From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee (MASC)

Annual Report 2018/2019
The Multinational Arabidopsis Steering Committee

Annual Report 2018/2019

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MASC Inc Annual Report 2018/2019

The Multinational Arabidopsis Steering Committee

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

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

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

Acknowledgements

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

The MASC report 2018/19 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
  http://Arabidopsisresearch.org

> uNASC, The Nottingham Arabidopsis Stock Centre:
  http://Arabidopsis.info/progresreports.html

> TAIR, The Arabidopsis Information Resource:
  http://www.Arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp

> GARNet:
  http://garnetcommunity.org.uk/reports

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Further information can be found on the MASC website: www.Arabidopsisresearch.org
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Executive Summary and Analysis

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC).

Our first task is to thank the many contributors who have submitted pieces for this annual report. Without their input then MASC would be unable to prepare this document that aims to track the progress and challenges of the global Arabidopsis community. MASC are delighted to welcome the Global Plant Council as a new Project contributor as well as five Country Representatives who have submitted new reports from Estonia, Poland, Saudi Arabia, Singapore and Taiwan.

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

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

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

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

History of MASC

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

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

The major goal stated in this roadmap is to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole organism, within populations and fields of plants. There is clear progress across each of these areas but perhaps most gratifying is in the range of community resources that are available for people to use. These range from the well-established genome and transgenic tools such as TAIR or SIGnAL through to newly released software such as Plant PTV Viewer (https://dev. bits.yh.projects/ptvviewer/index.php) and the Vona Visualising Variant tool (http://user1.bse.vt.edu:8380).

In 2017 MASC evolved into the not-for-profit MASC Inc. includes non-paid positions for the President (Nicholas Provart), Treasurer (Siobhan Brady) and Secretary (Geraint Parry). These officers are supported by a Board of eight Directors who oversee general activities. At 2020 MASC directors will fulfill 4-year terms of office that will often coincide with their involvement in the organisation of an ICAR meeting or with the development of a new community grant. In 2020 the terms of two directors, Michael Wrzaczek and Barry Pogson, will come to an end so MASC Subcommittees and community members are welcome to suggest if there is a need for a new subcommittee. In this case please contact the permanent members of MASC (Nicholas Provart, Siobhan Brady or Geraint Parry) to discuss your ideas. Suggestions will be gratefully received and likely approved so the next step in the official formation of new subcommittee would be to assemble a group of individuals knowledgeable in the area who could contribute to the submission to the annual report as well as becoming involved in the organisation of subcommittee-related meetings and workshops at ICAR meetings.

Arabidopsis Community Projects and Resources

A key component of the mature Arabidopsis research community is the variety of resources that have been developed over the course of the past 20 years. These community projects, stock centres and bioinformatic resources enable researchers to fully integrate their research from its initial phenotypic description through to full multi-omic characterisation.
Global collaboration across plant science is no-better exemplified by the activities of the International phenotyping community that have been awarded a set of large multi-country grants that encourage integration between users. Perhaps more importantly they also provide access to phenotyping facilities by researchers who do not have the means at the home institution (https://www.plant-phenotyping.org/).

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

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

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

Country Highlights

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

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

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

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

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

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

Activities of MASC

MASC web page: www.Arabidopsisresearch.org

MASC Inc has now been incorporated as a not-for-profit in Canada for over a year. This requires non-paid positions for the President, Treasurer and Secretary, the current incumbents are Nicholas Provart, Siobhan Brady and Geraint Parry respectively.

In 2017 eight directors were elected for a range of term lengths. These will ultimately be for four years once the first round of rotations has ended. These directors officially took up their positions at the MASC annual meeting that took place at ICAR2018 in Turku, Finland. To ensure that only two directors rotate off the board the initial term lengths will be less than 4 years. This is a list of the inaugural board of directors and the length of their terms:

- 2018-2020: Michael Wrzaczek (Finland), Barry Popson (Australia)
- 2018-2021: Xuelu Wang (China), Elizabeth Haswell (United States of America)
- 2018-2022: Blake Meyers (United States of America), Sean May (United Kingdom)
- 2018-2023: Rodrigo Gutierrez (Chile), Masatomo Kobayashi (Japan)

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

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

The three main MASC activities are:

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

This MASC report was assembled by Dr Geraint Parry who also organises the MASC annual meeting. Dr Parry fulfills this role in addition to his current position as the GARNET coordinator in the UK (http://garnetcommunity.org.uk). It is hoped that this role will continue for the foreseeable future, taking advantage of the full-time funding provided to the UK plant science community by the Biotechnology and Biological Sciences Research Council (BBSRC).
Overall we very much encourage Arabidopsis researchers to become involved in MASC activities, e.g. subcommittees, projects and resources or as country representatives.

**International Conference on Arabidopsis Research (ICAR)**

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

These are the locations for upcoming ICAR meetings:

- 30th ICAR, Wuhan China: June 16th-21st 2019: https://www.surveymonkey.com/r/5ZHYMYS
- 33rd ICAR, Asia. 2022
- 34th ICAR, The Americas. 2023
- 35th ICAR, Europe. 2024

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

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

**The MASC Code of Conduct**

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

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


**The MASC website**

http://Arabidopsisresearch.org/

The MASC website is hosted in Canada by Hostpapa, maintained by Geraint Parry and has two broad functions. Firstly it is an information resource for previous MASC related activities. These include:

Reports of the MASC Subcommittees

Bioinformatics

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

Arabidopsis Informatics – TAIR: Staff at The Arabidopsis Information Resource (TAIR) have continued updating Arabidopsis gene data in TAIR from published literature over the past year. From March 2018-Feb 2019, TAIR added 4,431 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations generated by TAIR curators, TAIR community, UniProt and Gene Ontology Consortium (GOC) to the database. A total of 536 articles were used to annotate to 1,696 distinct loci. We added 3,783 articles of which 2,302 were linked to 3,923 genes. We curated 849 new gene symbols, 164 alleles, 304 phenotypes and added/updated 5,867 gene summaries. We processed 610 annotations provided by 89 community members spanning 99 papers. TAIR database is updated weekly and the most up to date annotations are accessible via TAIR’s website and tools (www.Arabidopsis.org).

