähönen (University of Helsinki, Institute of Biotechnology): Stem cell dynamics in Arabidopsis root cambium (2013-2018). Funded by the Academy of Finland.

Dr. Michael Wrzaczek (University of Helsinki, Department of Biosciences): Understanding peptide ligands and their receptors in plants (2014-2019). Funded by the Academy of Finland.

The Viikki phenomics facility NAPPI Helsinki unit is partner with the Horizon2020 project EPPN2020 (10M€) and is supported by HiLIFE.

### Outlook for Arabidopsis Research

In Helsinki, the Viikki Plant Science Centre (ViPS) has now been expanded with 36 PIs, over 250 researchers and over 10 million € funding in 2016. Seven new PIs joined ViPS and two retired. While ViPS encompasses research on plants in general, Arabidopsis is one of the core tools used by most research teams to address fundamental questions and unravel molecular mechanisms. Plant Science has been named as a focus and marketing area of the new HiLife centre, with ViPS used as an example of an excellent and successful research program. A plant biology master's degree with heavy involvement of ViPS will begin in the autumn of 2017. The vision of ViPS is to attract internationally visible top level researchers; to stimulate multidisciplinary research environments; to participate in research and infrastructure core facilities also outside the University; to take an active role in post-graduate education.

Research on Arabidopsis or using Arabidopsis as a tool continues to be a major factor in Finnish plant science. Efforts include translation of knowledge from Arabidopsis towards tree research. As many research groups at ViPS use Arabidopsis as their model species there is a heavy emphasis on Arabidopsis research in the Doctoral Programme in Plant Sciences and Arabidopsis continues to be the primary model system to address fundamental research questions in all levels of education.

### Roadmap Related Activities

#### Tools and Resources

A community resource based on the saturating mutant screen for novel components in early stomatal signaling downstream of apoplast ROS is being carried out using next-generation sequencing and is identifying novel regulators of stomatal control but also novel alleles of known components. The group of Ari-Pekka Mähönen

has created a new multisite gateway system for easy construction of inducible cell-type specific expression constructs for Arabidopsis (Siligato *et al.*, 2016).

A software package for the analysis of heterogenous phenotypic data has been created as package in the programming language R during 2016 by Dr. Jarkko Salojärvi to allow analysis of phenotypic results independent of the phenotyping platform.

The Viikki phenomics facility NAPPI Helsinki unit is partnered with the Horizon2020 project EPPN2020 (10M€) and is supported by HiLIFE. The Arabidopsis image based phenotyping system is being developed towards in vitro systems to allow high throughput bioassays and hormone screens.

### Outreach Activities

Plant biology groups working with Arabidopsis at the University of Helsinki continue to introduce school classes to molecular plant biology and the importance of fundamental research using the model organism Arabidopsis. Outreach activities have been done towards high school students on scientific career choice and towards general public on genetically improved organisms.

The Fascination Plants Days continue to be a popular venue to introduce modern plant biology to the general public. NaPPI has partnered with the key international networks, IPPN, EPPN and ESFRI EMPHASIS. Currently efforts are being made to build networks in the Nordic region to address the specific local developments towards bioeconomy and also upon climate change.

### Conferences and Workshops

The 11th Finnish Plant Science Days (Kasvitieteen Päivät) have been held at the University of Turku, Turku, Finland. May 25-26, 2016

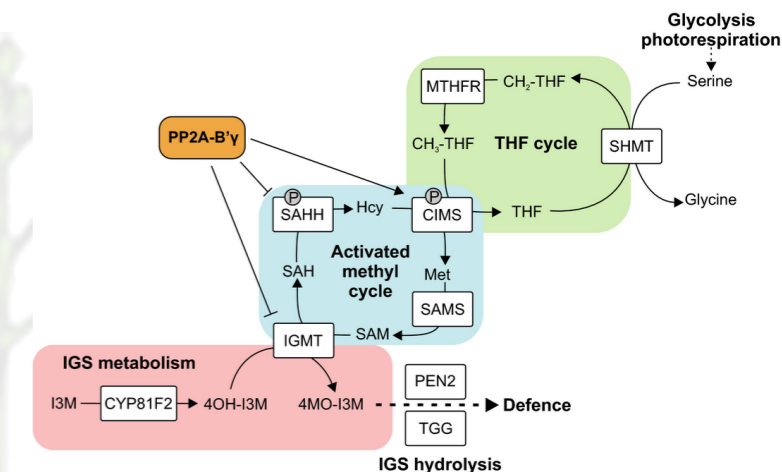
The biannual Finnish-Japanese plant science meeting was held in Saariselkä, Finland in September 2016.

Plant Biology Scandinavia 2017 will be held in Naantali, Finland from August 15-18 2017.

A PhD course on Plant Phenotyping Technologies will be organized in August 2017 by NaPPI and AGFOREE. Finland will host the International Conference on Arabidopsis Research 2018 from June 25-29 2018 in Turku Finland and is organized by researchers from the Universities of Helsinki, Turku and Oulu.

### Selected Publications

Cui, F., Brosché M, Lehtonen MT, Amiryousefi A, Xu E, Punkkinen M, Valkonen JPT, Fujii H and Overmyer K (2016) Dissecting abscisic acid signaling pathways involved in cuticle formation. (2016) *Molecular Plant* 9(6): 926-938.



**Figure 19.** Schematic representation of protein phosphatase 2A regulatory subunit B'Y (PP2A-B'Y) as a regulator of methionine metabolism in Arabidopsis. <http://dx.doi.org/10.1111/tpj.13326>

Hörok H, Sierla M, Töldsepp K, Wang C, Wang YS, Nuhkat M, Valk E, Pechter P, Merilo E, Salojärvi J, Overmyer K, Loog M, Brosché M, Schroeder JI, Kangasjärvi J, Kollist H. (2016) A Dominant Mutation in the HT1 Kinase Uncovers Roles of MAP Kinases and GHR1 in CO<sub>2</sub>-Induced Stomatal Closure. *Plant Cell*. 28(10):2493-2509.

Jakobson L, Vaahtera L, Töldsepp K, Nuhkat M, Wang C, Wang YS, Hörok H, Valk E, Pechter P, Sindarovska Y, Tang J, Xiao C, Xu Y, Gerst Talas U, García-Sosa AT, Kangasjärvi S, Maran U, Remm M, Roelfsema MR, Hu H, Kangasjärvi J, Loog M, Schroeder JI, Kollist H, Brosché M. (2016) Natural Variation in Arabidopsis Cvi-0 Accession Reveals an Important Role of MPK12 in Guard Cell CO<sub>2</sub> Signaling. *PLoS Biology* 14(12):e2000322.

Järvi S, Suorsa M, Tadini L, Ivanauskaite A, Rantala S, Allahverdiyeva Y, Leister D and Aro EM (2016) Thylakoid-bound FtsH proteins facilitate proper biosynthesis of Photosystem I. *Plant Physiology* 171(2): 1333-1343.

Pascual J, Vuorinen K, Overmyer K, Moffatt B, Ravanel S, Glawischnig E, Kangasjärvi S (2017) PP2A-B' modulates foliar trans-methylation capacity and formation of 4-methoxy-indol-3-yl-methyl glucosinolate in Arabidopsis leaves. *Rahikainen M, Trotta A, Alegre S, Plant Journal* 89112-127

### Major Funding Sources

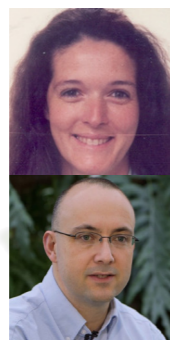
Academy of Finland (<http://www.aka.fi>)  
 University of Helsinki (<http://www.helsinki.fi/university>)  
 Finnish Cultural Foundation (<http://www.skr.fi>)



## France

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### General Activities

#### Research Facilities

Research on Arabidopsis is mainly carried out in a dozen of joint laboratories or research centers supported by research organizations like the Centre National de la Recherche Scientifique (CNRS, with National Institutes of Biological Sciences and Ecology and Environment), the Institut de la Recherche Agronomique (INRA, with divisions of Plant Biology and Breeding, and Plant health and the environment) in association with French Universities and higher education establishments (e.g. Ecole Normale Supérieure, AgroParisTech, or SupAgro).

Among the facilities developed in the context of the program "Investing for the future" (2011-2019), sponsored by the French government, are the Laboratory of Excellence (LabEx) coordinating research activities, training, teaching, innovation and transfer to applied research. Arabidopsis projects were represented in various LabEx (e.g. AGRO in Montpellier or MitoCross and NetRNA in Strasbourg).

Two LabEx, fully dedicated to plants, include a large number of Arabidopsis teams; the largest being the Saclay Plant Science LabEx (SPS, [https://www6.inra.fr/saclay-plant-sciences\\_eng/](https://www6.inra.fr/saclay-plant-sciences_eng/)) that develop research activities in genetic, molecular and cellular mechanisms that control plant physiology and development, as well as their interactions with fluctuating biotic or abiotic environments; the second is the LabEx is TULIP that networks 5 labs in the Toulouse area ([www.labex-tulip.fr](http://www.labex-tulip.fr)). TULIP strengthens the link between communities working on plant biology, agrobiosciences, biodiversity or ecology.

#### Arabidopsis Projects

Current research develops multidisciplinary approaches (from genomics, bioinformatics to biochemistry, genetics, physiology, development, biology, mechanobiology and modelling) and dedicated platforms with expertise in phenotyping, transcriptomics and RNA sequencing, proteomics, lipidomics, metabolomics and translational research.

#### Outlook

Research organizations such as CNRS, INRA or CEA provide recurrent funding to their laboratories in addition

to payment of salaries of permanent researchers and technicians.

The French national research agency, ANR (<http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency/>), provides funding for project-based research. The main calls are dealing with societal issues that do not very well support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is decreasing, although a new ANR call (2016-2017) is dedicated to fundamental mechanisms but still within the frame of the societal challenges.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

- The Arabidopsis Stock Centre at INRA Versailles continuously makes available T-DNA insertion mutants, natural accessions, RIL populations or nearly isogenic lines to the scientific community (<http://www-ijpb.versailles.inra.fr/en/plateformes/cra/index.htm>)

- Two high-throughput automated phenotyping platforms, PHENOSCOPE at Versailles (contact O. Loudet, <http://www.ijpb.versailles.inra.fr/en/plateformes/ppa/index.html>) and PHENOPSIS at Montpellier (contact C. Granier, [www1.montpellier.inra.fr/ibip/lepse/english/ressources/phenopsis.htm](http://www1.montpellier.inra.fr/ibip/lepse/english/ressources/phenopsis.htm)) are available to the community to grow up to 750 or 500 Arabidopsis plants, respectively, under fully controlled environment. PHENOPSIS DB is an information system providing comprehensible resources for the analysis of genotype x environment interactions in Arabidopsis (<http://bioweb.supagro.inra.fr/phenopsis/Accueil.php?lang=En>).

- A French plant phenomic network named PHENOME is also dedicated to high throughput phenotyping for crops ([https://www.phenome-fppn.fr/phenome\\_eng/](https://www.phenome-fppn.fr/phenome_eng/)). Tools for Functional Genomics on Arabidopsis are developed in the different teams of the labex SPS and can be reached through a commun web page ([https://www6.inra.fr/saclay-plant-sciences\\_eng/Infrastructures](https://www6.inra.fr/saclay-plant-sciences_eng/Infrastructures)).

- As part of the French National infrastructure of metabolomics and fluxomics MetaboHub, the laboratory of membrane biogenesis (LBM, Bordeaux) has created a lipidomic platform that brings together instrumentations and expertise dedicated to the analysis of the lipidome and the study of lipids in their diversity. It is dedicated to the study of many organisms, from animals and yeast to plants, including Arabidopsis (<http://www.biomemb.cnrs.fr/spip.php?article128&lang=en>).

- In 2016, the integration of a mass spectrometer Solarix FT-MS to the metabolomic platform at the IBMP offers outstanding facilities for molecule analysis and molecular imaging to scientists (<http://www.ibmp.cnrs.fr/plateformes/metabolomics/?lang=en>).

### Outreach Activities

The Scientific Group of Interest "Plant Biotechnologies" (GIS BV, <http://www.gisbiotechnologiesvertes.com/en/presentation-du-gis-bv>) is built on a large public-private partnership community, which gathers public research institutes (including work performed on model plants as Arabidopsis), seed companies, technical institutes, sector representatives, and competitive clusters.

A national association "Allenvi" (Alliance nationale de recherche pour l'environnement, <http://www.allenvi.fr>) gathers the different research organisms and universities to discuss and suggest scientific priorities to be supported at the national or European levels. Working groups deal with vast themes as "photosynthetic organisms (or plant biology)", "agroecology and soils" or "biodiversity".

### Conference and Workshops

- The SPS Summer School 2016 "From gene expression to genomic network", 2016 July 17th to 22nd - Centre Port Royal, Saint-Lambert

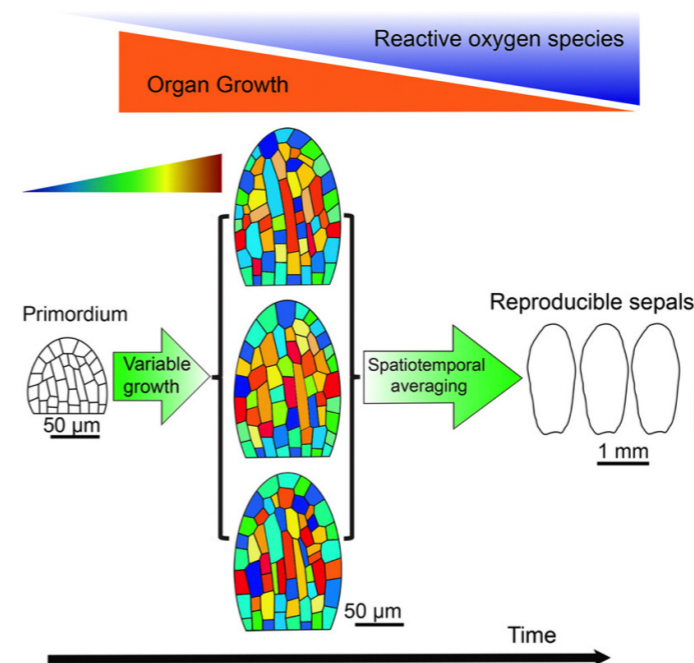
- Montpellier International School on Ion and Water Transport in Plants (MISTRAL) summer school held in July 2016 in Montpellier, France

- TULIP 2016 Summer School in integrative Ecology and Biology, July 2016 9-25

Highlights on coming international events:

- 12th Congress of the International Plant Molecular Biology. 5-10 August 2018 | Montpellier FRANCE <https://www.ipmb2018.org/>

- 23th IPGSA (International Plant Growth Substances Association) meeting. 2019 Paris FRANCE



**Figure 20.** Schematic representation on the role of ROS in the control of cell size. <http://dx.doi.org/10.1016/j.devcel.2016.06.016>

### Selected Publications

Hong, L.L., Dumond, M., Tsugawa, S., Sapala, A., Routier-Kierzkowska, A.L., Zhou, Y., Chen, C., Kiss, A., Zhu, M.Y., Hamant, O., Smith, R.S., Komatsuzaki, T., Li, C.B., Boudaoud, A., and Roeder, A.H.K. (2016). Variable Cell Growth Yields Reproducible Organ Development through Spatiotemporal Averaging. *Developmental Cell* 38, 15-32.

Muller, N.A., Wijnen, C.L., Srinivasan, A., Ryngajllo, M., Ofner, I., Lin, T., Ranjan, A., West, D., Maloof, J.N., Sinha, N.R., Huang, S.W., Zamir, D., and Jimenez-Gomez, J.M. (2016). Domestication selected for deceleration of the circadian clock in cultivated tomato. *Nature Genetics* 48, 89-+.

Petroutsos, D., Tokutsu, R., Maruyama, S., Flori, S., Greiner, A., Magneschi, L., Cusant, L., Kottke, T., Mittag, M., Hegemann, P., Finazzi, G., and Minagawa, J. (2016). A blue-light photoreceptor mediates the feedback regulation of photosynthesis. *Nature* 537, 563-+.

Shahzad, Z., Canut, M., Tournaire-Roux, C., Martiniere, A., Boursiac, Y., Loudet, O., and Maurel, C. (2016). A Potassium-Dependent Oxygen Sensing Pathway Regulates Plant Root Hydraulics. *Cell* 167, 87-+.

Wild, M., Daviere, J.M., Regnault, T., Sakvarelidze-Achard, L., Carrera, E., Diaz, I.L., Cayrel, A., Dubeaux, G., Vert, G., and Achard, P. (2016). Tissue-Specific Regulation of Gibberellin Signaling Fine-Tunes Arabidopsis Iron-Deficiency Responses. *Developmental Cell* 37, 190-200.

### Major Funding Sources

Basic research Research organizations as CNRS, INRA or CEA provide regular funding to a liated research laboratories in addition to payment of salaries of permanent researchers and technicians.

The French national research agency, ANR (<http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency/>), provides funding for project-based research. In 2014, novel rules and a two-step evaluation procedure were developed by the ANR.

Main work programme takes up the nine challenges identified in the "France Europe 2020" national strategic agenda largely based on "Horizon 2020" European framework programme which are not favorable to low TRL (Technology readiness level) thus not to work using the model plant Arabidopsis.

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



## Germany

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### General Activities

### Research Facilities

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

In order to maintain and enhance collaborations and communication, German Arabidopsis researchers count on the coordinating activities of the 'Arabidopsis Functional Genomics Network' (AFGN). Established in 2001 following the completion of the Arabidopsis genome sequencing, the AFGN was funded by the German Science Foundation (DFG) until 2010. Today the AFGN operates under the umbrella of the German Botanical Society (DBG) and its actions include the maintenance of a mailing list for advertising events, job postings, inquiries on seeds, plasmids and resources, as well as any other topic of interest for the plant community in Germany and Europe. A newly designed website has been recently launched and contains a complete description of the AFGN efforts in promoting networking among German researchers (<http://www.dbg-afgn.de/>).

### Arabidopsis Projects

The Arabidopsis functional genomics research is supported by German and European organizations. The DFG is the major funding body via several instruments exemplified below. In 2013 the DFG awarded Klaus Harter with a 3-year grant for the MASC/AFGN coordinator finalized in mid June 2016. German Arabidopsis researchers are also funded via grants awarded by the European Research Council (ERC), Marie Skłodowska-Curie actions, as well as from private initiative.

#### Individual Funding

Currently the DFG provides funding to a total of around 190 individual projects concerning Arabidopsis research. Of these projects, some are funded by the Emmy Noether Programme, some by the Heisenberg Programme, some are research fellowships and the majority are individual research grants.