TAIR also continues to provide publicly available releases of year-old datasets [https://www.Arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases]. The 18th public release from TAIR cumulative curated data set as of March 31, 2018. Educators can continue to request access to the “full” version of TAIR for teaching purposes. We look forward to integrating JBrowse into TAIR in the coming year.

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

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

DNA and RNA resources: John Brown’s lab in Dundee looked at how the Arabidopsis transcriptome responds at the level of alternative splicing, showing that hundreds of genes exhibit alternative splicing in response to cold [Calisto et al., 2018].

Marcus Schmidt’s group used INTACT to isolate phloem companion cell-specific transcripts and DNA for epigenomic analyses, identifying MRF1 as a regulator of flowering [Yoo et al., 2019].

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

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

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


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

A new Arabidopsis Interactions Viewer (AV2) was released by the Provart Lab [Dong et al., 2019]. The authors also predicted almost 10,000 protein-protein interactions (PPPs) using a docking algorithm, and have worked with BioGRID to incorporate 42,605 experimentally-determined PPPs into the new interface, along with 2.8M protein-DNA interactions. The new AV2 is available at http://bar.utoronto.ca/interactions2/.

Georgia Drakakis’s group published a cool study based on arrayed antibodies to identify the glycan contents of post-Golgi vesicles [Wilkop et al., 2019]. Youssef Belhadj’s group at GMI in Austria together with a number of collaborators published a leucine-rich repeat receptor kinase cell surface interaction network (CSRiRR) of 567 interactions between the extracellular domains of 225 LRR-RRks [Smakowska-Luzan et al., 2018]. These data are available in the AV2 mentioned earlier.

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

References
Reports from MASC Subcommittees

Selected Publication

Epigenetics and Epigenomics

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Roger Deal, roger.deal@emory.edu, Emory University

Open Tools and Resources for Arabidopsis Researchers

MASC Inc Annual Report 2018/2019
Figure 3: ZF108–TET1cd expression causes heritable late flowering and FWA up-regulation. (A) Schematic representation of the ZF108–YPet (Upper) and the ZF108–TET1cd fusions (Lower). (B) Flowering time of Col-0, fwa-4, and ZF108–TET1cd T1 plants. For each independent ZF108–TET1cd line, two different T3 populations were scored, one containing the ZF108–TET1cd transgene (+) and one that had the transgene segregated away in the T2 generation (−). For B and D, individual plants are depicted as colored dots. Leaf number corresponds to the total number of rosette and caulinar leaves after flowering. All plants above the dashed line are considered late flowering.

1) Targeted DNA demethylation of the Arabidopsis genome using the human TET1 catalytic domain (PNAS, 2018)
2) Paternal eosiRNAs regulate parental genome dosage in Arabidopsis (Nature Genetics, 2018)
3) Epigenetic activation of meiotic recombination near Arabidopsis thaliana centromeres via loss of H3K9me2 and non-CG DNA methylation (Genome Research, 2018)
4) Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation (PNAS, 2018)
5) Embryonic epigenetic reprogramming by a pioneer transcription factor in plants (Nature, 2018)

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

Selected Publications

- Cold Spring Harbor Asia meeting on Chromatin, Epigenetics & Transcription, Suzhou, China, April 2018 (Section on Epigenetic inheritance and Plant Epigenetics)
- Gordon Research Conference, Plant Molecular Biology, Holderness, NH, June 2018 (Session on Epigenetics)
- Midwest Chromatin & Epigenetics meeting, West Lafayette, IN, June 2018 (Session on Plant Epigenetics)
- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2018
- American Society for Plant Biologist, Montreal, Canada, July 2018 (Session on Plant Epigenetics)
- 29th International Conference on Arabidopsis Research, Turku, Finland, June 2018 (Session on Epigenetics)
- International Plant Molecular Biology meeting, Montpellier, France, August 2018 (Session on plant Epigenetics)
- Agricultural Bioscience International Conference, Weifang, Shangdong, China, September 2018 (Session on plant Epigenetics)
- International plant epigenetics symposium, Angers, France, October 2018
- UW-Madison Epigenetics symposium, Madison, WI, October 2018
- 2nd Uppsala Transposon symposium, Uppsala, Sweden, October 2018
- Plant Genomes in a changing environment, Cambridge, UK, October 2018
- Plant & Animal Genomes Conference, San Diego, CA, January 2019 (Session on Plant Epigenetics & Epigenomics)
- Japanese Society of Plant Physiologists 60th Annual Meeting, Nagoya, Japan, March 2019 (Session on inheritance and rewriting of cellular memory in plants)
- 10th International Conference on Arabidopsis Research, Wuhan, China, June 2019 (Plenary and concurrent sessions on Epigenetics)
- European workshop on plant chromatin, MPI Cologne, June 2019
- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2018
- Plant Epigenetics, Japan (hosted by Keiko Sugimoto and Toshito Ito) Date:TBD 2020

Selected Publications

- Cold Spring Harbor Asia meeting on Chromatin, Epigenetics & Transcription, Suzhou, China, April 2018 (Section on Epigenetic inheritance and Plant Epigenetics)
- Gordon Research Conference, Plant Molecular Biology, Holderness, NH, June 2018 (Session on Epigenetics)
- Midwest Chromatin & Epigenetics meeting, West Lafayette, IN, June 2018 (Session on Plant Epigenetics)
- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2018

Metabolomics

Kazuki Saito (Chair) kazuki.saito@riken.jp
RIKEN and Chiba University

Recently developed Open Tools and Resources for Arabidopsis Researchers

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

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

https://www.ebi.ac.uk/metabolights/METBLS528
Data resource: Metabolomics data deposited in MetaboLights (MTBLS528) - the natural variance of the Arabidopsis floral secondary metabolites (Tohge et al., 2018, Scientific Data, 5, 180051)

Recent activities of Subcommittee members.

Since metabolomics is an important component of Arabidopsis omics, a continuous goal of this subcommittee will be to promote metabolomics research of Arabidopsis leading to functional genomics and systems biology. Full integration of Arabidopsis-based metabolomics research with the activity of the Metabolomics Society (<http://www.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 metabolic datasets with other omics datasets. This will involve depositing metabolomic data in a usable format for data integration.

Future Activities of the Subcommittee.

The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where
Reports from MASC Subcommittees

the subcommittee members can join. The web interface will provide user with a user-friendly tool to search for Arabidopsis thaliana metabolomics data in available databases. In addition, the people in plant metabolomics community actively provide open tools and resources useful for Arabidopsis researchers as indicated above.

Conferences, Workshops and Training events

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

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

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

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

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

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

Selected Publications


Natural Variation and Comparative Genomics

J. Chris Pires
pirejs@missouri.edu
University of Missouri

Brian Dilkes
bdilkes@purdue.edu
Purdue University

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

Recently developed Open Tools and Resources for Arabidopsis Researchers

ViVa: Visualizing Variation in the Arabidopsis thaliana 1001 genomes project. Published at bioRxiv http://dx.doi.org/10.1101/488395 and Plant Direct (in press). The tool is available on the web (plantsynbolab.bse.vt.edu/viVa).

Questions can be directed to R. Clay Wright (wrightce@vt.edu)

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

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

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

Recent activities of Subcommittee members

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

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

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

Recent activities of Subcommittee members

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

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

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

Conferences, Workshops and Training events

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

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

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

Selected Publications

Aller EST et al. 2016. Comparison of the relative potential for genetic and epigenetic variation to contribute to plant defense evolution. G3 6(5):1733-1746


Proteomics
Joshua Heazlewood
jheazlewood@unimelb.edu.au
University of Melbourne
http://www.masc-proteomics.org/

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

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

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

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

Selected Publications


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

Systems and Synthetic Biology
Siobhan Brady
UC Davis
sbrady@ucdavis.edu

Recently developed Open Tools and Resources for Arabidopsis Researchers
- Pollak et al. (2019) Loop Assembly: a simple and open system for recursive fabrication of DNA circuits New Phytologist 222: 628-640

Conferences, Workshops and Training events
- Gordon Conference on Plant Molecular Biology: Dynamic Plant Systems June 10-15, 2018; Chai, Gloria Coruzzi (NYU); Vice-chair , Rob McClung (Dartmouth)
- 1st International Plant Systems Biology Meeting: https://sites.google.com/site/plantsystembiol/pictures
- EMBO Meeting: Integrating Systems Biology - From Networks to Mechanisms to Models, Heidelberg, April 2018 - organizers: Pascal Falter-Braun, Sandra Orchard, Sorina Popescu, Luis Serrano, Claudia Falter;
- SynBio: Crossing Frontiers, an international event bringing together scientists from the microbial, animal and plant field, 16-18 April 2018, Sainsbury Laboratory at the University of Cambridge, UK
- Open Plant Forum. 13-26 July 2018, Norwich, UK
- AICHE 2nd International Conference on Plant Synthetic Biology, Bioengineering, and Biotechnology, November 29 - December 1, 2018, Clearwater, Florida, USA
- Banbury Center: Revolutionizing Agriculture with Synthetic Biology, 2-5 December, 2018, Cold Spring Harbor, NV, USA
- International Association for Plant Biotechnology Congress, 19-24 August, Dublin, Ireland

Future Conferences or Workshops:
The Subcommittee is planning the 2nd International Plant Systems Biology in 2020, IPSB2020 in Venice! More details will be released shortly

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

Figure 6. Three TFs—CR4, SNZ, and CDF1—regulate 53% of the N-up-take/assimilation pathway genes. A time-based machine learning approach DFG was used to infer -target influence in a N-response gene regulatory network. The predicted gene targets are marked with different symbols. The different TFs are predicted by the GRN and validated by TF perturbations. The TFs are predicted by the GRN and validated by TF perturbations are shown by asterisks and thicker edge width. Gray circles indicate other cellular pathways that are predicted by the GRN and validated by TF perturbations are shown by asterisks and thicker edge width. Gray circles indicate other cellular pathways.
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> Extended Poster Session and Short Talks to Stimulate Discussions

www.garnetimaging19.weebly.com

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- Phillip Mullineaux (Essex)
- Myriam Charpentier (John Innes Centre)
- Giovanni Sesa (Imperial)
- Angiolillo Jones (Cardiff)
- George Littlejohn (Plymouth)
- Annalisa Rizza (SLCU)

- High Resolution Microscopy for Plant Cell Biology
- Imaging across Scales from Molecule to Organism
- Imaging with Novel Genetically Encoded Reporters

Arabidopsis Community Projects and Resources

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

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

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

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

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

Resource and Stock Centers

Arabidopsis Biological Resource Center (ABRC) (page 24)
Nottingham Arabidopsis Stock Centre (unNASC) (page 25)
RIKEN BioResource Center (BRC) (page 25)
The Arabidopsis Information Resource (TAIR) (page 26)
International Arabidopsis Informatics Consortium (IAIC) (page 27)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR) (page 29)
Adaptomics Project (page 31)
International Plant Phenotyping Resources (page 32)
Gramene (page 33)
Global Plant Council (page 35)

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

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

https://conf.Arabidopsis.org/display/COM/Resources
Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC)

www.abrc.osu.edu

David Somers
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ABRC Director

Emma Knee
knee.2@osu.edu
ABRC Associate Director

Recent Open Tools and Resources for Arabidopsis Researchers

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

The non-seed collection includes individual clones, and libraries from Arabidopsis thaliana and several other members of the Brassicaceae numbering almost 450,000 stocks as well as vectors, host strains, antibodies, cell lines and education resources. Most of the A. thaliana seed stocks donated in 2018 were T-DNA insertion mutant lines. These include lines from the GABI-Kat collection donated by B. Weisshaar through NASC and lines derived from the GABI-Kat collection - with many, many thanks to Bernd Weisshaar for such unstinting service to the community over the years.

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

Conferences, Workshops and Training events

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

Additional Information


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

Planned future activities of your project or resource.

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

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

If we (NASC and ABRC) can help you or promote your research to the community by distributing seed on your behalf then please do contact us - don’t wait for us to come to you.

See you in Wuhan!

The Nottingham Arabidopsis Stock Centre (uNASC)

http://www.Arabidopsis.info

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

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

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

For up-to-date details on stock donations or anything else that you wish to know, please do visit the NASC site, or contact curators@Arabidopsis.info at any time.