#### Priority Programmes

Arabidopsis researchers are involved in 3 priority programmes:

SPP 1710 (since 2014): Dynamics of thiol-based redox switches in cellular physiology

SPP 1529 (since 2011): Evolutionary plant solutions to ecological challenges: molecular mechanisms underlying adaptive traits in the Brassicaceae s.l.  
 SPP 1530 (since 2011): Flowering time control: from natural variation to crop improvement

#### Collaborative Research Centers

Arabidopsis researchers are involved in 13 collaborative research centers, out of which 3 mainly focus on Arabidopsis:

SFB 1101 (since 2014): Molecular encoding of specificity in plant processes  
 SFB 973 (since 2012): Priming and memory of organismic responses to stress  
 SFB 648 (since 2005): Molecular mechanisms of information processing in plants

#### Research Training Groups

GRK 2064 (since 2015): Water use efficiency and drought stress responses: from Arabidopsis to Barley  
 GRK 1525 (since 2009): The dynamic response of plants to a changing environment

#### Research Units

FOR 948 (since 2009): Nitrogen uptake, metabolism and remobilization in leaves during plant senescence  
 FOR 1186 (since 2009): Photorespiration: Origins and metabolic integration in interacting compartments  
 FOR 964 (since 2008): Calcium signaling via protein phosphorylation in plant model cell types during environmental stress adaptation

#### Cluster of Excellence

EXC 1028 (since 2012): Cluster of Excellence on Plant Sciences (CEPLAS) - from complex traits towards synthetic modules Excellence on Plant Sciences

#### European Research Council

The ERC currently funds several Arabidopsis research projects in Germany.

#### European Research Area

Arabidopsis functional genomics research is performed within the ERA-CAPS [www.eracaps.org](http://www.eracaps.org) for coordinating action in plant sciences, which is part of the 7th Framework Programme of the European Commission. 26 projects were funded following the first and second ERA-CAPS calls (funded projects). German Arabidopsis researchers participate in 8 of them, out of which 3 are coordinated in Germany:

Plasticity of flowering time in response to environmental signals in Arabidopsis  
 Molecular mechanisms of abiotic stress-induced senescence in plants  
 Decoding ligand-receptor specificities of LYSM-proteins in plant immunity and symbiosis

### Road Map Related Activities

#### Arabidopsis Tools and Resources

The new Arabidopsis Functional Genomics Network webpage (<http://www.dbg-afgn.de/>): updated research projects, funding options, events and outreach activities in Germany. A conference registration and abstract submission platform is now available for the community

1001 Genomes Project (<http://1001genomes.org/>): the "New 1001G Tools" for sequence download and strain identification are since recently online at <http://tools.1001genomes.org/>

German Plant Phenotyping Network ([http://www.dppn.de/dppn/EN/Home/home\\_node.html](http://www.dppn.de/dppn/EN/Home/home_node.html))

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

GABI Primary Database (<http://www.gabipd.org/>)

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

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

#### Outreach Activities

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

Two Arabidopsis related projects are exemplified below.  
 - PLANT-KBBE IV NESTOR (2014 - 2017): Nematode susceptibility targets for a durable resistance  
 - PLANT-KBBE IV DELLA-STRESS (2014 - 2017): Control of the abiotic stress response in plants by DELLA proteins and chemicals

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

- Wissenschaftsscheune, "The Science Barn" (<http://www.wissenschaftsscheune.de/>)  
 - Open House of the Tübingen MPI (<http://www.eb.tuebingen.mpg.de/institute/information-for-the-public.html>)  
 - Frag die Erbse, "Ask the Pea" booklet series ([http://www.mpimp-golm.mpg.de/22409/Frag\\_die\\_Erbse\\_Booklet](http://www.mpimp-golm.mpg.de/22409/Frag_die_Erbse_Booklet))

### Conference and Workshops

- Botanikertagung Kiel: 17-21 September 2017  
 - N-term 2017 - Proteostasis via the N-terminus, Halle ([nterm2017.org](http://nterm2017.org)): 11-13 September 2017  
 - 3rd Summer Academy in Plant Molecular Biology, Heiligkreuztal ([www.3rdsummeracademy.de](http://www.3rdsummeracademy.de)): 10-12 July 2017  
 - Plant Science Student Conference (<http://msbi.ipb-halle.de/pssc2017/>): 6-19 June 2017  
 - Conference Molecular Biology of Plants, Dabringhausen (<http://pflanzen-molekularbiologie.de/tagung-molekularbiologie-der-pflanzen.html>): 21-24 February 2017  
 - 10th Tri-National Arabidopsis Meeting: 14-16 September 2016, Vienna, Austria (<https://tnam.gmi.oeaw.ac.at/>)  
 - 22nd International Symposium on Plant Lipids: 03-08 July 2016, Göttingen (<http://www.eurofedlipid.org/meetings/goettingen2016/>)  
 - 1st SFB 1101 Symposium: 04-06 April 2016, Tübingen (<https://www.uni-tuebingen.de/en/research/core-research/collaborative-research-centers/sfb-1101/sfb-1101-1st-symposium.html>)

### Selected Publications

German Arabidopsis researchers were involved in over 400 publications since last year's report (search at NCBI using "Arabidopsis"[All Fields] AND "Germany"[Affiliation] AND "2017/03/20"[Date - Publication] : "3000"[Date - Publication]). Highlights are listed below.

Faden F, Ramezani T, Mielke S, Almudi I, Nairz K, Froehlich MS, Hoeckendorf J, Brandt W, Dohmen RJ, Schnittger A, Dissmeyer N (2016). Phenotypes on demand via switchable target protein degradation in multicellular organisms. *Nat. Comm.* 22;7:12202.

Hegenauer V, Furst U, Kaiser B, Smoker M, Zipfel C, Felix G, Stahl M, Albert M (2016). Detection of the plant parasite *Cuscuta reflexa* by a tomato cell surface receptor. *Science* 353, 478-481.

Schardon K, Hohl M, Graff L, Schulze W, Pfannstiel J, Stintzi A, Schaller A (2016). Precursor processing for plant peptide hormone maturation by subtilisin-like serine proteinases. *Science* 354, 1594-1597.

Von Wangenheim D, Fangerau J, Schmitz A, Smith RS, Leitte H, Stelzer EHK, Maizel A (2016). Rules and self-organizing properties of post-embryonic plant organ cell division patterns. *Curr. Biol.* 26, 439-449.

### Major Funding Sources

The German Science Foundation (DFG) is the major source financing Arabidopsis research in Germany (<http://www.dfg.de/en/index.jsp>). Contact: Catherine Kistner: [catherine.kistner@dfg.de](mailto:catherine.kistner@dfg.de)



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### General Activities

### Research Facilities

The major areas of research interest in India are: molecular processes involved in shoot and root development, leaf patterning, plant pathogen interaction, abiotic stress, light, hormone and sugar signaling.

The leading research centres in India on Arabidopsis continue to be:

- CCMB, Hyderabad
- IISc, Bangalore
- CCMB, Hyderabad
- NIT, Durgapur
- University of Delhi South Campus
- NIPGR, New Delhi
- NRCPB, New Delhi
- JNU, New Delhi
- IHBT, Palampur
- IISER, Thiruvananthapuram
- IISER, Mohali
- IISER, Bhopal
- IIT, Roorkee
- NCBS, Bangalore
- NISER, Bhubaneswar

Government agencies such as the Department of Biotechnology, the Council for Scientific and Industrial Research, Department of Atomic Energy, the Indian council for Agricultural Research, University Grants Commission and the Department of Science and Technology fund most of the projects as competitive grants to an individual or a group of collaborators across different institutes.

### Arabidopsis Projects

Some of the projects that were awarded by different funding agencies in 2016 are:

Dr. Sourav Datta (IISER, Bhopal); Study of root hair specific MATE transporters to engineer low phosphate and acid soil tolerance in plants. Department of Science and Technology, Govt. of India.

Two projects were awarded to Dr AshveryaLaxmi (NIPGR, New Delhi); (i) To study the role of glucose and its interaction with hormones in controlling shade stress



response in Arabidopsis and tomato and (ii) To study the interaction between glucose and salicylic acid signal transduction pathway in model plant Arabidopsis; both funded by the Department of Biotechnology, Govt. of India.

Dr. Mukesh Lodha (CSIR-CCMB, Hyderabad); Roles of cis regulatory motifs of SHOOT MERISTEMLESS (STM) and chromatin modifying factors in evolution of leaf complexity in plants, funded by the Department of Biotechnology, Govt. of India.

Prof. Asis Nandi (JNU, New Delhi); Interconnection between thermal acquired tolerance and systemic acquired resistance in plants. Funded by the UGC under Indo-Israel programme.

Prof. Sudip Chattopadhyay (NIT, Durgapur); Investigation of the modulation of transcriptional regulation of CAM7 by COP1 and Ca<sup>++</sup>/Mg<sup>++</sup> during Arabidopsis seedling development; funded by the Department of Science and Technology, Govt. of India.

Dr Shri Ram Yadav (IIT, Roorkee); Functional divergence of genetic regulation of ARs between dicot (Arabidopsis) and monocot (rice) model species, funded by the Department of Science and Technology, Government of India.

### Outlook

Although, Arabidopsis is being used as a model system for functional validation of genes identified from the heterologous plant by several groups, funds available for fundamental and basic research on Arabidopsis *per se* are very meager. The bias of funding agencies towards supporting applied research is very evident.

Currently, the policy and planning issues of various scientific bodies of the government of India are under a major review. Hopefully, the policy makers will come out with clear directives to support both fundamental and applied research.

### Road Map Related Activities

### Arabidopsis Tools and Resources

Jagreet Kaur's lab (University of Delhi, South Campus), using traditional genetic mapping and a whole genome association mapping has identified two major *Alternaria brassicae* resistance-conferring loci in Arabidopsis. It may be useful in breeding for resistance against this fungal pathogen in allied species.

### Outreach Activities

As stated in previous years, more than a dozen established researchers working on Arabidopsis meet every year to share their work and exchange ideas. This forum is open to graduate students and post-docs, as also others who wish to learn about the fine nuances in handling Arabidopsis as a model system. In other National/International

conferences that are organized in the country, several papers are presented dealing with Arabidopsis work, appreciating its utility in functional genomic studies.

### Conference and Workshops

Although many different conferences were organized but the one where there was greater coverage of Arabidopsis research was:

"National Symposium on "Challenges in Crop Physiology Research: From Molecular to Whole Plant" organized by the Indian Society of Plant Physiology at UAS, Bangalore, in December 2016.

### Selected Publications

Challa K. R., Aggarwal P., Nath U. (2016). Activation of YUCCA5 by the transcription factor TCP4 integrates developmental and environmental signals to promote hypocotyl elongation in Arabidopsis. *Plant Cell* 28: 2117–2130. [10.1105/tpc.16.00360](https://doi.org/10.1105/tpc.16.00360)

Kumar, S., Mazumder, M., Gupta, N., Chattopadhyay, S., and Gourinath, S. (2016). Crystal structure of Arabidopsis calmodulin7 and insight into its mode of DNA binding. *FEBS Letter* 590: 3029-3039.

Ram, H., Jain, M., Singh, M. and Chattopadhyay, S. (2016). Functional relationship of GBF1 with HY5 and HYH in genome-wide gene expression in Arabidopsis. *Plant Mol Biol Rep.* 34:211-220.

Rajarammohan, S., Kumar, A., Gupta, V., Pental, D., Pradhan, A K. and Kaur, J (2017) Genetic architecture of resistance to *Alternaria brassicae* in Arabidopsis: QTL Mapping reveals two major resistance-conferring loci. *Front. Plant Sci.* 8: 260. doi: [10.3389/fpls.2017.00260](https://doi.org/10.3389/fpls.2017.00260).

Roy S, Nandi AK. (2017) Arabidopsis methionine sulfoxidereductase B8 influences stress-induced cell death and effector-triggered immunity. *Plant Mol Biol.* 93:109-20.

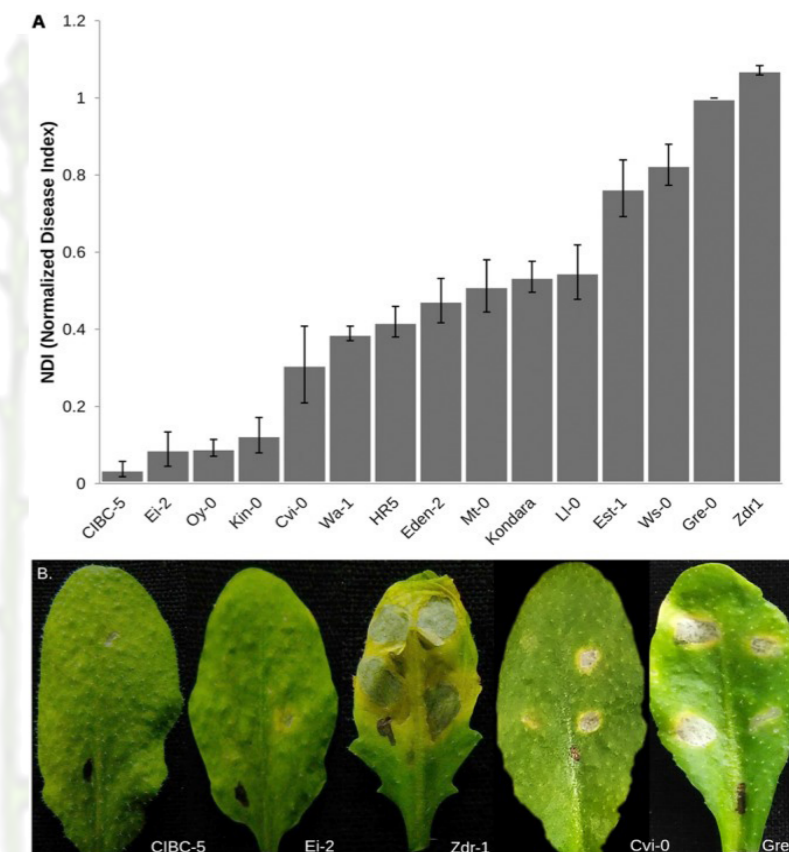
### Major Funding Sources

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/ser-index.htm>

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/vv>



**Figure 21.** Phenotypic variation in response to *A. brassicae* in 15 different accessions of Arabidopsis <http://dx.doi.org/10.3389/fpls.2017.00260>

## Ireland

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### General Activities

### Research Facilities

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 in Ireland.

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

1. Prof Charles Spillane, Genetics and Biotechnology Lab, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway (NUIG), Ireland.

2. Dr. Ronan Sulpice, Plant Systems Biology Lab, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway (NUIG), Ireland.

3. Dr. Sara Farrona, Plant Developmental Epigenetics Lab, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway (NUIG), Ireland.

4. Dr. Zoe Popper, Plant Cell Wall Lab, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway (NUIG), 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. Marcel Jansen, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.

10. Prof. Astrid Wingler, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.

11. Dr. Fuquan Liu, School of Biological Sciences, Queens University Belfast, Northern Ireland.

12. Dr. Emmanuelle Graciet, School of Biology, National University of Ireland Maynooth, Ireland.

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

### Arabidopsis Projects

There is no core funding for Arabidopsis research in Ireland. All research projects are externally funded from research grants.

A number of projects have been (or are) funded by Science Foundation Ireland on translational Arabidopsis research (e.g. Doohan, Farrona, Graciet, Spillane, Wellmer labs).

### Outlook

The Arabidopsis research community in Ireland faces major challenges to sustain fundamental research using Arabidopsis as national funding agencies have made a deliberate shift towards applied and translational research that is nearer-to-market. Greater integration of Arabidopsis research groups into EU and international research initiatives would be necessary to sustain Arabidopsis research activities in Ireland that are of a fundamental nature.

### Road Map Related Activities

### Arabidopsis Tools and Resources

The lab of Prof. Charles Spillane has conducted collecting missions for Arabidopsis accessions across Ireland, and established a low-cost phenotyping platform for analysing Arabidopsis growth.

The following Methods have been developed for Arabidopsis:

Kacprzyk, J. and McCabe, P.F., 2015. A root hair assay to expedite cell death research. *Plant Cell Expansion: Methods and Protocols*, pp.73-82.

McKeown, P.C., Fort, A. and Spillane, C., 2014. Analysis of genomic imprinting by quantitative allele-specific expression by pyrosequencing®. *Plant Epigenetics and Epigenomics: Methods and Protocols*, pp.85-104.

### Conference and Workshops

The 1st Irish Arabidopsis Meeting was held in NUI Galway in June 2014, with the 2nd Irish Arabidopsis Meeting held in Maynooth University in September 2015. The 3rd Irish Arabidopsis Meeting is expected to be held in September 2017.

### Selected Publications

de Marchi R, Sorel M, Mooney B, Fudal I, Goslin K, Kwasniewska K, Ryan PT, Pfalz M, Kroymann J, Pollmann S, Feechan A, Wellmer F, Rivas S, Graciet E., 2016. The N-end rule pathway regulates pathogen responses in plants. *Scientific reports*, 6.

Drost, H.G., Bellstädt, J., Ó'maoléidigh, D.S., Silva, A.T., Gabel, A., Weinholdt, C., Ryan, P.T., Dekkers, B.J., Bentsink, L., Hilhorst, H.W. and Ligterink, W., 2016. Post-embryonic hourglass patterns mark ontogenetic transitions in plant development. *Molecular biology and evolution*, 33(5), pp.1158-1163.

Flis, A., Sulpice, R., Seaton, D.D., Ivakov, A.A., Liput, M., Abel, C., Millar, A.J. and Stitt, M., 2016. Photoperiod-dependent changes in the phase of core clock transcripts and global transcriptional outputs at dawn and dusk in Arabidopsis. *Plant, cell & environment*, 39(9), pp.1955-1981.

Fort, A., Ryder, P., McKeown, P.C., Wijnen, C., Aarts, M.G., Sulpice, R. and Spillane, C., 2016. Disaggregating polyploidy, parental genome dosage and hybridity contributions to heterosis in Arabidopsis. *New Phytologist*, 209(2), pp.590-599.

Goñi, Oscar, Antoine Fort, Patrick Quille, Peter C. McKeown, Charles Spillane, and Shane O'Connell. "Comparative Transcriptome Analysis of Two Ascophyllum nodosum Extract Biostimulants: Same Seaweed but Different." *Journal of agricultural and food chemistry* 64, no. 14 (2016): 2980-2989.

Ryder, P., McHale, M., Fort, A. and Spillane, C., 2017. Generation of stable nulliplex autopolyploid lines of Arabidopsis using CRISPR/Cas9 genome editing. *Plant Cell Reports*, pp.1-4.

May, R.L., Warner, S. and Wingler, A., 2017. Classification of intra-specific variation in plant functional strategies reveals adaptation to climate. *Annals of botany*.