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

Conferences, Workshops and Training events

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

Additional Information

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

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

We have developed the Exp-Plant Catalog that provides the information of our Arabidopsis resources including natural accessions, individual mutants and transgenic lines, transposon-tagged lines, full-length cDNA clones, ORF clones of transcription factor genes, and genomic DNA clones to the community. In addition, a list of cultured cell lines such as Arabidopsis T87 cells and Tobacco BY2 cells are also available from the Catalog.


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

Planned future activities

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

The Arabidopsis Information Resource (TAIR)
www.Arabidopsis.org

Leonore Reiser
TAIR curator
lreiser@phoenixbioinformatics.org

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

Activities
The primary activity of TAIR is functional annotation of the Arabidopsis genome, with an emphasis on literature curation, to produce a ‘gold-standard’ reference genome dataset. From March 2018-Feb 2019, TAIR added 4431 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations generated by TAIR curators, TAIR community, UniProt and Gene Ontology Consortium (GOC) to the database. A total of 558 articles were used to annotate to 1960 distinct loci. We added 3783 articles of which 2302 were linked to 3921 genes. We curated 849 new gene symbols, 164 alleles, 304 phenotypes and added/updated 5867 gene summaries.

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

In the past year we have made many changes to the back end of TAIR that have significantly reduced downtime, as well as performance improvements to speed page loading. Other changes to enhance the data and user experience include (1) integration of the Bio Analytic Resource (BAR) eFP Expression Browser into TAIR locus pages, and (2) the complete integration of Araport 1.1 genome annotation into all of our tools (e.g. SeeViewer/GBrowse/Bulk downloads).

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

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

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

Planned future activities of your project or resource.

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

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

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


Additional Information
We gratefully acknowledge the support of the research community for their data contributions, suggestions for improvement and financial support.
Planned future activities of your project or resource.

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

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

Conferences, Workshops and Training events

The IAC held a workshop in May, 2018 in St. Louis, Missouri, USA, entitled “2018- Future of Arabidopsis Bioinformatics” to evaluate the current status of Arabidopsis bioinformatics and chart a course for future research and development. In advance of the meeting, organizers solicited input from the broader community via MASC, who distributed an online survey of plant bioinformatic needs (3). The workshop focused on several challenges, including the need for reliable and current annotation, community defined standard formats for data and metadata, and accessible and user friendly repositories/tools/methods for data integration and visualization.

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

The 2018 IAC workshop participants produced a white paper outlining the current state, challenges, and priorities for the future of Arabidopsis bioinformatics resources (4). See section (1) above for more details and linked article).

Additional Information

The IAC, and this material, are based upon work supported by the National Science Foundation under award #18062348. Any opinions, findings, and conclusions or recommendations expressed in this event, or in resulting work, are those of the participants and do not necessarily reflect the views of the National Science Foundation.

Open Tools and Resources for Arabidopsis Researchers

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

* 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or newer ePlant tool.
* 70,944 predicted protein-protein interactions plus 62,626 experimentally-determined PPIs (interologs also available) and ~2.8 million protein-DNA interactions, which can be explored with our new Arabidopsis Interactions Viewer 2 tool.
* 29,180 predicted protein tertiary structures and experimentally-determined structures for 402 Arabidopsis proteins.
* Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee’s site at 1001proteomes.masc-proteomics.org.
* Documented subcellular localizations for 11.7k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Recent activities of your project or resource.

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

We released a new Arabidopsis Interactions Viewer 2, which accesses our updated database of 91,175 experimentally-documented protein-protein interaction entries encompassing 62,626 unique pairs of proteins (through a collaboration with BioGRID, with some interactions being documented by multiple methods and/or groups; see Dong et al., 2019). We also predicted 9,065 protein-protein interactions by docking and validating a subset using X2H. These have added to the existing 70k PPIs predicted using the interolog method in our database (docking results are also described in Dong et al., 2019).

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

BAR Publications


German Research Priority Program ADAPTOMICS  
Evolutionary Plant Solutions to Ecological Challenges

– Molecular Mechanisms Underlying Adaptive Traits in the Brassicaceae.

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

Professor Dr. Ute Krämer  
Molecular Genetics and Physiology of Plants  
Ruhr University Bochum  
Bochum, Germany

Ute.Kraemer@ruhr-uni-bochum.de  
https://www.ruhr.de/mppg/Seiten_en/index_e.html

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

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

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

ADAPTOMICS brought together scientists specialized in different fields, for example ecology, molecular biology, genomics and population genetics, through collaborative research projects, two well-attended International Symposia held in Bad Neuenahr (Germany, 2014) and Berlin (Germany, 2017), as well as a number of specialized workshops. A joint project used shared data to examine genomic sequence variation across the Arabidopsis genus. The “Brassibase” database is a repository of taxonomy, systematics and evolution of the Brassicaceae, as well as of germplasm resources and specimen collections. Specific methodology was assembled in an “ADAPTOMICS Teaching Module”.

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

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

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

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

BrassBase is available here:  
https://brassicabase.uni-halle.de/
International Plant Phenotyping Resources
Roland Pieruschka
Julich Plant Phenotyping Centre
r.pieruschka@ifz-juelich.de

International Plant Phenotyping Network
http://www.plant-phenotyping.org/

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

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

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

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

EMPHASIS
http://www.emphasis.plant-phenotyping.eu/

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

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

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

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

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

Conferences, Workshops and Training events
EMPHASIS aims at organizing annual European plant phenotyping conferences starting in 2020. The first conference is in preparation.

European Plant Phenotyping Network 2020

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

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

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

Planned future activities of your project or resource.

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

Gramene: A comparative genomics and pathways resource for plants
Marcela Karey Tello-Ruiz (Project Manager)
tello.ruiz@cabi.edu
Doreen Ware (PI)
http://www.gramene.org

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

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

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

Within the past year, the alignments subset for A. thaliana grew from 34 to 57, and now includes alignments between A. thaliana and each of A. lyrata and A. halleri. In addition, A. lyrata was aligned to each of Medicago truncatula, Oryza sativa (japonica rice), Theobroma cacao (cacao), and Vitis vinifera (grapevine); and A. halleri to Japonica rice, cacao, and grapevine. Our synteny collection was also updated to include synteny maps for A. thaliana and each the following five species: A. halleri, Brassica rapa, Japonica rice, cacao, and grape; and for A. lyrata and grapevine. We continue to host 12.9 million Arabidopsis SNPs from the 1001 Arabidopsis Genomes Project. Variants are provided in the context of gene annotation, gene regulation, and protein domain structure, along with predicted functional consequences (e.g. missense variant), and genotypes. The Arabidopsis
SNP set was combined with phenotypic data for 95 inbred lines described in Atwell et al (2010). In our continued collaboration with the Expression Atlas project (EMBL-EBI), we provide baseline expression data for 23 species, including A. thaliana and A. lyrata through our Ensemble genome browser and Plant Reactome pathways interfaces. In addition, we provide direct links to differential gene expression data on the EMBL-EBI Expression Atlas website for a partially overlapping set of 23 species, including A. thaliana and A. lyrata. In collaboration with Reactome, Gramene hosts 293 metabolic and regulatory pathways curated in rice and inferred in 79 additional plant species (including the three Arabidopsis species in Gramene) based on orthology. Reactome pathways are checked and peer-reviewed prior to publication to ensure factual accuracy and compliance with the data model, and a system of evidence tracking ensures that all assertions (which use community standard controlled vocabulary ontologies) are supported by primary literature. Gramene's integrated search capabilities and interactive views facilitate visualizing gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, pathways, and cross-references to other bioinformatics resources, including ArabaPort, TAIR and NASC. Analysis tools to support comparative analyses of our data as well as user-provided data (e.g., BLAST/BLAT sequence aligner, sequence assembly converter for TAIR9/TAIR10 genome coordinates, genetic variant effect predictor, BioMart, Reactome pathways analysis/visualization of OMICS data and multi-species pathway comparisons). Gramene is committed to open access and reproducible science based on the FAIR (Findable, Accessible, Interoperable and Reusable) data principles. We are a phylogenomic resource, built upon best-of-class open source software, Ensembl, Reactome, and Expression Atlas infrastructure platforms. Thus, Gramene's genome portal was developed on the Ensembl infrastructure and in collaboration with the Ensembl Genomes project (EMBL-EBI); the pathways portal of the project is the Plant Reactome (http://plantreactome.graemene.org); and in collaboration with the Expression Atlas project (EMBL-EBI), we provide experimental baseline expression data from both our genomes and pathway browsers. Integrating across these platforms, Gramene has developed a powerful and flexible document-based architecture that enables advanced searching via a web-service accessible by a variety of programming languages, each platform supporting web-based and programmatic access through application programming interfaces (APIs).

Extensive use of ontologies, database cross-references, common data formats, metadata, community engagement and open-source software promotes interoperability within the ecosystem of informatics data and services. Gramene is supported by an NSF grant IOS-1127112, and partially from USDA-ARS (1907-21000-030-00D).

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

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

Conferences, Workshops and Training events

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

The Global Plant Council

Ibel Mendoza-Paudereux
isabel@globalplantcouncil.org

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

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

Planned future activities of your project or resource.

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

Conferences, Workshops and Training events

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

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

Additional Information

GPC is devoted to free dissemination of research information, specifically plant science events, resources and news from around the world. It is possible to follow the GPC updates by joining their 6,500 followers on Twitter (@GlobalPlantGPC), 2100 followers in Facebook, signing up to the monthly newsletter (http://tinyurl.com/GPCebulletin) or simply visiting their website (www.globalplantcouncil.org) for daily updates on news and events.
Analysis of Arabidopsis Publications

Outlook for 2018/19

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

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

The pre-eminence of China Plant Research

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

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

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

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

These technical improvements might include but aren’t limited to:
1- Improvements in next generation sequencing for genome and/or expression analysis
2- Advances in bioinformatics analysis of big datasets
3- Improved techniques for bulk transformation

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

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

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

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

Therefore we cannot claim that the numbers shown in figure 14 are a true representation of the absolute number of patents but rather it is the trend of the line that is most informative. The 2016 MASC report (Arabidopsisresearch.org/images/publications/mascreports/2016_MASCReport.pdf) showed that there was many more patents that include work from Arabidopsis importantly underpins those developed in other species. However gaining direct evidence for this relationship is almost impossible without undertaking an extremely rigorous analysis, which is outside the scope of this report.

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

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

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

Country Reports

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

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Argentina

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Use of Arabidopsis

There are more than 35 groups conducting varied research with Arabidopsis in Argentina. They work in different Institutes and Universities scattered throughout the country in cities such as Buenos Aires, Rosario, Mar del Plata, Santa Fe, Córdoba, Mendoza and Bariloche.

Selected Publications


Major Funding Sources
Fundamental and translational research can be funded by the Australian Research Council
www.arc.gov.au
Translational research is funded by the Grains Research Development Corporation
http://gsrc.com.au
Industry collaborations can be funded by the Australian Research Council Linkage Programs
www.arc.gov.au

Austria
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University of Natural Resources and Life Sciences BOKU, Vienna

Use of Arabidopsis
Although Austria is a small European country with around 8.8 mio inhabitants Arabidopsis research is highly active at seven institutions, the University of Natural Resources & Life Science Vienna (BOKU) (www.boku.ac.at/en), the Gregor Mendel Institute of Molecular Plant Biology (GMI) (www.gmi.oeaw.ac.at), the Max F Perutz Laboratories (MFPL) (https://www.mfpl.ac.at), the Institute of Science and Technology, Austria (IST Austria) (ist.ac.at/en), the AT Austrian Institute of Technology (https://www.ait.ac.at/), the University of Graz (https://botanik.uni-graz.at/de/forschung/molaeul-plant-physiology/).

The 23 research groups focus on molecular genetics (including population, epi-, and developmental genetics), physiology/). The 21st European Network on Plant Endomembrane Research, ENPR 2018; 4.-7. September 2018 (Main organisers Yasin Dagdas and Jürgen Kleine-Vehn)

Selected Publications


Root chip allowing for immediate treatments and simultaneous confocal live imaging


Root chip allowing for immediate treatments and simultaneous confocal live imaging

Figure 17 SMC7 proteins are evolutionary conserved across eukaryotes and primarily known for their function in nonsense mediated RNA decay (NMD). In contrast to other NMD factors, SMC7 proteins underwent independent expansions during evolution indicating their propensity to adopt novel functions. (A) Diagram of SMC7 and SMC7L genes with positions of T-DNA insertions and functional domains. (B) qRT-PCR analysis of SMC7L and SMC7 transcripts. Positions of the regions amplified by PCR are indicated in (A). Error bars represent SEM of three biological replicas. (C) Five week-old wild type and mutant plants. Taken from Capitao et al., 2018, doi: 10.3389/fpls.2018.01602.