Shtein, I., Shelef, Y., Marom, Z., Zelinger, E., Schwartz, A., Popper, Z.A., Bar-On, B. and Harpaz-Saad, S., 2017. Stomatal cell wall composition: distinctive structural patterns associated with different phylogenetic groups. *Annals of botany*, 119(6), pp.1021-1033.

Tabib, A., Vishwanathan, S., Seleznev, A., McKeown, P.C., Downing, T., Dent, C., Sanchez-Bermejo, E., Colling, L., Spillane, C. and Balasubramanian, S., 2016. A polynucleotide repeat expansion causing temperature-sensitivity persists in wild Irish accessions of Arabidopsis. *Frontiers in Plant Science*, 7.

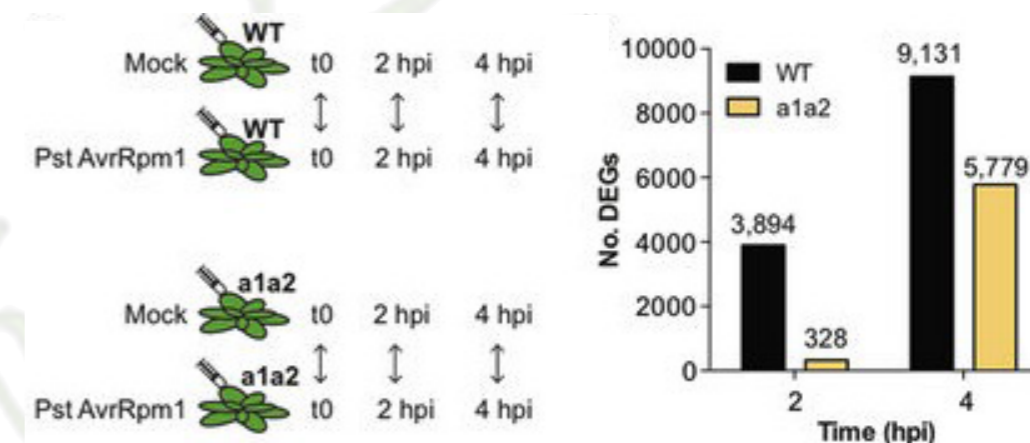
Liu, X., Wolfe, R., Welch, L.R., Domozych, D.S.,

Popper, Z.A. and Showalter, A.M., 2016. Bioinformatic identification and analysis of extensins in the plant kingdom. *PLoS one*, 11(2), p.e0150177.

### Major Funding Sources

Science Foundation Ireland ([www.sfi.ie](http://www.sfi.ie)) is currently the only funding source for Arabidopsis projects in Ireland.

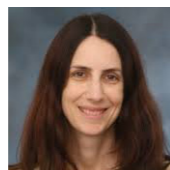
A number of projects have been (or are) funded by Science Foundation Ireland on translational Arabidopsis research (e.g. Doohan, Farrona, Graciet, Spillane, Wellmer labs).



**Figure 22** Experimental design of a transcriptomics experiment performed to compare the gene expression changes in wild-type and *ate1 ate2 (a1a2)* plants following inoculation with Pst AvrRpm1. <http://dx.doi.org/10.1038/srep26020>

## Israel

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5. Laying a foundation for a computational perspective of plant behavior under a changing environment, and predictions of selected genetic and environmental perturbations that will bring the plant to a desired metabolic or functional state. (<http://www.icore-plants.tau.ac.il/>). Effective funding, until 2021.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

In the context of the I-CORE, two research facilities have been established (<http://www.icore-plants.tau.ac.il/infrastructure/>):

(1) High throughput plant phenomics system was established At Tel Aviv University with the ability to monitor: Morphometrics (RGB), water content (Near Infra Red camera), chlorophyll fluorescence (FluoCaM) and Fluorescent proteins (e.g. GFP). The system was designed and manufactured by Photon Systems Instruments (PSI, Czech Republic).

(2) Center for simulating and analyzing effects of climate change on whole plant functional phenotyping was established at the Faculty of Agriculture of the Hebrew University (Rehovot). The new greenhouse allows simultaneous soil-plant-atmosphere measurements of all of the plants in the array in an easy-to-use, non-destructive and non-invasive manner, allowing for the genuine comparison of different plants and treatments. The system calculates the following physiological traits of the whole plant: daily biomass gain, daily water loss, water-use efficiency, transpiration rate, stomatal conductance, root water flux, relative water content and individual stress index (DRI).

In Bar Ilan University:

Use of chromosome conformation capture technology (3C, 4C and Hi-C) to unravel the folding patterns of the genome, to catalogue genes with their distant regulatory loci, and to characterize their nuclear spatial environment.

#### Outreach Activities

- > Summer course 2016: Plant Epigenetics and Gene Expression in Changing Environments.
- > Summer course 2017: Plant Metabolomics: Advances, Applications, and Techniques.

#### Conference and Workshops

1. Israeli Society of Plant Sciences (ISPS) Meeting. Sept, 2016, Tel Aviv
2. CropSym: Crop Abiotic Stress workshop. May 16-18, 2017, Faculty of Agriculture of the Hebrew University (Rehovot).

#### Selected Publications

About 60 research articles employing Arabidopsis were published since the beginning of 2016 and until March 2017.

#### Major Funding Sources

The Israel Science Foundation (ISF). <http://www.isf.org.il/>

Areas of research include plant physiology, biochemistry, development and genomics. Research labs using Arabidopsis established by young PIs:

1. Dr. Yasmine Meroz, School of Plant Sciences and Food Security at Tel Aviv University (postdoctoral training in the lab of L. Mahadevan, Harvard University, USA).
2. Dr. Michal Lieberman Lazarovich, Ph.D. (Postdoctoral training in the lab of in the lab of Prof. Jerzy Paszkowski, University of Geneva, Switzerland)
3. Dr. Tamar Avin-Wittenberg, The Hebrew University of Jerusalem, (postdoctoral training in the lab of Dr. Alisdair Fernie, Max Planck Institute of Molecular Plant Physiology, Germany).

#### Arabidopsis Projects

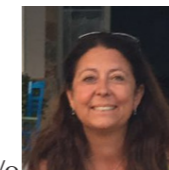
The Israeli Centers of Research Excellence (I-CORE) program is aimed at fundamentally strengthening the long term positioning of Israel's academic research, promote national and international research collaborations, and to assist in the recruitment of new excellent researchers, by the gradual establishment of "Centers of Excellence" – leading research centers specializing in innovative and groundbreaking research in a range of fields.

The I-CORE PLANT ADAPTATION TO CHANGING ENVIRONMENT, includes Arabidopsis and crop research, brings together plant biologists and computer scientists with the following research approaches:

1. Deciphering the genetic and epigenetic factors affecting short- and long-term (trans-generational) phenotypic plasticity and adaptation to environmental changes.
2. Elucidating the mechanisms underlying the interactions of the environment with intrinsic developmental programs, and the role of phytohormones in stress responses.
3. Elucidating the key factors regulating plant metabolism and catabolism under stress with focus on the switch-points driving cell death versus cell vitality.
4. Dynamics of cell structures (cell wall, membranes, organelles, and protein complexes) and their role in stress responses.

## Italy

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### General Activities

#### Arabidopsis Research Facilities

A few Italian groups, mainly consisting of laboratories in the University of Rome, Milan, Parma and of the CNR (National Research Council) continue to utilize Arabidopsis as a model organism for plant biology research and their results are published in high impact journals. Work is mainly performed in individual laboratories with networks and collaborations. Research is mainly focused on root and flower development, seed germination, xylem differentiation, plant defense responses and plant response to environment.

#### Current Research Projects

The Italian Ministry of Education, University and Research funded:

Large project on "The control of plant root growth: a systems biology approach" awarded to the groups of I. Ruberti (IBPM-CNR, Rome), C. Tonelli (University of Milan) and S. Sabatini/P. Costantino (Sapienza University, Rome); this project is coordinated by Paolo Costantino and involves also other partners performing RNAseq and proteomic analysis (2013-2016);

Project (PRIN 2014-2017) on 'Genetic and epigenetic control of ovule number and fertility in Arabidopsis'. Coordinator Lucia Colombo;

Project FIRB (Futuro in Ricerca 2014-2017) for young researcher. Principal investigator Raffaele Dello Ioio;

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

Local funding from: Sapienza University of Rome (Coordinator Maria Maddalena Altamura); 'Roma Tre' University of Rome, University of Parma, University of Milan (Coordinator: Ignacio Ezquer)

Istituto Pasteur fondazione Cenci Bolognetti, [www.istitutopasteur.it/](http://www.istitutopasteur.it/) has funded a project on 'Study of the role of DAG1 and GAI in embryogenesis and seed germination in Arabidopsis'. Coordinator Paola Vittorioso

(2014-2016). Other funding comes from the EU: ERC grant awarded S. Sabatini/P. Costantino and F. Cervone/G. de Lorenzo, and from MC-IRSES - "The physiology and genetics of fruit formation: from genes to networks" (FRUIT-look) FP7-PEOPLE-2013-IRSES, Coordinator: UNIMI Italy. Period: 2014-2017

### Outlook

Arabidopsis research in Italy is getting little or no financial support. Many programs have limited funding from Universities. New fundings have been obtained by young researchers with dedicated grants. Future work will focus on the continuation of the main research projects while young researchers are developing independent research lines. Many groups are seeking fundings for applied research on crop species.

### Roadmap Related Activities

#### Tools and Resources

Cardarelli/Costantino group unveiled an important developmental role of the anther tissue middle layer in stamen development and Dello Ioio compared the development of Arabidopsis and Cardamine root to understand the genetic basis underlying anatomical differences in plants.

M. Kater/L. Colombo group recent advances point out to the discovery of key genetic and molecular markers for seed and fruit quality

#### Outreach Activities

Several Arabidopsis researchers from Milan and Rome were involved in planning and organizing the Fascination of Plants day under the umbrella of EPSO (European Plant Science Organisation) on May 2016.

M. Kater /L. Colombo have a strong outreach program related to flower, fruit and seed development in the frame European Researcher's night (Meet me Tonight).

#### Conferences and Workshops

Giovanna Serino is the organizer -together with the COST Proteostasis network- of the 2017 ZOMES IX conference on "PCI complexes and Ubiquitin defining a hub for protein homeostasis" ([www.zomesix.com](http://www.zomesix.com)) which took place in Rome in February 2017 and includes many talks focused on Arabidopsis by Internationally renowned speakers.

The Italian Federation of Life Sciences (FISV) in collaboration with the University of Parma organizes the 3rd "PARMA" NANO-DAY, 12-14 July 2017 - An international meeting to bring together students, researchers, enterprises dedicated to nanomaterials and nanotechnologies. It will feature oral presentations on

ecotoxicology and toxicology on model systems, including Arabidopsis

C Tonelli was a keynote speaker at the Gordon Conference "Salt and drought stress" 2016, Lese Diablerets CH

**Selected Publications**

Balanzà V, Roig-Villanova I, Di Marzo M, Masiero S, Colombo L. Seed abscission and fruit dehiscence required for seed dispersal rely on similar genetic networks. *Development*. 2016 Sep 15;143(18):3372-81

Cecchetti V, Celebrin D, Napoli N, Ghelli R, Brunetti P, Costantino P, and Cardarelli M. (2017) An auxin maximum in the middle layer is necessary for stamen and pollen maturation in Arabidopsis *New Phytologist* Feb; 213(3):1194-1207

Ezquer I, Mizzotti C, Nguema-Ona E, Gotté M, Beauzamy L, Viana VE, Dubrulle N, Costa de Oliveira A, Caporali E, Koroney AS, Boudaoud A, Driouich A, Colombo L. The Developmental Regulator SEEDSTICK Controls Structural and Mechanical Properties of the Arabidopsis Seed Coat. *Plant Cell*. 2016 Oct;28(10):2478-2492.

Gan X, Hay A, Kwantes M, Haberer G, Hallab A, Dello Iorio R, Hofhuis H, Pieper B, Cartolano M, Neumann U, Nikolov LA, Song B, Hajheidari M, Briskine R, Kougioumoutzi E, Vlad D, Broholm S, Hein J, Meksem K, Lightfoot D, Shimizu KK, Shimizu-Inatsugi R, Imprialou M, Kudrna D, Wing R, Sato S, Huijser P, Filatov D, Mayer KF, Mott R, Tsiantis M. The *Cardamine hirsuta* genome offers insight into the evolution of morphological diversity. *Nature Plants*. 2016 Oct 31;2(11):16167. doi: 10.1038/nplants.2016.167.

Shu K, Chen Q, Wu Y, Liu R, Zhang H, Wang P, Li Y, Wang S, Tang S, Liu C, Yang W, Cao X, Serino G, Xie Q (2016). ABI4 mediates antagonistic effects of abscisic acid and gibberellins at transcript and protein levels. *Plant Journal*, 85:348-61

**Major Funding Sources**

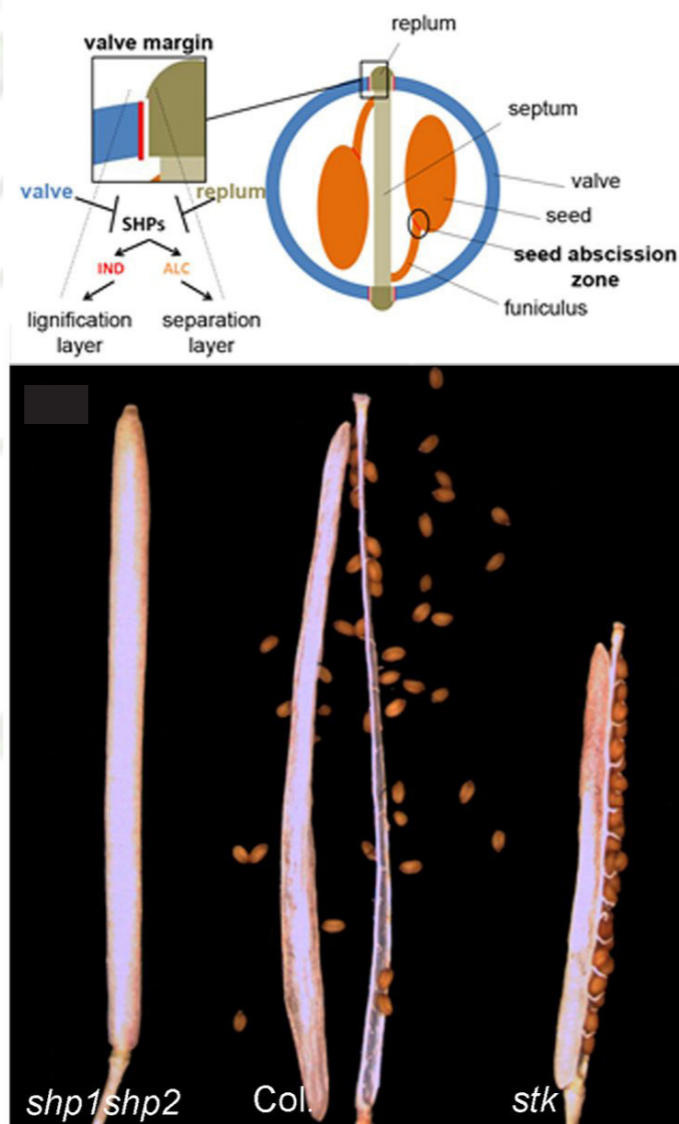
European Commission program "Horizon 2020" (<https://ec.europa.eu/programmes/horizon2020/>).

Italian Ministry of University and Scientific Research ([www.istruzione.it](http://www.istruzione.it))

Institute Pasteur - Cenci Bolognetti Foundation ([www.istitutopasteur.it](http://www.istitutopasteur.it))

Sapienza University, Rome (<http://www.uniroma1.it>)  
Parma University ([www.unipr.it](http://www.unipr.it))

University of Milan ([www.unimi.it](http://www.unimi.it))



**Figure 23** Arabidopsis wild-type and fruit phenotypes from SHAT-TERPROOF 1/2 (*shp1/2*) or SEEDSTOCK (*stk*) mutant plants. <http://dx.doi.org/10.1242/dev.135202>

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David Gifford [david.gifford@riken.jp](mailto:david.gifford@riken.jp)  
RIKEN Center for Sustainable Resource Science



**General Activities**

**Research Facilities**

Coordinated projects continuing in 2016/2017:  
Kazusa DNA Research Institute (<http://www.kazusa.or.jp/e/>) Laboratory of Plant Genomics and Genetics, Plant DNA Analysis Group, Metabolomics Team, Bioresources team, Biomass Team. Genome Informatics Group developed the portal site Plant Genome DataBase Japan PGDBj (<http://pgdbj.jp/?ln=en>) integrating databases related to plant omics studies. Manually curated literature information on DNA markers of 55 plants.

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) (<http://www.csr.riken.jp/en/>) CSRS (Director Kazuo Shinozaki), established in 2013 to conduct basic research integrating plant scientists, chemists and chemical biologists to work for solutions to critical scientific, technical and social issues with special focus on Green Innovation and sustainable production of energy and resources. CSRS contributes to many United Nations 2015 Sustainable Development Goals (SDGs) and COP21 Paris Agreement goals by applied research through interdisciplinary innovation for sustainable production of energy, efficient engineering and production of useful plant biomass, renewable chemical materials and bioplastics, efficient catalysts, as well as crop production under climate change. In addition to Arabidopsis, CSRS uses other plants such as Sorghum, Cassava, Setaria, Brachypodium and others.

RIKEN National Science Institute - BioResource Center (BRC) (<http://epd.brc.riken.jp/en/>), ([plant@brc.riken.jp](http://plant@brc.riken.jp)) The Experimental Plant Division (Masatomo Kobayashi) collects, preserves and distributes plant resources developed in Japan. The project is funded by the Japanese government through the National BioResource Project (NBRP, <http://www.nbrp.jp/index.jsp>). The Arabidopsis resources in RIKEN BRC include seeds (mutants, transgenic lines, and natural accessions), DNA materials (full-length cDNA clones, ORF clones of transcription factors, and TAC clones), and cultured cells (T87 and At wt cell lines). The center also distributes full-length cDNA clones and cultured cells of model plants such as rice, Brachypodium distachyon and tobacco to the international research community.

AIST Advanced Industrial Science and Technology National Institute - BioProduction Research Institute (<https://unit.aist.go.jp/bpri/>) Plant research includes studies of plant gene regulation, plant molecular biology, plant biotechnology, biomaterial production, and genetic resources. Plant Gene Regulation Research Group (Kaoru Suzuki, Nobutaka Mitsuda, Sumire Fujiwara, Masaru Ohme-Takagi and others) (<http://bit.ly/1QlwEjP>) focuses on study of plant transcription factors and related molecules and techniques. Group developed CRES-T gene-silencing and other technologies for functional analysis and engineering of important traits in model and economic plants.