**Major Funding Sources**

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

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

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


Major Funding Sources

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework (cordis.europa.eu)
- Belgian Federal Science Policy Office (www.belspo.be)
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; www.iwt.be)
- Fonds de la Recherche Scientifique (FRS; http://www.frs-frs.be)
- European Research Council (erc.europa.eu)
Use of Arabidopsis

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

Hence, other species are usually employed, particularly crop species, given that dedicated grants programs are usually only starting to use Arabidopsis and there is a gradual increase in the usage of Arabidopis as a model plant to molecular and genetic studies due to its power as an easily developed model plant. Only starting to use Arabidopsis there is a gradual increase in the usage of Arabidopsis as a model plant to molecular and genetic studies due to its power as an easily developed model plant.

Conferences, Workshops and Outreach events

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

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

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

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

Selected Publications


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

Major Funding Sources

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

Although funding in Brazil is available through several calls, it is becoming increasingly difficult to obtain funding for basic research, particularly to finance Arabidopsis research, given that the general trend is a more supportive program for applied research.
Canada
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Use of Arabidopsis
Approximately 55 groups conduct varied research with Arabidopsis in Canada.

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

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

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

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

A new Arabidopsis Interactions Viewer (AV2) was released by the Provart Lab (Dong et al., 2019). The authors also predicted almost 10,000 protein-protein interactions (PPIs) using a docking algorithm, and have worked with Biogrid to incorporate 42,605 experimentally-determined PPIs into the new interface, along with 2.8M protein-DNA interactions.

The new AV2 is available at: http://bar.utoronto.ca/interactions2.

Yousof Belhkadir’s group at GMI in Austria together with a number of colleagues published a leucine-rich repeat receptor kinase cell surface interaction network (CSLRR) of 567 interactions between the extracellular domains of 225 LRR-RKs (Smakowska-Luzan et al., 2018). These data are available in the AV2 mentioned earlier.

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

Selected Publications


Conferences, Workshops and Outreach events

January 9th - 10th, 2018

**Course: "Genetical Improvement in Pseudocereals and the Socio-Cultural Implications."**

This course was held at Universidad de Chile, Santiago - Chile.

The Ph.D. program "Ciencias Silvoagropecuarias y Veterinarias" offered the course entitled "Genetical improvement in Pseudocereals and the socio-cultural implications" to students.

Organizer: Escuela de Postgrado, Facultad de Ciencias Agropecuarias, Universidad de Chile.

July 26th - 24th, 2018

**2nd Scientific Meeting on Vegetal Biology and Biotechnology**

The meeting was held in Salón Bicentenario de la U. de Talca, Campus Lircay, Talca – Chile.

The meeting was organized including three thematic areas: Biotic and abiotic stress, phylogenetics resources, and molecular and functional ecology.

Organizer: Ph.D. program on Sciences, mention plant genetics on Instituto de Ciencias Biológicas de Universidad de Talca – Chile.

August 21st, 2018

**Seminar Wayne Parrott: Plant Breeding and CRISPR**

Seminar presented by Wayne Parrott Ph.D., an international expert on the research of new techniques of genetic improvement of agronomical species from the University of Georgia.

Organizer: American Academy of Science and Technology, UC Davis Chile, Universidad Andrés Bello and Universidad de Talca.

October 2nd - 3rd, 2018

**Workshop on Plant Cell Wall**

This workshop was held at Plant Biotechnology Center at Universidad Andres Bello, Santiago – Chile.

Organizers: Plant Biotechnology Center, Universidad Andrés Bello and Chilean Society of Plant Biologists.

November 29th, 2018

**Workshop "Applied Plant Biology III"**

This workshop was held at Auditorio Instituto de Ciencias Biológicas, Talca – Chile.

Organized by The Functional Genomics, Biochemistry & plant physiology group, ICB – Universidad de Talca.

Guests: Dr. Jorge Paiva, Dr. Hannelin Roschhättt, Dr. Ross Atkinson

### December 3rd - 6th, 2018

**XII Chilean Plant Biology Meeting**

The last meeting was held at Enjoy Hotel in Puerto Varas - Chile. It included several symposiums for instance Plant Biotic Interactions, Natural Variation & Plant Breeding, Ecophysiology and Plant-Water Relationship, Iron Homeostasis and Plant Nutrition, Plant Biotechnology for Agriculture Development, Postharvest. Nearly 250 abstracts were submitted, including works from national and international research centers, presented by undergraduate and graduated students, young scientist, and faculty from the major plant research centers in the country.

Organizer: Chilean Society of Plant Biologists

January 14th - 20th, 2019

**International Graduate Course on Ecophysiology of the Rhizosphere**

This workshop was held at Parque Katalapi, Región de Los Lagos, Chile.

Main topics of the course: Soil properties, Plant nutrition, Rhizosphere components, Mycorrhizae diversity, Nitrogen fixation, Salt tolerance, Cluster roots functioning, Rhizodeposition, organic matter and soil microorganisms, Plant growth promoting rhizobacteria (PGPR), Endophyte, Phytohormones, Molecular plant microbe-interaction.

Organizers: Luisa Basquín, Universidad de Concepción; Alex Valentine, Stellenbosch University; Alejandro Zúñiga Feist, Universidad Austral de Chile.