WPI ITbM (<http://www.itbm.nagoya-u.ac.jp/>) World Premier International Research Center (WPI) Institute of Transformative Bio-Molecules (ITbM) of Nagoya University is the first MEXT WPI institute to study plant science. Ambitious full-scale collaboration between synthetic chemists, plant and animal biologists, and theoreticians led by Director Kenichiro Itami, Vice-director Tetsuya Higashiyama and others.

Determining principles in the birth of new plant species: elucidation of lock-and-key molecular systems in sexual reproduction (<http://bit.ly/2mrqD4T>) Project goal to clarify primary mechanism in the birth of new species by revealing a whole picture of molecule-level understanding of "lock-and-keys" in plant reproduction through active interdisciplinary collaborative research. Scientific Research on Innovative Areas MEXT Grant-in Aid Project FY2016-2020. Multi-organization representative: Tetsuya Higashiyama, ITbM/Nagoya University.

Integrative system of autonomous environmental signal recognition and memorization for plant plasticity (<http://www.rs.tus.ac.jp/plantmemory/en/>) Project goal to clarify distributed response of cells and tissues of plants and determine how plants control such information through plant unique whole-organism dynamic signal transduction system in response to environmental stimuli. Scientific Research on Innovative Areas MEXT Grant-in Aid Project FY2015-2019. Multi-organization representative: Toshinori Kinoshita, ITbM/Nagoya University.

Multidimensional Exploration of Logics of Plant Development (MEXT) (2013-2017) (<http://bit.ly/1TyA7Fg>) Project to delineate systems coordinating intercellular and intracellular signals, functions of key differentiation genes, and control of metabolism, under combined efforts of 9 core research groups, 4 supporting facilities/teams, and 19 research groups (2013-2017) using multiple model species. Four facilities/teams assist in metabolomics, use of an Arabidopsis transcription factor library, development of a new model system, *Marchantia polymorpha*, and mathematical modeling. Multidisciplinary collaborative approach will explore unprecedented research directions. Led by Hirokazu Tsukaya.

The Plant Cell Wall as Information Processing System (2012-2017) (<https://www.plantcellwall.jp/en/>) Program goal to elucidate molecular processes for information processing and self-regulation capabilities of the cell wall by understanding molecular mechanisms by which land plants sense and interact with environment via information processing systems in cell walls. Led by Kazuhiko Nishitani, Tohoku University. Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Creation of fundamental technologies contribute to the elucidation and application for the robustness in plants against environmental changes” Started 2015, Core Research for Evolutional Science and Technology (JST-CREST) (<http://bit.ly/1TyzoDT>) coordinated with PRESTO (Sakigake). Goal to establish environmentally-adaptive-plant design systems for stable food supply in age of climate change via highly precise quantitative analysis of environmental response mechanisms of plants, modeling of plant environmental response mechanisms, and evaluation of plant characters modified by sophisticated reconstruction of genes or genotype. At present, nine highly competitive research groups each composed of experts in plant physiology, genetics, genomics, breeding and bioinformatics, are participating in this project. This project will continue to 2022. Led by Satoshi Tabata (Kazusa DNA Research Inst.). CREST is led by Satoshi Tabata (Kazusa DNA Research Inst.). Two PRESTO programs are led by Kiyotaka Okada and Masashi Ninomiya, respectively.

Creation of essential technologies to utilize carbon dioxide as a resource through the enhancement of plant productivity and the exploitation of plant products. Started in 2011, Core Research for Evolutional Science and Technology (JST-CREST) (<http://bit.ly/2217neA>). Goal to create basic technologies to use plant photosynthetic functions and biomass that will enable efficient carbon dioxide utilization. Led by Akira Isogai (Nara Institute of Science and Technology).

JST-ALCA Japan Science and Technology Agency - Advanced Low Carbon Technology Research and Development Program (<http://www.jst.go.jp/alca/en/index.html>) provides competitive funding for research up to ten year period in biotechnology, chemical and energy processes and systems, materials.

JST-NSF “Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low- Carbon Society” (<http://1.usa.gov/1LVBpa>), research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and K. Saito (RIKEN), Oliver Fiehn (Univ. of California at Davis) and M. Arita (NIG).

ERATO Higashiyama Live-Holonics Project (2010-2016) (<http://www.liveholonics.com/en/>) headed by T. Higashiyama, Nagoya University. Project studies intercellular signaling in multicellular organisms with

complete control of cells and molecules under microscope by developing new live-cell analysis technologies.

Japan Advanced Plant Science Research Network (<http://www.psr-net.riken.jp/>) 2011-2017. (RIKEN CSRS) Nine centers of excellence in universities and research institutes support plant research for green innovation. Plant Science Center for Advanced Research Network (PSR-net) ended at the end of 2016. Reviewed subjects applied for in February 2017. After April 2017, system to mainly support research institutions such as joint-use organizations, collaborative research centers and world-class research center programs.

NC-CARP Network of Centers of Carbon Dioxide Resource Studies in Plants (<http://nc-carp.org/index>) Program in GRENE; Green Network of Excellence. Organizer: Shigeru Otani RIKEN CSRS. 2011-2016. Innovation of plant biomass technology by collaboration among Plant Science, Agriculture, Engineering and Chemistry, and education. NC-CARP project ended in March 2016, but the University-Industry Collaborative Consortium decided to continue.

DREB project: Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat supported by MAFF and JIRCAS; (<http://bit.ly/227H1Tp>) (Kazuko Yamaguchi-Shinozaki U. Tokyo, Kazuo Shinozaki RIKEN, Kazuo Nakashima JIRCAS and others of IRRI, CIAT, CIMMYT, Embrapa) After identifying and applying DREB genes in Arabidopsis, DREB gene function in stress tolerance were recognized as well conserved in any important crops. Project develops stress-tolerant soybean, rice and wheat. Recently, transgenic rice lines with Arabidopsis Gols2 gene were shown to produce higher amount of seeds than non-transgenic rice in the dry field conditions.

Advancement of cassava molecular breeding by cutting-edge technologies. RIKEN CSRS Plant Genomic Network Research Team (Motoaki Seki, Yoshinori Utsumi and Hiroki Tokunaga) (<http://pgn.riken.jp/English/>), CIAT (Manabu Ishitani), AGI (Ham Huy Le, Dong Van Nguyen, Vu Anh Nguyen), Yokohama City Univ. (Hiroyuki Tsuji) and NARO (Seiichi Toki)

### Current Arabidopsis Projects

*Kazusa DNA Research Institute*  
Kazusa Metabolomics Database (KOMICS) web portal to databases, tools and other information was developed through plant metabolomics studies of Daisuke Shibata, including integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, co-ex- pressed gene search tools and regulatory network research. (<http://www.kazusa.or.jp/komics/en/>)

*AIST Bioproduction Research Institute, Gene Regulation Research Group*  
CRES-T was applied to more than 1,600 Arabidopsis

transcription factors and most T2 seeds were harvested individually. For transcriptional repressors, the group produced more than 300 VP16-fused constructs and harvested individual T2 seeds. The group also prepared Gateway entry clones of ca. 2,000 transcription factors (without stop codon) in collaboration with M. Matsui group in RIKEN. The group developed yeast one-/two-hybrid library using the entry clones and established high-throughput screening system. (<http://bit.ly/1QlWtEJP>)

*RIKEN National Science Institute - BioResource Center (BRC)*  
SABRE2: database connecting plant EST/Full-Length cDNA Clones with Arabidopsis information. Plant resources with homologous genes are searched, together with related TAIR gene models and annotations, by specifying a Resource ID, a TAIR AGI code or a keyword. All SABRE resources are available from the core facilities of NBRP (National BioResource Project) (<http://sabre.epd.brc.riken.jp/>)

*RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS)*

- Metabolome platform using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi, Tetsuya Sakurai). CSRS established the Arabidopsis metabolomics platform (<http://prime.psc.riken.jp/>), consisting of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics.
- Hormonome platform and RIKEN Plant Hormone Research Network: (Hitoshi Sakakibara, Mitsunori Seo) CSRS established highly sensitive high-throughput phytohormone quantification platform consisting of mass spectrometry-based technology. Platform is conducting a wide range of collaborative research in plant hormone biology (<http://hormones.psc.riken.jp/>)
- Proteome platform: Plant Phosphoproteome Database (RIPP-DB) CSRS (Hirofumi Nakagami, Ken Shirasu) and Keio University (Yasushi Ishihama, Naoyuki Sugiyama) High-throughput shotgun phosphoproteomics tool for plants and phosphorylation site databases (<http://bit.ly/224sjjk>) (<http://pepbase.iab.keio.ac.jp>)
- Phenome platform RIKEN Activation tagging lines Database and Full-length-cDNA-overexpressing (FOX) Arabidopsis lines (M. Matsui) (<http://bit.ly/1WdrX2Z>), Rice FOX Arabidopsis line Database (<http://ricefox.psc.riken.jp/>), RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary (Takashi Kuromori, T. Sakurai, K. Shinozaki) (<http://rarge-v2.psc.riken.jp/>)
- The Chloroplast Function Database II (Fumiyoshi Myouga, K. Shinozaki) Comprehensive database analyzed by combining genotypic and phenotypic multiparametric analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins. (<http://bit.ly/1P2YMty/>)
- Analysis of small Open Reading Frame (Kousuke Hanada, M. Matsui, M. Seki) Identified ~8,000 sORFs with high coding potential in intergenic regions of the Arabidopsis genome.

- MassBank (Masanori Arita, Takaaki Nishioka, K. Saito) Public repository of mass spectral data for sharing spectra among research communities. The data is useful for chemical identification and structure elucidation of metabolites detected by mass spectrometers. (<http://www.massbank.jp/en/about.html>)
- PosMed Positional Medline (Y. Makita, N. Kobayashi, T. Toyoda) Semantic web association study (SWAS) search engine ranks resources including Arabidopsis genes and metabolites, using associations between user-specified phenotypic keywords and resources connected directly or inferentially via a semantic web of biological databases such as MEDLINE, OMIM, pathways, co-expressions, molecular interactions and ontology terms (<http://bit.ly/2qEPFuy>)
- High-throughput genome-wide biochemical analysis using wheat germ cell-free-based protein array technology. The method developed by Proteo-Science Center of Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) (<http://bit.ly/21ssVcQ>) and RIKEN CSRS (M. Seki and K. Shinozaki) is useful for in vitro screening of substrate protein, interacting protein or chemical compound.
- RIPPS (RIKEN Plant Phenotyping System) (K. Shinozaki, Miki Fujita, Kaoru Urano and Takaya Tanabata) Automated system for evaluating plant growth under environmental stress conditions developed by the Gene Discovery Research Group of CSRS. RIPPS provides high-throughput and accurate measurements of plant traits, facilitating understanding of gene function in a wide range of environmental conditions (<http://bit.ly/1sObBEE>)
- PASMET - Prediction, Analysis and Simulation of Metabolic Reaction Networks (Kansuporn Sriyudthsak, Masami Hirai) PASMET is a web-based platform for predicting, modelling and analyzing metabolic systems. Non-commercial and user-friendly tool to assist non-experts in mathematical modelling, in silico computing or programming to work on computational biology (<http://pasmnet.riken.jp/>)
- Plant-PrAS (Plant-Protein Annotation Suite) (A. Kurotani, Y. Yamada, AA. Tokmakov, Y. Kuroda, Y. Fukami, K. Shinozaki, T. Sakurai) Analyzed predicted multiple physicochemical and secondary structural parameters using over 20 analysis tools with whole amino acid sequences from genomes of representative plant species (Arabidopsis, Glycine max, Populus trichocarpa, Oryza sativa, Physcomitrella patens, and Cyanidioschyzon merolae) for which genome sequencing was achieved, and organized those results as Plant-PrAS. (<http://plant-pras.riken.jp/>)
- “Development of Synthetic Promoters for Acceleration of Biomass Production” JST-ALCA project (<http://bit.ly/1SRr7de>) led by Yoshiharu Yamamoto (Gifu Univ.). (<http://bit.ly/2qAm2L8> and <http://bit.ly/2qEmmby>)
- New dataset of Arabidopsis TSS and extended 5’UTR intro for genome annotation, called “Max 5’UTR”, have been released (Tokizawa *et al*, Plant J, 2017).(<http://bit.ly/2my30D8>) (sub. Yoshiharu Yamamoto)

## Road Map Related Activities

### Arabidopsis Tools and Resources

Kazusa DNA Research Institute

- PGDBJ Plant Genome DataBase Japan (<http://pgdbj.jp/?ln=en>)
- Arabidopsis EST Index (<http://bit.ly/2217Ehl>)
- KATANA Kazusa Arabidopsis Annotation Abstract (<http://bit.ly/1M6noqN>)
- TACWeb Database of the transformation-competent bacterial artificial chromosome (TAC) vectors for Arabidopsis (<http://bit.ly/22kE5CY>)
- KOMICS Kazusa Metabolomics Database portal (<http://bit.ly/1QWjzok>)
- KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (<http://kpv.kazusa.or.jp/>)
- MassBase: a plant metabolome database (<http://bit.ly/1Rlf9Dd>)
- KomicMarket Kazusa omics data market: metabolite eaks annotations database (<http://bit.ly/1YY8dly>)
- MS-MS Fragment Viewer (<http://bit.ly/1QWjPUm>)
- KAGIANA co-expressed gene search tool (<http://bit.ly/253kFEO>)
- CoP co-expressed gene search tool (<http://bit.ly/2qABGpP>)
- RnR regulatory network research (<http://bit.ly/2qAEpzl>)
- MFSearcher molecular formula searcher (<http://bit.ly/1RN2BFp>)

Gifu University

- Plant Promoter Database, ppdb (<http://ppdb.agr.gifu-u.ac.jp>) Yoshiharu Yamamoto (<http://bit.ly/1LVwnep>) updated ver. 3.0. Large TSS data of NGS incorporated into database.

RIKEN BRC

- Resources including seed catalogs (<http://epd.brc.riken.jp/en/>)
- Experimental Plant Division Arabidopsis Seed, DNA, Cell line (<http://bit.ly/2mri7Tq>)
- Phenotype database of natural accessions (<http://bit.ly/2mrkm9m>)
- The ABRANA (Arabidopsis-Brassica Network Access) DB. Resources related with TAIR cDNAs and annotations through sequences (<http://www.abrana.jp/>)
- SABRE2: Database connecting plant EST/Full-Length cDNA clones with Arabidopsis information. (<http://sabre.epd.brc.riken.jp/>)

RIKEN CSRS

- PRIME Platform for RIKEN Metabolomics (<http://prime.psc.riken.jp/>). Arabidopsis metabolomics platform publicly available platform resources:
- Widely-targeted metabolomics (<http://bit.ly/227pkDi>)
  - LC-MCS Branch (<http://bit.ly/1P2Zhtnt>)
  - AtMetExpress Arabidopsis metabolome expression database (<http://bit.ly/1P2YByw>)
- PRIME Web Applications

- PASMET - Prediction, Analysis and Simulation of Metabolic Reaction Networks (<http://pasmnet.riken.jp/>)
- Standard Spectrum Search (<http://bit.ly/1TyDxaT>)
- MS2T Arabidopsis MS/MS spectral tag viewer (<http://bit.ly/1XgNdod>)
- ReSpect RIKEN MSn Spectral database for phytochemicals (<http://bit.ly/1P2ZaIv>)
- PRIMeLink integrates 3 above databases (AtMetExpress, MS2T and ReSpect) for bi-directional search from gene or metabolite (<http://bit.ly/1RCX4Bc>)
- HiFi Heteroatom-containing Ion Finder (<http://bit.ly/2qAwaUe>)
- MeKO Metabolomic characterization of knock-out mutants of Arabidopsis (<http://bit.ly/1QQBwYl>)
- SpinAssign annotation of metabolites by NMR from 13C-HSQC peaks (<http://bit.ly/1LVE58h>)
- Correlated Gene Search (<http://bit.ly/1RCXbwn>)
- Cluster Cutting (<http://bit.ly/227pNoU>)

Distribution and Redistribution

- MetBoard standard compounds (<http://bit.ly/24U5A8B>)
- Drop Met mass-spec based metabolome analyses (<http://bit.ly/1LVEfwq>)
- Simple BL-SOM (<http://bit.ly/1TyE10E>)

Other RIKEN CSRS developed tools and resources:

- Plant Hormone Research Network (<http://hormones.psc.riken.jp/>)
- UniVIO Uniformed Viewer for Integrative Omics (<http://univio.psc.riken.jp/>)
- RARGE II Arabidopsis Genome Encyclopedia II (<http://rarge-v2.psc.riken.jp/>)
- The Chloroplast Function Database II (<http://bit.ly/1P2YMTy>)
- RAPID Phenome Analysis of Ds transposon-tagging line in Arabidopsis (<http://bit.ly/1TQBvdb>)
- RARTF RIKEN Arabidopsis Transcription Factor database (<http://bit.ly/1P2YO4N>)
- Arabidopsis Activation Tagging Line Database (<http://bit.ly/1WdrX2Z>)
- RIPP-DB Plant Phosphoproteome Database (<http://bit.ly/224sjjk>)
- 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) (<http://plant-pras.riken.jp/>)

### Conference and Workshops

- Mar. 16-18, 2017: 58th Annual Meeting of Japanese Society of Plant Physiologists Kagoshima University (<http://bit.ly/2mrkfux>)
- Feb. 27-28, 2017: International Symposium "Environmental Stress Adaptation & Memory in Plants" RIKEN, Yokohama Campus. Sponsorship: RIKEN CSRS; Bioscience and Biotechnology Center, Nagoya Univ.; JST CREST (<http://bit.ly/1TKqm6O>)

## The Netherlands

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### General Activities

#### Research Facilities

Leiden University: Auxin and pattern formation (Offringa), DNA repair and recombination (Hooykaas). Metabolomics facility for plant defence compounds (Klinkhamer).

Utrecht University: Plant-Microbe Interactions (Pieterse, van den Ackerveken): Molecular networks in plant immunity; root microbiome and plant health. Molecular Plant Physiology (Smeekens): Sugar-, light- and high temperature-mediated signal transduction mechanisms and how this controls plant growth. Plant Ecophysiology (Voesenek, Pierik): physiological and molecular mechanisms of plant adaptation to abiotic stress (flooding stress and/or dense, competitive environments)

Wageningen University: Floral transcription factor networks (Angenent), Root development and stem cells (Scheres), Embryogenesis (Weijers/de Vries).

University of Amsterdam/VU: Abiotic stress response, lipid signalling, volatile signaling (Testerink/Haring), Chromatin structure (Koes).

Urecht Plant Growth Facility (19 high-quality climate chambers for Arabidopsis research).

#### Current Arabidopsis Projects

- Dose-dependent BBM action (2015-2019-Boutillier)
- EMBO Long term fellowship (Oct2015-Oct2017) Scott Hayes, with Ronald Pierik. Mechanism and functional significance of salt-mediated inhibition of plant shade avoidance.
- ERA-CAPS: European Plant Embryology Consortium (2014-2017, Weijers, Scheres)
- ERA-CAPS: Plasticity of flowering time in response to environmental signals in Arabidopsis (FLOWPLAST) (2014-2017 Angenent)
- ERC Advanced Grant: The Plant Immune System: a multidisciplinary approach to uncover how plants simultaneously deal with beneficial and parasitic organisms to maximize profits and protection (Pieterse 2011-2017)

- Nov. 29-Dec. 2, 2016: Cold Spring Harbor Asia Conference in Japan, "Latest Advances in Plant Development and Environmental Response" Awaji Island, Kobe (<http://bit.ly/1TKqqDK>)

### Selected Publications

- Adams E, Miyazaki T, *et al* (2017) A novel role for methyl cysteinyl, a cysteine derivative, in cesium accumulation in Arabidopsis. *Scientific Reports* 7, Article number: 43170 doi: [10.1038/srep43170](https://doi.org/10.1038/srep43170)
- Hirakawa Y, Shinohara H, *et al* (2017) Cryptic bioactivity capacitated by synthetic hybrid plant peptides. *Nat Commun.* Feb 6;8:14318. doi: [10.1038/ncomms14318](https://doi.org/10.1038/ncomms14318).
- Mizukami AG, Inatsugi R *et al* (2016) The AMOR Arabinogalactan Sugar Chain Induces Pollen-Tube Competency to Respond to Ovular Guidance. *Curr Biol.* Apr 25;26(8):1091-7. doi: [10.1016/j.cub.2016.02.040](https://doi.org/10.1016/j.cub.2016.02.040).
- Nakayama T, Shinohara H *et al* (2017) A peptide hormone required for Casparian strip diffusion barrier formation in Arabidopsis roots. *Science.* Jan 20;355(6322):284-286. doi: [10.1126/science.aai9057](https://doi.org/10.1126/science.aai9057).
- Petroustos D, Tokutsu R, *et al* (2016) A blue-light photoreceptor mediates the feedback regulation of photosynthesis. *Nature.* 22;537(7621):563-566. doi: [10.1038/nature19358](https://doi.org/10.1038/nature19358).
- Sriyudthsak K, Mejia R, *et al* (2016) PASMET: a web-based platform for prediction, modelling and analyses of metabolic systems. *Nucleic Acids Res* 44 (W1): W205-W211. doi: [10.1093/nar/gkw415](https://doi.org/10.1093/nar/gkw415)

### 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>)
- ALCA (Advanced Low Carbon Technology Research and Development Program) (<http://www.jst.go.jp/alca/en/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>)

- Microtubule organization in the Arabidopsis embryo (with Bela Mulder, AMOLF, NL and Dolf Weijers, WUR, NL). Funded by IP/OP WUR – 2013 – 2017.
- NWO Graduate Programme Horticulture and Starting Materials (1M Euro/yr since 2012)
- NWO-ALW (2012-2017) Niels Anten (WUR), with Ronald Pierik. The power of phenotypic plasticity in competition for light.
- NWO-ALW (2014-2017) Ronald Pierik. Unravelling molecular mechanisms of plant competition: the interplay between above- and belowground competitive responses in Arabidopsis.
- NWO-ALW (Sep2015-Sep2019) A novel role for ethylene in conferring anoxia tolerance: mechanism and significance
- NWO-DBT (Jan2016-Jan2020) Understanding responses to simultaneously and sequentially occurring abiotic stresses typical of climate change in rice and Arabidopsis
- NWO-GSU (2016-2021) Ronald Pierik. Moving from tip to base: how local far-red signalling regulates distant growth.
- NWO-GSU (Sep2015-Sep2019) Rens Voeselek. NO problem: ethylene-induced regulation of nitric oxide confers flooding tolerance in plants
- NWO-VENI: Evolutionary aspects of the MADS domain transcription factor FUL (2014-2017, Bemer)
- NWO-VIDI (2013-2018) Ronald Pierik. When growing tall is not an option: down-regulation of shoot elongation in the shade.
- NWO-VIDI (2015-2019) Kirsten ten Tusscher. Lateral root patterning in plants: multi-scale modelling of complex feedbacks.
- NWO-VIDI Bert De Rybel - The molecular and cellular basis of vascular tissue formation (2014-2019)
- Role of TCP transcription factors in growth (2013-2017, Immink)
- Stem cells and regeneration (with Keygene, NL). Funded by seed companies. 2015 – 2019.
- Stress signalling in the root stem cell niche (with Chuanyou Li Institute of Genetics and Developmental Biology Chinese Academy of Science, Beijing) Funded by CAS sep 2016 – dec 2017).
- STW Perspective Programme Back2Roots (national programme; 3 MEuro 2016-2022)
- STW Perspective Programme Green Defenses Against Pests (national programme; 3M Euro 2014-2020)
- NWO-Building Blocks of Life (2017-2021) Ronald Pierik. Photoreceptor control of plant development: molecular signalling shoot to root.
- NWO-VICI Dolf Weijers - The evolutionary and structural basis for specificity in plant hormone response (2015-2020)

**Outlook**

Flooding and low oxygen stress biology: We have used Arabidopsis as a model system to investigate flooding and low oxygen stress responses, as well as multiple stress combinations and identify the genetic basis of stress variation using natural variation in *A. thaliana*.

Projects related to this have utilized a combination of physiology and genomics and have yielded very valuable datasets that provide considerable new insight into how plants cope with flooding stress. We have also identified several candidate genes and processes previously unexplored functions in resistance to flooding stress. These form very promising leads for future research directions and funding opportunities.

**Photobiology:**

Plant photobiology research has centred on Arabidopsis, due to the tremendous versatility of resources for research. Although we are expanding this to other species, Arabidopsis will continue to form the backbone of research efforts. A combination of molecular biology, genetics, physiology, mathematical modelling and natural variation is used to identify novel regulators of plant growth adjustments to light quality cues perceived by the photoreceptors and beyond. Although light signals are typically sensed in the shoot, we are also studying impacts at the whole-plant level, including the root system and including both wet lab and modeling approaches.

**Road Map Related Activities**

**Outreach Activities**

- Fascination of Plants Day (national activities, see link via EPS)
- EPSO workshop on Plant Microbiomes (Vienna, 23 February 2017)
- NWO-Building Blocks of Life (2017-2021) Ronald Pierik. Photoreceptor control of plant development: molecular signalling shoot to root. A collaborative project between theoretical biologist Kirsten ten Tusscher and plant photobiologist Ronald Pierik, with applied plant research industry pitching in.

**Conference and Workshops**

- Experimental Plant Sciences annual meeting 11-12 April, 2016.
- 9th International Utrecht PhD Summer School on Environmental Signaling in Plants
- Summerschool Environmental Signalling in Plants, Utrecht University & EPS, Utrecht, the Netherlands. 28-30 August 2017.

**Selected Publications**

Das D, St. Onge KR, Voeselek LACJ, Pierik R, Sasidharan R (2016) Ethylene- and shade-induced hypocotyl elongation involve shared transcriptome patterns and functional regulators. *Plant Physiology* 172: 718-733

de Wit M, Keuskamp DH, Bongers FJ, Hornitschek P, Gommers CMM, Reinenen E, Martinez-Cerdon C., Fankhauser C, Pierik R. (2016) Integration of phytochrome and cryptochrome signals determines plant growth during competition for light. *Current Biology*, 26: 3320-3326

**New Zealand**



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**General Activities**

**Research Facilities**

As agriculture plays a major role in the New Zealand economy, plant science largely focusses on forage crops such as rye, legumes and brassicas, for dairy cattle and other stock, and horticultural crops such as grapes, kiwifruit, apples, stone fruits and potatoes. 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. Basic research into plant development is also conducted using Arabidopsis within universities.

In New Zealand research using Arabidopsis is conducted in both universities and Crown Research Institutes (CRIs), government-owned companies that carry out scientific research. Universities working with Arabidopsis include the University of Auckland (School of Biological Sciences; Plant Molecular Science), the University of Canterbury (Biological Sciences), Lincoln University (Bio-Protection Research Centre), Massey University (Institute of Fundamental Science; Institute of Agriculture & Environment) and the University of Otago (Department of Biochemistry). The major Crown Research Institutes using Arabidopsis in research programs are AgResearch and Plant and Food Research. Research in the universities and the Crown Research Institutes is often linked, with several researches having joint appointments in two facilities.

**Current Arabidopsis Projects**

Major themes of plant research in New Zealand that include work with Arabidopsis:

- Flowering time. Investigating how external cues such as day length, light quality and cold regulate flowering. The University of Auckland, the University of Otago and Plant and Food Research.
- Plant pathogen interactions and stress responses. Lincoln University, Massey University, the University of Otago and Plant and Food Research
- Plant Growth and Development. Investigating the molecular control of various aspects of plant development such as plant reproduction, organ size, regulation of branching. AgResearch, Massey University, the University of Otago and Plant and Food Research.

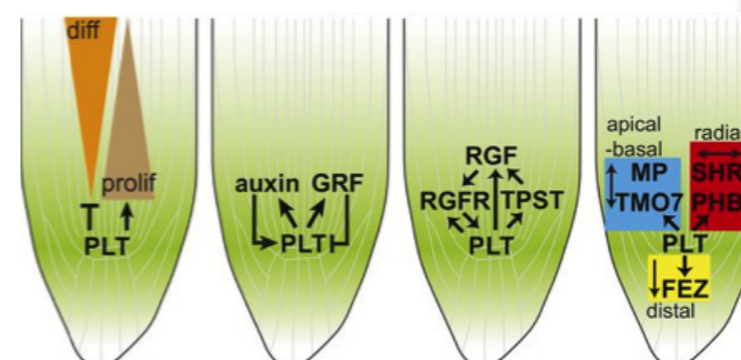
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Toen, M.P.M, Davila Olivas, N.H., Kloth, K.J., Coolen, S., Huang, P.-P., Aarts, M.G.M., Bac-Molenaar, J.A., Bakker, J., Bouwmeester, H.J., Broekgaarden, C., Bucher-Lange, J., Cheng, X., Fradin, E.F., Jongma, M.A., Julkowska, M.M., Keurentjes, J.J.B., Ligterink, W., Pieterse, C.M.J., Ruyter-Spira, C., Smant, G., Testerink, C., Usadel, B., Van Loon, J.J.A., Van Pelt, J.A., Van Schaik, C.C., Van Wees, S.C.M., Visser, R.G.F., Voorrips, R., Vosman, B., Vreugdenhil, D., Warmerdam, S., Wieggers, G.L., Van Heerwaarden, J., Kruijer, W., Van Eeuwijk, F.A. and Dicke, M. (2017). Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. *New Phytologist* 213: 1346–1362.

van Veen H, Vashisht D, Akman M, Girked T, Mustrup A, Reinen E, Hartman S, Kooiker M, van Tienderen P, Schranz ME, Bailey-Serres J, Voeselek LACJ and Sasidharan R (2016) Transcriptomes of eight Arabidopsis accessions reveal core conserved, genotype- and organ-specific responses to flooding stress. *Plant Physiology* 172: 668–689

**Major Funding Sources**

Nederlandse Organisatie voor Wetenschappelijk Onderzoek (NWO) ([www.nwo.nl](http://www.nwo.nl))



**Figure 24.** PLT target genes regulate differentiation progression, regulatory feedback on PLT levels and patterning <http://dx.doi.org/10.1105/tpc.16.00656>

iv) Control of gene expression. Transcriptional regulation, intron-mediated transcriptional control, uORFs and translation regulation. The University of Otago and Plant and Food Research.

v) Colour and nutrition. Characterization of the molecular pathways controlling the production of pigments and nutritional compounds in plants. The University of Auckland, the University of Otago and Plant and Food Research.

vi) Plant metabolism. Lipid biosynthesis, photosynthesis, photorespiration and nitrogen metabolism.

### Outlook

As agriculture and horticulture play major roles in the New Zealand economy, Arabidopsis will continue to play a key role in plant research as a model for gene discovery, the characterization of molecular pathways and the testing of the function of genes from crop species. Basic plant science at the universities will also continue using Arabidopsis.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

SNPFreqPlot - A web application for the easy visualization of the frequency at which SNPs occur across a genomic region of all Arabidopsis accessions by extracting key information from VCF files, such as those downloaded from the 1001 Genomes Project. The application is available at: <http://snpfreqplot.otago.ac.nz/SNPFreqPlot/>.

A rapid method for the identification of candidate targets of plant transcription factors was described in: Bond DM, Albert NW, Lee RH, Gillard GB, Brown CM, Hellens RP and Macknight RC. (2016) Infiltration-RNAseq: transcriptome profiling of Agrobacterium-mediated infiltration of transcription factors to discover gene function and expression networks in plants. *Plant Methods* 12:41.

### Outreach Activities

The plant research environment in New Zealand strongly supports the flow of information from university to applied plant scientists and plant breeders, largely through the Crown Research Institutes that are Government-owned companies. Both Plant and Food and AgResearch have scientists with a range of skills from gene discovery and characterization to plant breeding. There are also a number of researchers that have joint appointments at both a university and a Crown Research Institute. Additionally, research funding from the Ministry of Business, Innovation and Employment (MBIE) is dependent upon collaborations between research scientists and potential end users being established early in a research program.

### Conference and Workshops

QMB Plant Molecular Biology Meeting, September 1- 2, 2016, Nelson, New Zealand.

Plant Science Central, 4-6 July, 2017, Palmerston North, New Zealand.

AustralAsia Genetics Society Meeting, July 3-6, 2017, Dunedin, New Zealand.

### Selected Publications

Le J, Joshi N, Pasini R, Dobson RCJ, Allison J and Leustek T. (2016) Inhibition of Arabidopsis growth by the allelopathic compound azetidine-2-carboxylate is due to the low amino acid specificity of cytosolic prolyl-tRNA synthetase. *The Plant Journal* 88: 236-24.

Peters B, Casey J, Aidley J, Zohrab S, Borg M, Twell D and Brownfield L. (2017). A conserved cis-regulatory module determines germline fate through activation of the transcription factor DUO1 promoter. *Plant Physiology* 173: 280-293.

Ridge S, Susmilch FC, Hecht V, Vander Schoor JK, Lee R, Aubert G, Burstin J, Macknight RC, Weller JL. (2016) Identification of LATE BLOOMER2 as a CYCLING DOF FACTOR Homolog Reveals Conserved and Divergent Features of the Flowering Response to Photoperiod in Pea. *Plant Cell* 28: 2545-2559.

Zheng X, Tan DX, Allan AC, Zuo B, Zhao Y, Reiter R J, ... Zhou, J. (2017). Chloroplastic biosynthesis of melatonin and its involvement in protection of plants from salt stress. *Sci Rep*, 7.

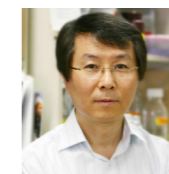
### Major Funding Sources

Basic research in plant sciences in New Zealand is largely supported by the Marsden Fund administered by the Royal Society of New Zealand (<http://www.royalsociety.org.nz/programmes/funds/marsden/>) along with funding from universities.

Translational research is funded through the Ministry for Business, Innovation and Employment (MBIE) through core funding to the Crown Research Institutes and contestable funding through the Science Investment Rounds. MBIE also supports international collaborations through the Catalyst Fund. Funding for translational research is also available through The Agricultural and Marketing Research and Development Trust (AGMARDT: <http://agmardt.org.nz/>). The Crown Research Institutes also receive funds from royalties of commercialized products.

## South Korea

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### General Activities

#### Research Facilities

The major topics include abiotic and biotic stress, plant senescence and life history, plant hormones, photosynthesis, protein targeting and trafficking, transporters and channels, phloem development, light signaling, and circadian clock. In addition, plant biotech-related topics are also actively studied for the purpose of developing plants as a bioreactor.

- Multi-omic approaches for systems study on plant senescence
- Phenomics center
- Mass analysis system for plant hormones and secondary metabolites
- Plant factory for GM plant growth

#### Current Arabidopsis Projects

- Systems & Synthetic Agrobiotech Center (~ 9 M USD/yr for 10 years by Rural Development Administration, Korea.
- Systems understanding of plant senescence and life history (~9 M USD/yr for 10 years by Institute of Basic Research )
- Global research lab project (0.5 M\$/yr for 10 years by National Research Foundation, Korea
- Woojangchoon Project focusing on ABA signaling and synthetic biology (0.9 M USD/yr for 5 years) supported by Rural Developmental Agency, Korea
- Woojangchoon Project focusing on chloroplast development and photosynthesis of C3 and C4 systems (0.9 M USD/yr for 5 years) supported by Rural Developmental Agency, Korea

### Outlook

Currently, the direction of research in plant science is more toward application using crop plants. Thus, basic research using Arabidopsis is less promising. In addition, a major funding for the basic research is given to the newly established organization, the Institute of Basic Research.

In this institute, the research funding is distributed to its center with a small number of scientists. Thus, it is likely that the basic research, in particular plant science using Arabidopsis, in university will suffer in the near future.

### Road Map Related Activities

#### Conference and Workshops

- Plant Winter Conference of Korean Society of Plant Biologists

- Annual meeting of Korean Society of Plant Biologists
- ICAR2016 Gyeongju Korea
- The 8th International Symposium on Plant Senescence

### Selected Publications

- Jeon J, Cho C, Lee MR, Van Binh N, Kim J (2016) CYTOKININ RESPONSE FACTOR2 (CRF2) and CRF3 Regulate Lateral Root Development in Response to Cold Stress in Arabidopsis. *Plant Cell* 28(8):1828-43.

- Kim J, Song K, Park E, Kim K, Bae G, Choi G (2016) Epidermal Phytochrome B Inhibits Hypocotyl Negative Gravitropism Non-Cell-Autonomously. *Plant Cell* 28(11):2770-2785.

- Lee HG, Seo PJ (2016) The Arabidopsis MIEL1 E3 ligase negatively regulates ABA signalling by promoting protein turnover of MYB96. *Nat Commun* 7:12525.

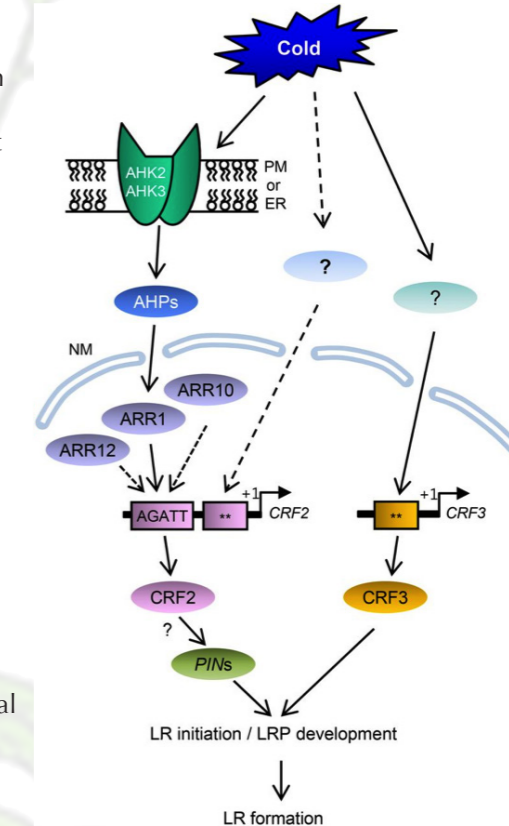
- Park Y, Xu ZY, Kim SY, Lee J, Choi B, Lee J, Kim H, Sim HJ, Hwang I (2016) Spatial Regulation of ABCG25, an ABA Exporter, Is an Important Component of the Mechanism Controlling Cellular ABA Levels. *Plant Cell* 28(10):2528-2544.