January 9th, 2019

**Seminar: Orange on Top: Is There Mutual Exclusion Between Anthocyanin and Carotenoids Biosynthesis in Petunia Flowers?**

This seminar was held at Facultad de Ciencias de Universidad de Chile (Santiago – Chile)

Organizers: Universidad de Chile – Santiago, Chile. Guest: Dr. Julian Verdón, Wageningen University, The Netherlands

### Selected Publications


China

Yuling Jiao ylijiao@genetics.ac.cn
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China

Use of Arabidopsis

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

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

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

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

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

Transcription factor library

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

Shoot cell type-specific transcriptome profiling lines

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

New Software Tools

- Arabidopsis Root Cell Atlas
  http://wanglab.ippe.ac.cn/rozrootatlas/

- HD2.0: Arabidopsis hormone database 2.0
  http://ahd.chi.pku.edu.cn

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

- PlantTFDB: Plant transcription factor database
  http://planttfdb.chi.pku.edu.cn/invlink.php

- PSRobot: Plant small RNA analysis toolbox
  http://omicslab.genetics.ac.cn/psRobo/

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

Selected Publications


**Major Funding Sources**

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

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

Use of Arabidopsis

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

Selected Publications


**MASC Country Reports**

**Czech Republic**

Viktor Žárský
viktor@natur.cuni.cz

**Use of Arabidopsis**

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

**Conferences, Workshops and Outreach events**

- 43rd FEBS Congress 7.-12. July, 2018 Prague, Czech Republic
- Plant Biology CS 2019, University of South Bohemia and Biology Centre CAS, Ceske Budejovice, Czech Republic: 25th–30th 2019 www.plantbiologycs.cz

**Selected Publications**


**Major Funding Sources**

1. Czech Science Foundation/GACR, Prague
http://www.gacr.cz

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

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

4. Ministry of Agriculture, National Agency for Agricultural Research
https://goo.gl/PJGc1O

**Figure 24. EXO70H4 recruits PMR4 to the ingrowths of the trichome cell wall.** A. Left, Overall view of the trichome expressing mCh-EXO70H4 (magenta) and GFP-PMR4 (green). Projection of 14 sections. Yellow dotted square depicts detailed view on the right. Right, Detailed view of a single section with cell wall ingrowths decorated by EXO70H4 and PMR4 with a 2D histogram for the colocalization (Pearson’s R value, 0.35; Lin ICQ value, 0.127).
**Denmark**

Michael Palmgren

palmgren@plen.ku.dk

University of Copenhagen, Department of Plant and Environmental Sciences

**Use of Arabidopsis**

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

**Conferences, Workshops and Outreach events**

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

**Selected Publications**


**Major Funding Sources**

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

**Estonia**

Liina Jakobson

liina.jakobson@taltech.ee

Tallinn University of Technology

**Estonian University of Life Sciences**

Hanna Hörrak

hanna.horrak@emu.ee

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

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

Gas exchange analysis equipment, new improved and much faster version #3, which enables real-time gas exchange measurements such as stomatal conductance, transpiration, photosynthesis etc of single intact Arabidopsis plants in controlled and adjustable conditions. Air temperature, air composition (humidity, CO2, O3 etc) and light conditions can be manipulated throughout the experiment.

**Selected Publications**


**Major Funding Sources**

Estonian Research Council

www.etag.ee

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

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

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

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

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

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

National Plant Phenotyping Infrastructure (http://www.plantphenotyping.inria.fr)
PhenomatoR: An R Package for the Analysis of Large-Scale Phenomic Data (https://github.com/jsalojar/PhenomatoR)
PhenomatoR https://helsinki.fi/en/infrastructures/national-plant-phenotyping/initiated or funded in 2018 or early 2019

Selected Publications


Major Funding Sources

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

Selected Publications


Figure 28 DET1 controls histone H2B monoubiquitination levels by opposing DUBm activity. Proposed model depicting the CID complex activity in regulating histone H2Bub homeostasis through ubiquitin-mediated control of the DUBm stability. UB2P2 is a Ub-like monoubiquitin binding and ubiquitin-conjugating enzyme 1 involved in ubiquitination of the DUBm. DUBm activity is regulated by ubiquitin binding and ubiquitin-conjugation enzymes, which are involved in ubiquitination of the DUBm. DUBm activity is regulated by ubiquitin binding and ubiquitin-conjugation enzymes.

Major Funding Sources

- Research organizations such as CNRS, INRA, CEA or Universities provide reciprocal 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-ant/about-the-french-national-research-agency/, provides funding for project-based research. The main calls deal with societal issues that do not very well support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is decreasing, although since 2017 ANR calls include again calls dedicated to fundamental mechanisms.

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

- NQuire: a statistical framework for ploidy estimation

- German Plant Phenotyping Network http://www.dppn.de/dppnEHome EHome_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.gabiip.org

- SNOMED CT Terminology Database

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

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

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

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

Germany

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University of Tübingen, Tübingen

Use of Arabidopsis

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

Selected Publications

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

- German Plant Phenotyping Network http://www.dppn.de/dppnEHome EHome_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.gabiip.org

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

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

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

- NQuire: a statistical framework for ploidy estimation

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

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


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

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


- 24th EUCARPA Matze and Serghium Conference, 09. – 09.10.2019, Weihenstephan/Freising, Germany (https://www.events.turn.de/intend/index.php/subs=120)


Workshops

miRNA mobility is regulated independently from small protein movement. a–d Free GFP expressed in phloem companion cells (pSUC2:GFP) diffuses throughout a, c young sink leaves, but behaves cell autonomously in b, d mature source leaves. e–h In p35S:3xNLS-GFP mobility at defined cell-cell interfaces governs their impact as positional signals. Nature Comm. 9:3107; doi: 10.1038/s41467-018-05571-0.


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

Outreach Events

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

- Open House of the Tübingen MPI [http://www.mpi-tuebingen.mpg.de/institute/information-for-the-public.html]
- Open House of the Tübingen MPI [http://www.mpi-tuebingen.mpg.de/institute/information-for-the-public.html]
- 5th Plants and People (P&P) Conference, 03. – 04.09.2019, Potsdam, Germany [https://plants-and-people.mpg.de/]
- Major Funding Sources

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

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- Open House of the Tübingen MPI [http://www.mpi-tuebingen.mpg.de/institute/information-for-the-public.html]
- Open House of the Tübingen MPI [http://www.mpi-tuebingen.mpg.de/institute/information-for-the-public.html]
- 5th Plants and People (P&P) Conference, 03. – 04.09.2019, Potsdam, Germany [https://plants-and-people.mpg.de/]

Selected Publications


Use of Arabidopsis

These institutions conduct some research with Arabidopsis:
- Agricultural University of Athens, Athens, Greece
- Aristotle University of Thessaloniki, Thessaloniki, Greece
- National and Kapodistrian University of Athens, Athens, Greece
- University of Crete, Crete, Greece