- Seo DH, Ahn MY, Park KY, Kim EY, Kim WT (2016) The N-Terminal UND Motif of the Arabidopsis U-Box E3 Ligase PUB18 Is Critical for the Negative Regulation of ABA-Mediated Stomatal Movement and Determines Its Ubiquitination Specificity for Exocyst Subunit Exo70B1. *Plant Cell* 28(12):2952-2973.

### Major Funding Sources

National Research Foundation  
[www.nrf.re.kr/](http://www.nrf.re.kr/)

Rural Developmental Agency  
[www.rda.go.kr/](http://www.rda.go.kr/)



**Figure 25.** Model Showing CRF2 and CRF3-Mediated Lateral Root Formation in Arabidopsis under Cold Stress. Solid arrows indicate +ve regulation. Dotted arrows indicate putative signaling pathways. Double asterisks indicate unknown cis-elements. ER, endoplasmic reticulum; NM, nuclear membrane; PM, plasma membrane. <http://dx.doi.org/10.1105/tpc.15.00909>



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root phototropism and growth through regulation of proliferation-to-differentiation transition. *Plant Cell* 28: 1372-1387.

Wu Q, Zhang X, Peirats-Llobet M, Belda-Palazon B, Wang XF, Cui S, Yu XC, Rodriguez PL and An CC (2016) Ubiquitin ligases RGLG1 and RGLG5 regulate abscisic acid signaling by controlling the turnover of phosphatase PP2CA. *Plant Cell* 28: 2178-2196.

### Major Funding Sources

About 80 grants from the Ministry of Economy, Industry and Competitiveness of Spain fund Arabidopsis research projects at individual laboratories. Authors from laboratories studying Arabidopsis in Spain published about 400 papers in the last year.vWvW

### Road Map Related Activities

### Conference and Workshops

The 'Plant Organ Growth Symposium 2017' was held on 15-17 March 2017 in Elche (Spain), organized by J.L. Micol, M.R. Ponce, D. Wilson-Sánchez and R. Sarmiento-Mañús ([POGS2017.edu.umh.es](http://POGS2017.edu.umh.es)).

### Selected Publications

Belda-Palazon B, Rodriguez L, Fernandez MA, Castillo MC, Anderson EM, Gao CJ, Gonzalez-Guzman M, Peirats-Llobet M, Zhao Q, De Winne N, Gevaert K, De Jaeger G, Jiang LW, León J, Mullen RT and Rodriguez PL (2016) FYVE1/FREE1 interacts with the PYL4 ABA receptor and mediates its delivery to the vacuolar degradation pathway. *Plant Cell* 28: 2291-2311.

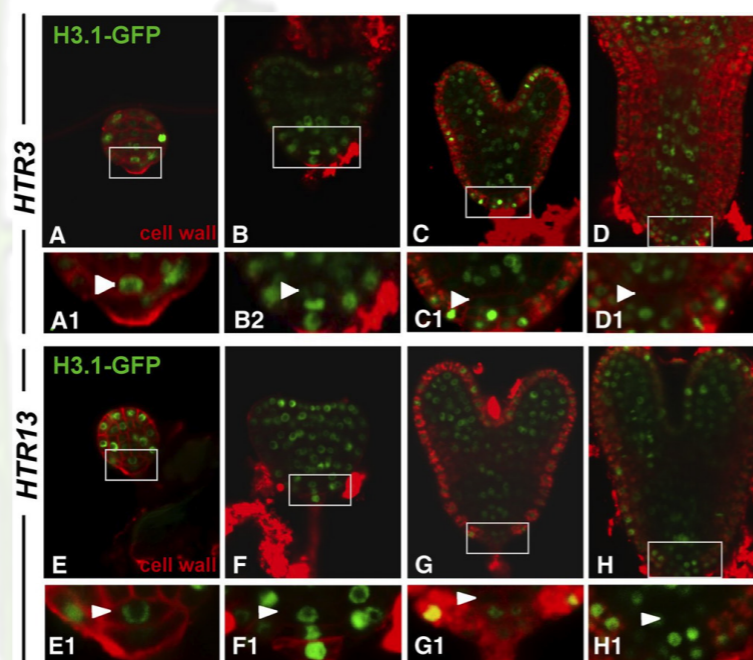
González-Grandío E, Pajoro A, Franco-Zorrilla JM, Tarancón C, Immink RGH and Cubas P (2017) Abscisic acid signaling is controlled by a BRANCHED1/HD-ZIP 1 cascade in Arabidopsis axillary buds. *Proceedings of the National Academy of Sciences of the United States of America* 114: E245-E254.

Martín G, Leivar P, Ludevid D, Tepperman JM, Quail PH and Monte E (2016) Phytochrome and retrograde signalling pathways converge to antagonistically regulate a light-induced transcriptional network. *Nature Communications* 7: 11431.

Otero S, Desvoyes B, Peiró R and Gutierrez C (2016) Histone H3 dynamics reveal domains with distinct proliferation potential in the Arabidopsis root. *Plant Cell* 28: 1361-1371.

Perea-Resca C, Carrasco-López C, Catalá R, Tureckova V, Novak O, Zhang WP, Sieburth L, Jiménez-Gómez JM and Salinas J (2016) The LSM1-7 complex differentially regulates Arabidopsis tolerance to abiotic stress conditions by promoting selective mRNA decapping. *Plant Cell* 28: 505-520.

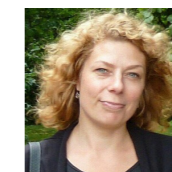
Silva-Navas J, Moreno-Risueno MA, Manzano C, Téllez-Robledo B, Navarro-Neila S, Carrasco V, Pollmann S, Gallego FJ and del Pozo JC (2016) Flavonols mediate



**Figure 26.** Histone H3.1 Labeling Pattern during Arabidopsis Embryo Development. Embryos of plants expressing H3.1(HTR3)-GFP ([A] to [D]) or H3.1(HTR13)-GFP ([E] to [H]) are shown at different stages: globular ([A] and [E]), early ([B] and [F]) and late ([C] and [G]) heart, and torpedo ([D] and [H]). Cell membranes were stained with FM4-64 (red). Insets focus on the region containing the QC (white arrowheads) in each case. <http://dx.doi.org/10.1105/tpc.15.01003>

## Sweden

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of Biochemistry and Biophysics(<http://www.dbb.su.se/research>)

- The Linnean Centre; comprising Departments at Uppsala University and SUAS in Uppsala (<http://lcpu.se/>)

- The Evolutionary Biology Centre, Uppsala University, Uppsala (<http://www.ebc.uu.se/Research/>)

- Umeå Plant Science Centre UPSC comprising Departments at Umeå University and SUAS in Umeå (<http://www.upsc.se/research/research-groups.html>)

### General Activities

### Research Facilities

There are no dedicated Arabidopsis centres, however, a larger part of the community of plant researchers do use Arabidopsis as their main model system together with additional agricultural or forestry crop model systems. Thus, the researchers employing Arabidopsis are spread over more than ten Universities in Sweden.

The Arabidopsis associated research themes span across a broad range of subjects, from basic cell biology, developmental biology, stress biology, photosynthesis, wood biology and ecological work focussed on local adaptation.

Sweden's Governmental Agricultural Board's benign approach to field testing (following a strict application procedure) also enable large scale testing of Genetically Modified (GM) traits in the field using Arabidopsis or other species of interest, greatly facilitating research on adaptive traits and/or future improvements of crops.

Major sites of Arabidopsis research are (from South to North):

- Lund University, Department of Biology, Molecular Plant Biology (<http://www4.lu.se/molecular-plant-biology>)

- The University of Agricultural Sciences (SUAS) in Alnarp is based for instance at the Dept. of plant-protection-biology (<http://www.slu.se/en/departments/plant-protection-biology/>)

- The Plant Link' (<http://www.plantlink.se/>) coordinate plant research at Lund University and University of Agricultural Sciences (SUAS) in Alnarp with a focus on bringing basic and applied work on Arabidopsis and crops together.

- Gothenburg University, Department of Biological and Environmental Sciences, Plant Cell and Molecular Biology (<http://bioenv.gu.se/english/research/physiology-and-cell-biology/plant-cell-and-molecular-biology>)

- Örebro University, Life Science Centre,, Molecular Biochemistry, (<https://www.oru.se/english/research/research-environments/ent/lsc/>)

- Stockholm University, Department of Ecology, Environment and Plant Sciences (<http://su.se/deep/english/research/research-areas/plant-sciences>); Department

### Current Arabidopsis Projects

There are several ongoing, larger projects awarded from the major funding bodies which uses Arabidopsis as the major model system. About 100 papers of primary work using Arabidopsis from modelling and theoretical analysis to plant development, molecular biology, biochemistry, physiology and molecular ecology were published during the last year, with Swedish scientists as lead or co-authors. Among those papers a notable part focussed on auxin and cytokinins metabolism and their role in stem cells or light regulation of plant development.

Larger awarded grants 2016; Prof. Markus Schmid, Umeå University recieved a grant from the Knut and Alice Wallenberg Foundation (28,680,000 Swedish krona over five years) for the project "Epigenetic and metabolic control of flowering time".

Dr. Charles Melnyk was awarded a Wallenberg Academy Fellowship from the Knut and Alice Wallenberg Foundation providing long-term career development and funding for the project "Grafted plants – how do they connect their vascular systems?" at the Swedish University of Agricultural Sciences, Uppsala.

For other funded Arabidopsis projects please see research at individual Centres (listed above).

### Outlook

All listed major funding bodies (below), regularly advertise open calls where Arabidopsis research qualifies for funding. However, as noted in the previous year, additional grant calls aimed at applied research using other model systems or certain "products" are on the increase.

### Road Map Related Activities

### Arabidopsis Tools and Resources

National resources used by the Arabidopsis research community;

• Max Lab hosted by Lund University; <http://www.maxlab.lu.se/maxlab>, a facility dedicated to high-throughput,

nanovolume characterization and crystallization of biological macromolecules.

- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government, <http://www.scilifelab.se>
- Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis <http://www.upsc.se>, found under “resources”.
- The Swedish Metabolomics Centre in Umeå is a national resource, <http://www.swedishmetabolomicscentre.se/>
- The Swedish National Infrastructure for Computing (SNIC), <http://www.snic.vr.se/>

### Outreach Activities

‘Fascination of Plants Day’ is celebrated at most major plant science centres across Sweden, which also regularly host outreach activities to highlight research on plants. Also, on March 9, 2017, a popular science seminar day was filmed by Swedish TV (UR, Kunskapskanalen) to showcase the breadth of plant research at Umeå Plant Science Centre.

### Conference and Workshops

- The Umeå renewable energy meeting, February 14 - 17, 2017, Umeå, Sweden

Upcoming meetings:

- Society of Experimental Biology Symposium, July 3 - 6, 2017, Gothenburg, Sweden
- 8th International Symposium on Root Development, May 29 - June 1, 2017, Umeå, Sweden
- 8th European Symposium on Plant Lipids, July 2 - 5, 2017, Malmö, Sweden
- ICPB 2017: 19th International Conference on Proteomics and Bioinformatics, July 13 - 14, 2017, Stockholm, Sweden
- 1st International Plant Spectroscopy Conference, August 29 - 30, 2017, Umeå, Sweden

### Selected Publications

Gruel J, Landrein B, Tarr P, Schuster C, Refahi Y, Sampathkumar A, Hamant O, Meyerowitz EM, Jönsson H (2016) An epidermis-driven mechanism positions and scales stem cell niches in plants. *Science Advances* 2: e1500989.

Kirscht A, Kaptan SS, Bienert GP, Chaumont F, Nissen P, de Groot BL, Kjellbom P, Gourdon P, Johanson, U (2016) Crystal Structure of an Ammonia-Permeable Aquaporin. *PLOS Biology* 14: e1002411.

Mehdi S, Derkacheva M, Ramstrom M, Kralemann, L, Bergquist J, Hennig L (2016) The WD40 Domain Protein MS11 Functions in a Histone Deacetylase Complex to

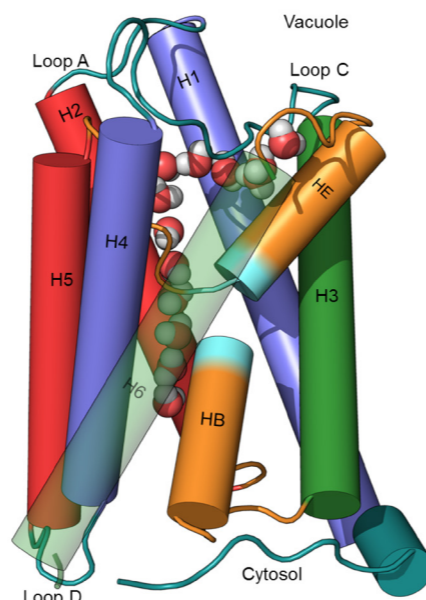
Fine-Tune Abscisic Acid Signaling. *Plant Cell* 28: 42-54.

Muller, CJ, Valdes AE, Wang GD, Ramachandran P, Beste L, Uddenberg D, Carlsbecker A (2016) PHABULOSA Mediates an Auxin Signaling Loop to Regulate Vascular Patterning in Arabidopsis. *Plant Physiol* 170:956-970.

Porco S, Pencik A, Rashed A, Voss U, Casanova-Saez R, Bishopp A, Golebiowska A, Bhosale R, Swarup R, Swarup K, Penakova P, Novak, O, Staswick P, Hedden P, Phillips AL, Vissenberg K, Bennett MJ, Ljung K (2016) Dioxygenase-encoding AtDAO1 gene controls IAA oxidation and homeostasis in Arabidopsis. *Proc Natl Acad Sci U S A* 113:11016-11021. <https://doi.org/10.1371/journal.pbio.1002411>

### Major Funding Sources

- The Swedish Research Council (VR; <http://www.vr.se>) a core funder of researcher-initiated basic research.
- The Swedish Foundation for Strategic Research (<http://www.stratresearch.se>) supports strategic research in natural science, engineering and medicine.
- The Swedish Agency for Innovation Systems (VINNOVA; <http://www.vinnova.se>) promotes sustainable growth by funding needs-driven research and the development of effective innovation systems.
- The Royal Academy of Science/ (<http://www.kva.se>) Agriculture and Forestry (<http://www.ksla.se>)
- The Swedish Research Council Formas (<http://www.formas.se>) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.
- The Wallenberg Foundations (<http://www.wallenberg.org/en>) private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.
- Carl Tryggers Foundation for Scientific Research (<http://www.carltryggersstiftelse.se/>) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.
- The Kempe Foundations (<http://www.kempe.com>) private foundations devoted to support scientific research in Northern Sweden
- Stiftelsen Olle Engkvist Byggmästare (<http://engkviststiftelserna.se/>)



**Figure 27.** Topology and structure of At-TIP2;1. Eight water molecules form a single file in the main pore of the monomer, connecting the cytosolic and vacuolar vestibules. At the top right, five additional water molecules are seen in a side pore underneath loop C.

## Switzerland

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### General Activities

#### Research Facilities

- Swiss Plant Science Web (Swiss-wide network of plant science, <https://swissplantscienceweb.ch/>) It is composed of Zurich-Basel Plant Science Center (competence center linking and supporting the plant science research community of the University of Zurich, ETH Zurich and the University of Basel, <http://www.plantsciences.uzh.ch/index.html>), Arc lémanique plant science (<http://www.unil.ch/alps/home.html>), and BeNeFri network.
- Functional Genomics Center Zurich (e.g. genome sequencing of Arabidopsis halleri)
- Genetic Diversity Center (e.g. genome-wide polymorphisms of Arabidopsis halleri)
- The Neuchâtel Platform of Analytical Chemistry (the Mass Spectrometry and Metabolomics Unit and the Nuclear Magnetic Resonance Unit, <http://www.unine.ch/npac>)
- Bio-molecular Analysis Platform (collaborative basis, <http://biveg.unige.ch/en/services/bma/>)

#### Current Arabidopsis Projects

Plant research projects and researchers are listed at the website of Swiss Plant Science Web. <https://swissplantscienceweb.ch/research/research-portfolios/>, <https://swissplantscienceweb.ch/research/researchers/>

There are a large number of projects supported by Swiss National Science Foundation.

1. IDP BRIDGES is an Innovative Doctoral Program supporting 14 PhD students for work in the most challenging areas of plant sciences. In IDP BRIDGES, a cohort of 14 PhD fellowships - funded by 7th Framework Program of the European Union for 36 months - is linked to the training program Science & Policy.
2. SystemsX.ch  
 PlantGrowth2 In a Changing Environment, Apr. 2013 – Mar. 2017 (<http://www.systemsx.ch/projects/research-technology-and-development-projects/plantgrowth2/>)  
 MecanX Understanding Physics of Plant Growth, Apr. 2013 – Mar. 2017 (<http://www.systemsx.ch/projects/research-technology-and-development-projects/mecanx/>)

### Outlook

The National Centre of Competence in Research (NCCR) “Plant Survival – Plant Survival in Natural and Agricultural Ecosystems” finished in 2013. It would be valuable for proposing Arabidopsis related researches in the next calls.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

1. Swiss-Prot database contributes to TAIR database
2. Briskine RV, Paape T, Shimizu-Inatsugi R, Nishiyama T, Akama S, Sese J & Shimizu KK. (2016) Genome assembly and annotation of Arabidopsis halleri, a model for heavy metal hyperaccumulation and evolutionary ecology. *Mol Ecol Resour.* 2016 Sep 27.
3. Gan X, Hay A, Kwantes M, Haberer G, Hallab A, Ioio RD, Hofhuis H, Pieper B, Cartolano M, Neumann U, Nikolov LA, Song B, Hajheidari M, Briskine R, Kougioumoutzi E, Vlad D, Broholm S, Hein J, Meksem K, Lightfoot D, Shimizu KK, Shimizu-Inatsugi R, Imprialou M, Kudrna D, Wing R, Sato S, Huijser P, Filatov D, Mayer KF, Mott R, Tsiantis M. (2016) The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. *Nat Plants.* 2016 Oct 31;2(11):16167.
4. Novikova PY, Hohmann N, Nizhynska V, Tsuchimatsu T, Ali J, Muir G, Guggisberg A, Paape T, Schmid K, Fedorenko OM, Holm S, Säll T, Schlötterer C, Marhold K, Widmer A, Sese J, Shimizu KK, Weigel D, Krämer U, Koch MA, Nordborg M. (2016) Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. *Nat Genet.* 2016 Sep;48(9):1077-82

### Outreach Activities

1. Agora outreach program of Plant Science Center
2. Continuing Education Program in Plant Sciences for Secondary School Teachers <http://www.plantsciences.uzh.ch/outreach/atschool.html>

Plant research was a missing element in continuing education and is, therefore, very well received by the teachers and collaborators in the regional learning centers. At the interface we now offer several workshops with an innovative format, topics at the forefront of current plant science research but well linked to the curricula of secondary schools, exchange with active researchers in interactive discussion, robust teaching material that can be transferred easily to classroom teaching, and guidance and support through our flying trainer during and after the workshop. Topics have been discussed with teachers before setting up the training to make sure that they are meeting the requirements of teachers and school classes. Participation in our workshops is fully accredited as continuing education in the teacher’s portfolio.

- Plant Molecular Biology II: Angewandte evolutionsforschung mit Gemüse aus dem Supermarkt (2), Evolution du Broccoli (Development in 2014 / first time offered in Dec 2014) (WSV)
- 3. PSC Discovery Program for Youth (Swiss National Science Foundation) (2015-)

### Conference and Workshops



1. SwissPlant 2017, Leukerbad, 25-27 Jan. 2017  
<https://swissplantscienceweb.ch/swissplant-2017-symposium/>
2. LS<sup>2</sup> Annual Meeting 2017, Zurich, 2-3 Feb. 2017, SWISS PLANT SCIENCE WEB (SPSW) Plant Genomics Session (This session is supported by the URPP Evolution in Action)
3. Plant lectures at the latest Lausanne Genomics Days, 9-10 Feb. 2017, Lausanne  
<http://www.genomyx.ch/thu-feb-9-fri-feb-10-2017-lausanne-genomics-days-2017/>
4. PSC Summer school 2016, Einsiedeln, 11-16 Sep. 2016, Zürich, 19 Sep. 2016, Agriculture in Transformation - New Concepts for an Agriculture Production that is Socially Fair, Environmentally Safe and Economically Viable
5. PSC Summer school 2017, Einsiedeln, 29 May - 2 June 2017  
Understanding Risks and Resilience in Plant Systems
6. Gordon Research Conference, Les Diablerets, 29 May - 3 June, 2016  
Salt & Water Stress in Plants  
<https://www.grc.org/programs.aspx?id=12420>
7. Network Meeting of the Marie Curie Innovative Training Network (ITN) "CALIPSO" (Ca<sup>2+</sup> and Light Signals in Photosynthetic Organisms), Les Diablerets, 21-24 Sep. 2016.  
<http://itn-calipso.univie.ac.at/>

### Selected Publications

1. Kohnen M., Schmid-Siegert E., Trevisan M., Allenbach Petrolati L., Sénéchal F., Müller-Moulé P., Maloof J.N., Xenarios I., Fankhauser C. (2016) Neighbor Detection Induces Organ-specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-specific Growth. *Plant Cell*. 2016 Dec;28(12):2889-2904.
2. Wild R, Gerasimaite R, Jung JY, Truffault V, Pavlovic I, Schmidt A, Saiardi A, Jessen HJ, Poirier Y, Hothorn M, Mayer A. (2016) Control of eukaryotic phosphate homeostasis by inositol polyphosphate sensor domains. *Science*. 2016 May 20;352(6288):986-90.
3. Paape T, Hatakeyama M, Shimizu-Inatsugi R, Cereghetti T, Onda Y, Kenta T, Sese J, Shimizu KK. (2016) Conserved but Attenuated Parental Gene Expression in Allopolyploids: Constitutive Zinc Hyperaccumulation in the Allotetraploid *Arabidopsis kamchatica*. *Mol Biol Evol*. 2016 Nov;33(11):2781-2800.
4. Zürcher E, Liu J, di Donato M, Geisler M, Müller B. (2016) Plant development regulated by cytokinin sinks. *Science*. 2016 Sep 2;353(6303):1027-1030.
5. Doblaz VG, Smakowska-Luzan E, Fujita S, Alassimone J, Barberon M, Madalinski M, Belkhadir Y, Geldner N. (2017) Root diffusion barrier control by a vasculature-derived peptide binding to the SGN3 receptor. *Science*. 2017 Jan 20;355(6322):280-284.

### Major Funding Sources

1. Swiss National Science Foundation (SNSF)  
<http://www.snf.ch/en/Pages/default.aspx>
2. European Research Council (ERC), <https://erc.europa.eu/>
3. SystemsX.ch, <http://www.systemsx.ch/>
4. Syngenta (Plant Science Center - Syngenta Fellowship), <https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html>
5. Research and Innovation Staff Exchange (RISE) of European Commission  
[http://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange\\_en](http://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange_en)
6. State Secretariat for Education, Research, and Innovation (SERI), <https://www.sbf.admin.ch/sbf/en/home.html>
7. University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Beat Keller, Ueli Grossniklaus, University of Zurich)  
<http://www.evolution.uzh.ch/en.html>
8. Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), <https://www.jst.go.jp/kisoken/crest/en/>

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### General Activities

#### Arabidopsis Research Facilities

The UK has active Arabidopsis research occurring at over 40 academic departments and research institutes. The major funder of this research in the Biotechnology and Biological Science Research Council (BBSRC) who show continued support of Arabidopsis research as a model for discovery and as a pathway to translation. The BBSRC supports the Nottingham Arabidopsis Stock Centre (uNASc) that, as one of two global stock centres hold over 1 million genotypes and annually supply over 100,000 tubes of seed.

The BBSRC research institutes of the John Innes Centre, Rothamsted Research, the Institute of Biological Environmental and Rural Science (IBERS) and The Earlham Institute have a plant science focus that includes Arabidopsis research. The National Plant Phenomics Centre, NPPC is located at IBERS Aberystwyth. BBSRC also supports CyVerseUK (and the Centre for Integrative Biology, CPIB in Nottingham).

The Gatsby Charitable Foundation supports two plant science research institutions. The Sainsbury Laboratory, Norwich and the Sainsbury Laboratory Cambridge University both have significant Arabidopsis research programmes.

#### Current Arabidopsis Projects

The majority of UK Arabidopsis grants are awarded to individual research groups, although the BBSRC also fund a number of 'Networks in Industrial Biotechnology and Bioenergy' (NIBB) that have the aim of encouraging the translation of fundamental research, most of which is occurring in Arabidopsis. These NIBBs include the 'High Value in ChemicalNetwork (<http://hvcp.net/>)' and the 'Lignocellulosic Biorefinery Network (<http://lb-net.net/>)'. By early-2017 the BBSRC funds around 90 active individual research grants that include most aspects of Arabidopsis research, awarded to over 75 different academics. This amounts to over £35.5M of support.

Since the start of 2016 there have been 29 grant holder awarded to a value around £8million.

Amongst these recent grants, highlights include:  
- £582K: EpiSpiX - Cellular and biochemical context of Arabidopsis circadian-clock components. Seth Davis (University of York).  
<http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN018540%2f1>

- £533K: The twilight zone: the initiation of starch degradation in leaves. Alison Smith (John Innes Centre).  
<http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN001389%2f1>

- £511K: Understanding the mechanism of chloroplast immunity. Murray Grant (University of Warwick).  
<http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fP002560%2f1>

- £493K: Perception and integration of nutritional signals in plant root systems: Solving the mystery of K-Fe-P interactions. Anna Amtmann (University of Glasgow)  
<http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN018508%2f1>

- £493K: Role of the chloroplast ubiquitin E3 ligase SP1 in abiotic stress tolerance in plants. Paul Jarvis (University of Oxford).  
<http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN006372%2f1>

UK-based plant scientists have also benefited from individual EU grants: Daniel Gibbs (University of Birmingham) and Diane Saunders (John Innes Centre) gained a ERC Starting Grants whilst Daniel Zilberman and Christine Faulkner (both at John Innes Centre) have gained ERC Consolidator Grants.

#### Outlook on Arabidopsis Research

The BBSRC funding provided to Arabidopsis-focused grants showed a slight decline in 2016 (£7.1M 2016, £10M, 2015; £21M, 2014; £10.2M, 2013, 10.9M, 2012). This suggests that we are at an important moment for the future of funding of Arabidopsis research in the UK. As part of its Global Challenges Research Fund (GCRF) and in funding calls associated with Developing Countries, the BBSRC is increasing its funding for research in crops species. It remains important to ensure that this funding is underpinned by fundamental research. However at this time it is unclear whether basic research that feeds into the crop-development pipeline will be funded. This will become clear as the first round of the successful GCRF grants are announced in early 2017.

By late 2017 the UK Plant Science Federation plan to publish a 'Roadmap for UK Plant Science'. This will recommend that aspects of the future UK bioeconomy dependent on plant science require maintaining the close links between basic academic research and potential industrial partners. The report states that removal of this basic research base will have a detrimental effect on UK productivity in this area.

### Road Map Related Activities

#### Arabidopsis Tools and Resources

Development of software tools as part of the CyVerseUK mode of CyVerseUS. <http://cyverseuk.org/>

John Brown (James Hutton Institute) is the corresponding author of the 'Arabidopsis Reference Transcript Dataset 2 (AtRTD2)'. This Arabidopsis transcriptome is designed for the accurate representation of levels of alternative splicing: <http://biorxiv.org/content/early/2016/05/06/051938>

BioDare (Biological Data Repository) is an online resource for the sharing, processing and analysis, with the main focus on timeseries data produced in circadian experiments. This resource was developed by a consortium of researchers from Edinburgh Synthesis (<https://www.biodare.ed.ac.uk/robust/>).

CPIB at the University of Nottingham continue to add free-to-use tools for phenotypic analysis on different scales <https://www.cpiib.ac.uk/tools-resources>.

Sofortios Tsafaris (University of Edinburgh) and colleagues have developed the PhenoTiki software and cheap-to-use hardware tool for the automated phenotyping of Arabidopsis rosettes (<http://phenotiki.com>).

The Cambridge University-JIC iGEM synthetic biology team developed a cheaper version of the GeneGun designed for facile assembly and subsequent bombardment of plant tissues <http://2016.igem.org/Team:Cambridge-JIC/Biologistics>

Wendy Harwood (John Innes Centre) and Nicola Patron (Earlham Institute) have established a resource for the transformation of barley and Brassica oleracea that is in part designed for the translation of genes whose functions have been discovered in Arabidopsis <http://www.bract.org/>

#### Outreach Activities

The BBSRC-funded GARNet community network continues to support UK plant science by providing regular updates regarding new developments that involve Arabidopsis research. This is provided via the @GARNetweets feed, the 'Weeding the Gems' blog <http://blog.garnetcommunity.org.uk/>, the GARNet website (<http://www.garnetcommunity.org.uk/>) and through the ArabUK email group. The dissemination of a weekly Arabidopsis Research Roundup provides an update on newly published papers and includes occasional audio-descriptions by leading academics.

The bi-annual GARNish newsletter continues to inform the worldwide community about recent events and technical developments (<http://www.garnetcommunity.org.uk/newsletters>). We have re-launched a YouTube channel that features interviews about important papers from UK Arabidopsis researchers.

### Conferences and Workshops

In 2016 GARNet organised three meetings that will bring together Arabidopsis researchers from the UK and beyond.

April: Integrating Large Data into Plant Science: From Big Data to Discovery, Exeter: [www.garnetcommunity.org.uk/sites/default/files/GARNetEgenis\\_Book.pdf](http://www.garnetcommunity.org.uk/sites/default/files/GARNetEgenis_Book.pdf)

September: GARNet2016- Innovation in the Plant Sciences, Cardiff University: [www.garnetcommunity.org.uk/sites/default/files/GARNet2016\\_Book\\_Online.pdf](http://www.garnetcommunity.org.uk/sites/default/files/GARNet2016_Book_Online.pdf)

December: GARNetNatVar16: Natural Variation as a tool for gene discovery and crop improvement, University of Cambridge: [www.garnetcommunity.org.uk/sites/default/files/GARNetNatVar16\\_Online\\_Final.pdf](http://www.garnetcommunity.org.uk/sites/default/files/GARNetNatVar16_Online_Final.pdf)

In April 2016 the UK hosted a set of meetings that brought together Arabidopsis researchers.

- The Sainsbury Lab, Cambridge University: Induced Plant Development
- UK Plant Science Federation (UKPSF): Plants in a changing world: molecule to ecosystem (John Innes Centre)
- Plant Proteases 2016: From Roles in Life and Death to Understanding Regulation and Action (University of Oxford)

In 2017 GARNet will organise three workshops and conferences that will involve Arabidopsis researchers:

- March- CyVerseUK Workshop at University of York. To introduce the software tools developed as part of the CyVerseUK grant for analysis of plant science data.
- April- Monogram2017 at the University of Bristol. GARNet will sponsor a session of the MonogramUK cereal meeting to encourage interaction between Arabidopsis and crop researchers.
- December- From Proteome to Phenotype: role of post-translational modifications at University of Edinburgh. SEB and GARNet will organise this meeting that introduces this exciting area of research

#### Selected Publications

During 2016 UK researchers authored over 160 papers that involved work on Arabidopsis, 64% of which were

#### Open Access.

These papers are documented weekly on the GARNet Blog: <http://blog.garnetcommunity.org.uk>

Abley K, Sauret-Güeto S, Marée A, Coen E (2016) Formation of polarity convergences underlying shoot outgrowths *eLife* 5:e18165 <http://dx.doi.org/10.7554/eLife.18165>

Arnold B, Lahner B, DaCosta J, Weisman C, Hollister J, Salt D, Bomblies K, Yant L (2016) Borrowed alleles and convergence in serpentine adaptation *PNAS* 113 (29) 8320–8325 doi: 10.1073/pnas.1600405113

## United States of America



<https://www.araport.org/community/group/naasc>

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### General Activities

#### Research Facilities

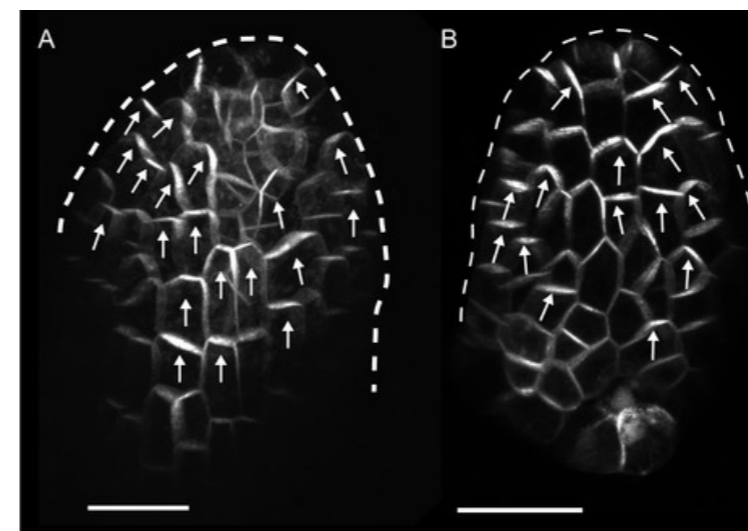
There are a large number of US institutions, companies, and facilities that conduct Arabidopsis research and it would be impossible to list them all. Therefore we list ABRC, the US stock center which, in partnership with NASC, the European Stock Centre (UK) and RIKEN BioResourceCenter (Japan), provide valuable Arabidopsis seed (and other) resources to the global community:

The Arabidopsis Biological Resource Center (ABRC) collects, preserves, reproduces and distributes diverse seed and other stocks of Arabidopsis and related species. Resources are donated by researchers from around the world. ABRC has been providing Arabidopsis and related species seed and other resources for research and education since 1991. At present ABRC has about 4,000 characterized mutant and 2,000 transgenic lines. Overall the seed collection is approaching half a million (~490,000) counting all the characterized and uncharacterized T-DNA lines, as well as the natural accessions. More than 100,000 samples are shipped annually to researchers and educators from 60 countries. ABRC holdings include: Arabidopsis seed stocks and clones, Arabidopsis cell lines and protein chips, seed and clone resources from related species, Cloning vectors and host strain, Education kits.

#### Current Arabidopsis Projects

There are a large number of US Arabidopsis projects that include many partners and encompass a vast array of topics. It would be impossible to parse out the 'major projects' within the report's space restrictions; therefore we list two NAASC-initiated and/or led community consortium proposals that focus on: (1) Research and training for plant biology in the 21st Century and (2) the Arabidopsis reference genome and related resources.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st



**Figure 28.** PIN1::PIN1:GFP expression in young WT and *kan1kan2* leaf primordia. (A) WT primordium of leaf 1, showing abaxial epidermis (a total of 10 leaves were imaged over 2 separate experiments). (B) As for A, but for a *kan1kan2* primordium (a total of 15 leaves were imaged over three separate experiments). White arrows indicate inferred polarities. Dashed white lines indicate leaf outlines. <http://dx.doi.org/10.7554/eLife.18165.003>

Choi K, Reinhard C, Serra H, Ziolkowski PA, Underwood CJ, Zhao X, Hardcastle T, Yelina N, Griffin C, Jackson M, Mézard C, McVean C, Copenhaver G, Henderson I (2016) Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. *PLoS Genet* 12(7): e1006179. doi:10.1371/journal.pgen.1006179

Feikea D, Seung D, Grafa A, Bischof S, Ellick T, Coiro M, Soyk S, Eickeb S, Mettler-Altman T, Lub K, Tricka M, Zeemanb SC, Smith A (2016) The Starch Granule-Associated Protein EARLY STARVATION1 Is Required for the Control of Starch Degradation in Arabidopsis Leaves *The Plant Cell* 28 6 1472-1489 <http://dx.doi.org/10.1105/tpc.16.00011>

Simonini S, Deb J, Moubayidin L, Stephenson P, Valluru M, Freire-Rios A, Sorefan K, Weijers D, Friml J, Østergaard L (2016) A noncanonical auxin-sensing mechanism is required for organ morphogenesis in Arabidopsis *Genes & Dev.* 2016. 30: 2286-2296 <http://dx.doi.org/10.1101/gad.285361.116>

#### Major Funding Sources

Biotechnology and Biological Sciences Research Council (BBSRC) <http://www.bbsrc.ac.uk/>  
The Gatsby Charitable Foundation <http://www.gatsby.org.uk/>  
European Research Council [http://ec.europa.eu/research/era/index\\_en.htm](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/>

century (ART-21); June 2015-May 2020; [http://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1518280](http://www.nsf.gov/awardsearch/showAward?AWD_ID=1518280)

(2) NSF Award #1262414 (PI C. Town, Co-PIs G. Micklem, M. Vaughn, A. Chan, J. Miller, K. Krampos) ABI Development: The Arabidopsis Information Portal; Sept. 2013- Aug. 2018; [http://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1262414](http://www.nsf.gov/awardsearch/showAward?AWD_ID=1262414)

We list here five US Arabidopsis researchers (3 are current or past NAASC members) selected in the past year as Howard Hughes Medical Institute (HHMI) or HHMI-Simons Foundation Faculty Scholars. These scholars are early-career scientists who have great potential to make unique contributions to their field. These awards support the research of each investigator for five years. <http://media.hhmi.org/FacultyScholars2016-gallery/>

US Arabidopsis faculty scholar awarded 2016: (1) Siobhan Brady (HHMI), University of California, Davis, maps the gene networks that regulate the development of plant roots. Comparing these networks in different cell types across different species, including important crops such as tomato and sorghum, reveals how some plants adapt to frequent droughts and other harsh environmental conditions.

(2) José Dinneney (HHMI-Simons), Carnegie Institution for Science, looks at the mechanisms plants use to sense water availability and adapt to drought conditions. He takes a holistic approach in his research, emphasizing the importance of developmental pathways and molecular genetic mechanisms in guiding acclimation and homeostatic processes.

(3) Elizabeth Haswell (HHMI-Simons), Washington University in St. Louis, is studying how plants use mechanosensitive ion channels to sense and respond to mechanical forces such as tension, touch, or vibration. She is also developing research tools that will enable her to measure membrane tension in live cells and to explore electrical signaling during trap closure in a carnivorous aquatic plant.

(4) Jennifer Nemhauser (HHMI), University of Washington, studies plant signaling pathways to learn how multicellular organisms develop and respond to their environment. She gleans information about molecular networks in natural systems and then synthetically programs these core functions into yeast cells to measure the effect of evolved and engineered changes. Her ultimate aim is to develop technologies that support small-hold farmers and foster global health.

(5) Daniel Zilberman (HHMI-Simons), University of California, Berkeley, investigates how epigenetic regulation of gene expression functions and evolves. His work with diverse, distantly related species aims to elucidate the evolutionary history of eukaryotic DNA methylation, understand how methylation patterns are

faithfully inherited across generations, and determine the influence of such epigenetic inheritance on the agricultural characteristics of crops.

### Outlook

NAASC has focused in the past 2 years on a community reassessment of training needs for 21st century plant biology, an effort supported through a grant to NAASC from the US National Science Foundation (PI Siobhan Brady). The Arabidopsis Research and Training for the 21st century (ART-21) Research Collaboration Network (RCN) has several activities to convene plant biologists with scholars from computational, quantitative, and education-oriented fields to assess the changing training needs for 21st century plant biology.

One focus of the five year program include revamping training to enable better understanding of the complexity of biological systems and associated new datatypes and increasing datasets that are available; this will require a larger focus on quantitative, systems and computational approaches in combination with biological experimentation. A second focus involves honing in on interdisciplinary training and education to enable translation of skills and knowledge gained in basic research to applied research that will support agricultural objectives. A third focus reflects the reality that non-academic 21st century biology careers will continue to grow and outnumber those in academia while the US student population continues to increase in diversity, mirroring larger national trends; requiring new approaches to training for diverse careers.

The NAASC-led series of collaborative activities includes: participatory workshops that address the key program foci and produce summary white papers to disseminate assessment and recommendations; support of US scientists to participate in the annual International Conferences on Arabidopsis Research (ICAR), in particular, early-career scientists and populations under-represented in US science; support of novel scientific sessions at the 2017 ICAR, and ongoing reassessment of community needs via surveys, workshops, and outreach activities.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; [http://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1518280](http://www.nsf.gov/awardsearch/showAward?AWD_ID=1518280)

### Road Map Related Activities

#### Arabidopsis Tools and Resources

Cistrome and Epicistrome of Arabidopsis transcription factors  
In O'Malley *et al.*, a novel method was developed that allows rapid analysis of the genomic DNA sequences that transcription factors are able to bind across the genome. In this study the authors utilize the nearly complete library of cloned transcription factors in Arabidopsis to

survey the genomic loci that transcription factors are able to bind using the DAP-Seq in vitro assay. In total, 529 transcription factors were characterized leading to the largest compendium of potential regulatory interactions in plants. The method uses fragmented genomic DNA and thus is sensitive to the effects of methylation on transcription factor binding. By comparing PCR amplified and native genomic DNA preps, the authors were able to identify transcription factors whose binding is methylation sensitive. These data have been integrated into an interactive web-based database that allows users to browse the transcription factors that are predicted to bind loci of interest ([http://neomorph.salk.edu/dap\\_web/pages/index.php](http://neomorph.salk.edu/dap_web/pages/index.php)).

O'Malley RC, Huang SS, Song L, Lewsey MG, Bartlett A, Nery JR, Galli M, Gallavotti A, Ecker JR (2016) Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell*. 2016 May 19;165(5):1280-92. doi: [10.1016/j.cell.2016.04.038](https://doi.org/10.1016/j.cell.2016.04.038). Erratum in: *Cell*. 2016 Sep 8;166(6):1598.

### Outreach Activities

Santa Fe, New Mexico (USA)- February 2017: NAASC organized a participatory workshop entitled "Workshop on Training and Education for Plant Biology Emerging 'Omics Technologies, Big Questions in Plant Biology, and Diverse Careers'. The activity, funded by an award to NAASC by the US National Science Foundation, included 20 participants (Arabidopsis/plant biology faculty, students, and staff), that spent 1.5 days in small group discussions of training needs and recommendations. NAASC co-developed an outreach activity on one evening that involved NAASC workshop participants traveling to a nearby community college for a networking and outreach dinner and career discussion with local college students and teachers. The outreach event was a collaboration between NAASC and members of the SoyMap project (also funded by the US National Science Foundation) including Michael Gonzales (New Mexico), Scott Jackson, and Bob Schmitz (University of Georgia).

ICAR 2017 (St. Louis, USA)- NAASC are the conference organizing committee and will fund participation of 110+ scientists in the 28th ICAR including 58 US and international invited speakers and conference committee members, 14 US under-represented minorities, 36 early-career researchers from US institutions, and several participants that will receive funding to defray childcare costs. Beyond the scientific sessions, a significant number of these supported participants will be involved in conference-related outreach activities including to locally-based agricultural biotech companies. Outreach to early-career researchers attending ICAR will also take place via several planned career workshops.

### Conference and Workshops

June 2017: St. Louis, Missouri, USA. 28th International Conference on Arabidopsis Research

(ICAR 2017). NAASC comprises the organizing committee for this annual main Arabidopsis conference taking place June 19-23. The ICAR is on track to have a significantly smaller turnout than in recent years (approximately 500 attendees, primarily from the US), due in part to an uncertain political climate and immigration policies of the new US government, led by the Trump administration.

Pre-ICAR Hands-On Workshop and Hackathon. NAASC, as part of their RCN award (1), are organizing a pre-ICAR hands-on workshop and hackathon at the Danforth Center to engage early-career scientists in learning key computational and bioinformatic skills via a one day 'Data Carpentry' workshop followed by an optional second day of wet-lab experimentation (Instructor: Roger Deal, Emory University) or 'learn by doing' hackathon for high-throughput phenotyping, programming, statistics, and plant biology education (Instructors, R. Cody Markelz and Nathan Miller, Univ. of WI- Madison).

The Data Carpentry workshop teaches basic concepts, skills and tools for working more effectively with data. The focus of the workshop will be on working with genomics data and data management and analysis for genomics research. It will cover data organization, connecting to and using cloud computing, the command line for sequence quality control and bioinformatics workflows. The phenotyping hackathon, running concurrent with the Data Carpentry workshop, will be joined by some of the workshop participants the second day, while the remainder will participate in an ATACseq wetlab taught by Roger Deal. The 2-3 hour lab will guide students through ATACseq including, for example, data generation, comparison of DNase hypersensitive data to ATACseq data, determination of open chromatin regions and transcription factor foot printing.

February 2017: Santa Fe, New Mexico, USA. NAASC RCN (1) Steering Committee members Joanna Friesner and Sarah Assmann convened the grant's second focus group with 20 participants entitled "Workshop on Training and Education for Plant Biology Emerging 'Omics Technologies, Big Questions in Plant Biology, and Diverse Careers". Workshop discussion topics were: What are the next big questions in plant biology (pure and applied)? How can genomics, proteomics, metabolomics, and other 'omics approaches help to answer these questions? What are the emerging 'omic experimental biology technologies needed by plant scientists of the 21st century? What are the bottlenecks to the technologies? How and where does Arabidopsis fit in? Training and education to address plant biology in the 21st century. Broader Impact, Diversifying, Training in Multiple Disciplines. A workshop white paper with recommendations and analysis will be forthcoming.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; [http://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1518280](http://www.nsf.gov/awardsearch/showAward?AWD_ID=1518280)

**Selected Publications**

Efroni I, Mello A, Nawy T, Ip PL, Rahni R, DelRose N, Powers A, Satija R, Birnbaum KD (2016) Root Regeneration Triggers an Embryo-like Sequence Guided by Hormonal Interactions. *Cell*. 165(7):1721-33. doi: [10.1016/j.cell.2016.04.046](https://doi.org/10.1016/j.cell.2016.04.046).

Yangnan Gu, Sophia G. Zebell, Zizhen Liang, Shui Wang, Byung-Ho Kang, Xinnian Dong<sup>4</sup>, Correspondence information about the author Xinnian Dong (2016) Nuclear Pore Permeabilization Is a Convergent Signaling Event in Effector-Triggered Immunity *Cell* 166, Issue 6, p1526–1538.e11

Heather M Meyer José Teles Pau Formosa-Jordan Yassin Refahi Rita San-Bento Gwyneth Ingram Henrik Jönsson James C W Locke Adrienne H K Roeder (2017) Fluctuations of the transcription factor ATML1 generate the pattern of giant cells in the Arabidopsis sepal. Fluctuations of a transcription factor that coincide with the G2 phase of the cell cycle pattern two interspersed cell fates in a multicellular system. *Elife* doi: [10.7554/eLife.19131](https://doi.org/10.7554/eLife.19131)

Xingyun Qi Soon-Ki Han Jonathan H Dang Jacqueline M Garrick Masaki Ito Alex K Hofstetter Keiko U Torii (2016) Autocrine regulation of stomatal differentiation potential by EPF1 and ERECTA-LIKE1 ligand-receptor signaling The stomatal precursor cell uses autocrine peptide-receptor kinase signaling to self-inhibit its differentiation potential in order to ensure proper stomatal development on the plant epidermis. doi: [10.7554/eLife.24102](https://doi.org/10.7554/eLife.24102)

Liang Song, Shao-shan Carol Huang, Aaron Wise, Rosa Castanon, Joseph R. Nery, Huaming Chen, Marina Watanabe, Jerushah Thomas, Ziv Bar-Joseph, Joseph R. Ecker (2016) A transcription factor hierarchy defines an environmental stress response network. *Science* Vol. 354, Issue 6312, aag1550 doi: [10.1126/science.aag1550](https://doi.org/10.1126/science.aag1550)

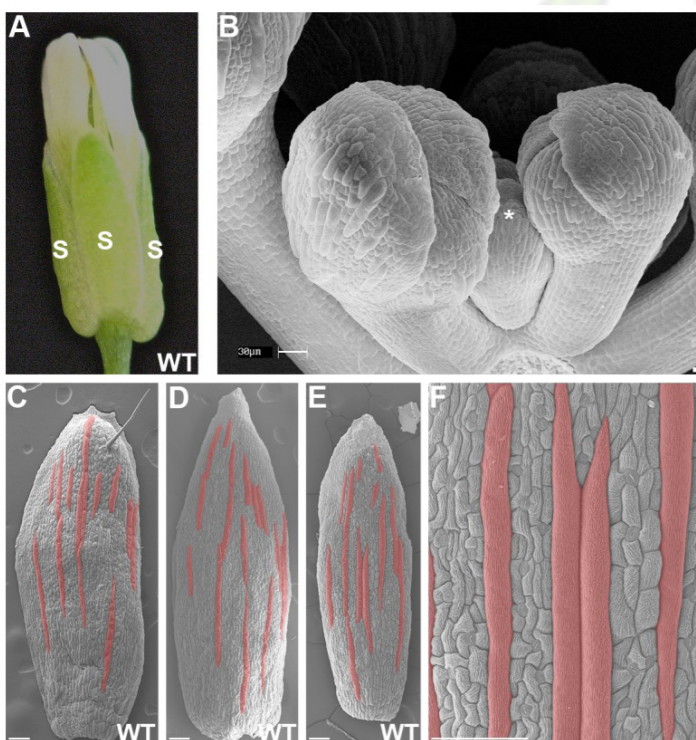
**Major Funding Sources**

Government  
US Arabidopsis Research is primarily supported by the National Science Foundation (NSF): <http://www.nsf.gov/>

Additional support:  
US Department of Agriculture (USDA): <http://www.usda.gov/>  
US Department of Energy (DOE): <http://energy.gov/>  
National Institutes of Health (NIH): <http://www.nih.gov/>

Private  
HHMI-GBMF: <http://news.sciencemag.org/2011/06/biomedical-institute-adds-15-plant-biologists-its-roster>  
<https://www.hhmi.org/scientists>

Bill and Melinda Gates Foundation: <http://www.gatesfoundation.org/>



**Figure 29.** The Scattered Pattern of Giant Epidermal Cells. <http://dx.doi.org/10.7554/eLife.19131>

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# Multinational Arabidopsis Steering Committee Annual Report 2016/17



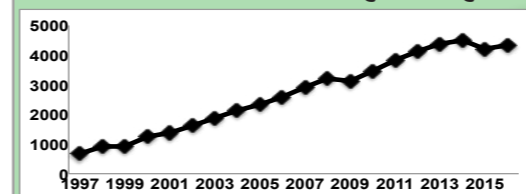
Download Full MASC Report: <http://arabidopsisresearch.org/index.php/en/publications>

## Country Highlights

- > **Argentina:** Legris *et al* (2016) Phytochrome B integrates light and temperature signals in Arabidopsis. *Science*.
- > **Australia:** Several Australian researchers working with Arabidopsis were listed in the Thomson Reuters High Cited Researcher for 2016.
- > **Austria:** Nine holders of current ERC Starting and Consolidator grants.
- > **Belgium:** New ERC Grants for Bert De Rybel and Daniel Van Damme.
- > **Canada:** Continued outstanding development of BAR resource and its integration with Araport.
- > **Chile:** Creation of Chilean Society for Plant Biologists.
- > **China:** Yao *et al* (2016) A non-canonical hormone receptor for strigolactone. *Nature*.
- > **Czech Republic:** Hosted EPSO plant biology congress "Plant Biology Europe EPSO/FESPB 2016".
- > **Denmark:** Olsen *et al* (2016) Mother-plant-mediated pumping of zinc into the developing seed. *Nature Plants*.
- > **Finland:** Hosting 29<sup>th</sup> ICAR in Turku in June 2018.
- > **France:** Continued development of outstanding resources at Saclay Plant Sciences Centre.
- > **Germany:** Updated AFGN website: <http://www.dbg-afgn.de/>
- > **India:** Challa *et al* (2016). Activation of YUCCA5 by the transcription factor TCP4 integrates developmental and environmental signals to promote hypocotyl elongation in Arabidopsis. *The Plant Cell*.

- > **Ireland:** Fort *et al* (2016) Disaggregating polyploidy, parental genome dosage and hybridity contributions to heterosis in Arabidopsis thaliana. *New Phytologist*.
- > **Israel:** Strong support for fundamental research at Israeli Centers of Research Excellence (I-CORE).
- > **Italy:** Ezquer *et al* (2016) The Developmental Regulator SEEDSTICK Controls Structural and Mechanical Properties of the Arabidopsis Seed Coat. *The Plant Cell*.
- > **Japan:** 75 scientists selected as Highly Cited Researchers 2016.
- > **Netherlands:** Arabidopsis research remains well funded.
- > **New Zealand:** Peters *et al* (2017) A conserved cis-regulatory module determines germline fate through activation of the transcription factor DUO1 promoter. *Plant Physiology*.
- > **Spain:** Martin *et al* (2016) Phytochrome and retrograde signalling pathways converge to antagonistically regulate a light-induced transcriptional network. *Nature Communications*.
- > **South Korea:** Welcomed 1000 delegates from 29 countries to ICAR2016 in Gyeongju.
- > **Sweden:** Porco *et al* (2016) Dioxygenase-encoding AtDAO1 gene controls IAA oxidation and homeostasis in Arabidopsis. *PNAS*.
- > **Switzerland:** Doblás *et al* (2017) Root diffusion barrier control by a vasculature-derived peptide binding to the SGN3 receptor. *Science*.
- > **United Kingdom:** BBSRC funded GARNet continues to support all aspects of Arabidopsis research.
- > **United States:** Hosting the 2017 ICAR conference.

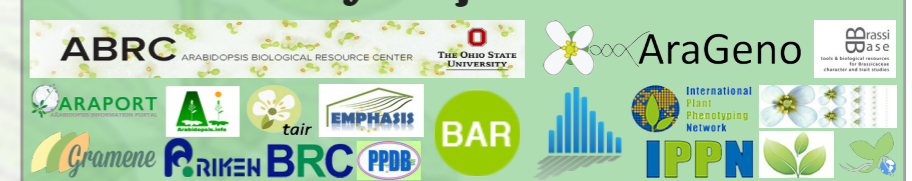
## Annual Global Arabidopsis Papers



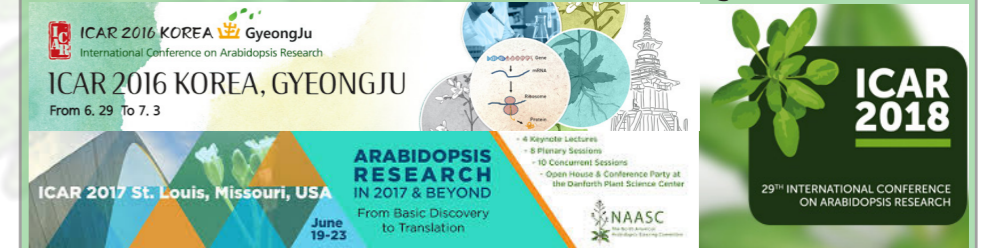
## 2016 Arabidopsis publications



## Community Projects and Resources



## International Conference for Arabidopsis Research







A French network for research, teaching, training and innovation in plant sciences

**Understanding the genetic, molecular and cellular mechanisms controlling the physiology and development of plants, as well as their interactions with fluctuating biotic and abiotic environments**

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