Selected Publications


Major Funding Sources

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


Hellenic Foundation for Research and Innovation (HRF) www.efkev.gr/en/homepage/

Figure 30 Auxin signaling and transport and cytokinin signaling, as detected by the DR5::GFP, PIN1::PIN1-GFP and TCS::GFP reporter genes respectively, in Arabidopsis thaliana flower stage 9 and 12 gynoecia. (a–d) DR5::GFP expression in (a) wild-type (WT), (b) gcn5-1, (c) clv1-1 and (d) clv1-1gcn5-1 gynoecia. (e–h) PIN1::PIN1-GFP expression in (e) WT, (f) gcn5-1, (g) clv1-1 and (h) clv1-1gcn5-1 gynoecia. (i–l) TCS::GFP expression in (i) WT, (j) gcn5-1, (k) clv1-1 and (l) clv1-1gcn5-1 gynoecia. Bars, 250 μm. GCN5, GENERAL CONTROL NON DEREPRESSIBLE 5; CLAVATA1, CLAVATA.
**MASC Country Reports**

**Ireland**

Prof. Charles Spillane
Genetics & Biotechnology Lab, Plant & AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway, University Road, Galway H91 REW4, Ireland
charles.spillane@nuigalway.ie  www.spillanelab.org

**Use of Arabidopsis**

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

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

1. Prof Charles Spillane, Genetics and Biotechnology Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUIGalway), Ireland.
2. Dr. Ronan Sulpice, Plant Systems Biology Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUIGalway), Ireland.
3. Dr. Zoe Popper, Plant Cell Wall Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUIGalway), Ireland.
5. Dr. Fiona Doohan, School of Biology & Environmental Sciences, University College Dublin, Dublin, Ireland.
6. Dr. Emanuelle Graciet, School of Biology, National University Belfast, Northern Ireland.
7. Dr. Rainer Melter, School of Biology and Environmental Science, University College Dublin, Dublin, Ireland.
8. Dr. Mario Fares, Smurfit Institute of Genetics, Trinity College Dublin.
9. Dr. Rainer Melter, School of Biology and Environmental Science, University College Dublin, Dublin, Ireland.
10. Prof. Charles Spillane, Genetics & Biotechnology Lab, Plant & AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUIGalway), Ireland.

**Selected Publications**


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**Major Funding Sources**

Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/
Department of Science & Technology (DST), Government of India http://www.dst.gov.in/
Science and Engineering Research Board (SERB), Government of India http://www.serbonline.in/
Council of Scientific and Industrial Research (CSIR), New Delhi http://www.csirhrdg.res.in/
Indian Council of Agricultural Research (ICAR), New Delhi http://www.icar.org.in/
University Grants Commission, New Delhi https://www.ugc.ac.in/
Use of Arabidopsis

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

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

Conferences, Workshops and Outreach events

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

Publications


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

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

Conferences, Workshops and Outreach events

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

Selected Publications


Use of Arabidopsis

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

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Conferences, Workshops and Outreach events

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

Selected Publications


Mozota Seki, mozota.seki@rikken.jp
RIKEN CSRS
Masatomo Kobayashi, masatomo.kobayashi@rikken.jp
RIKEN BRC

Use of Arabidopsis
Approximately 350 labs in Japan use Arabidopsis in their research.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019
RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) (http://www.css.riken.jp/)
PRIMePlatform for RIKEN Metabolomics (http://prime.psc.riken.jp/)
Arabidopsis metabolomics platform publicly available platform resources:
- AmiExpress Arabidopsis metabolome expression database (http://bit.ly/1P2BYgw)
- LC-MICS Branch (http://bit.ly/1P2Zhm)
- PRIMe Web Applications
- PRIMELink integrates 3 above databases
(AmiExpress, MS2T and ReSpect) for bi-directional search from gene or metabolite (http://bit.ly/TRX48c)
- ReSpect RIKEN MSn Spectral database for phytocompounds (http://bit.ly/1P2Zau)
- Hifi Heteroatoms-containing Ion Finder (http://bit.ly/1nR3j6)
- PASMet - Prediction, Analysis and Simulation of Metabolic Reaction Networks (http://pasmet.riken.jp/) Distribution and Redistribution
- Drop Met mass-spect pre-processed metabolome analysis (http://bit.ly/1LV5xgv)
- Other RIKEN CSRS developed tools and resources:
  - AtGenExpress Arabidopsis Gene Expression profile database (http://bit.ly/1P2YTb)
  - Plant/PrAS (Plant-Protein Annotation Suite) database of phytochemical and structural properties, and novel functional region in plant protomers (http://plant.pras.riken.jp/)
  - MassBank: Public repository of mass spectral data for sharing spectra among research communities (http://www.massbank.jp/)
  - Plant/PrAS (Plant-Protein Annotation Suite) (http://plant-pras.riken.jp/)

Major Funding Sources
The Italian Ministry of Education, University and Research funded:
- Project SIR (2015-2018) for independence of young researchers, on ‘MADS box transcription factor SHORT VEGETATIVE PHASE, understanding the molecular mechanism and involvement in sense and antisense transcript regulation. RSB114BT.2. Coordinator Veronica Gregis.
- Local funding from: Sapienza University of Rome, Roma Tre University of Rome and University of Milan

Further funding:
- Project Horizon 2020 EU RISE project “EXPOSEED” Exploring the molecular control of seed yield in crops (https://ec.europa.eu/research/mariecurieactions/about-research-innovation-staff-exchange_en)
- Project Promotion of consumer health of the National technological cluster Agrifood. Participant Ida Ruberti.
- Project Promotion of consumer health of the National technological cluster Agrifood. Participant Ida Ruberti.
- Project Horizon 2020 EU RISE project “EXPOSEED” Exploring the molecular control of seed yield in crops (https://ec.europa.eu/research/mariecurieactions/about-research-innovation-staff-exchange_en)
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- Project Promotion of consumer health of the National technological cluster Agrifood. Participant Ida Ruberti.


Figure 35: Dose-response test of the AtPep3/AT13 peptide affected in salinity stress tolerance. (Left) Representative images of plants from the AT13.5 dose-response test. https://doi.org/10.1038/s41467-018-07763-z


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/grant/)
- CREST of Japan Science and Technology Corporation (http://bit.ly/22I8avZ)
- ERATO of Japan Science and Technology Corporation (http://www.jst.go.jp/erato/en/index.html)
- MIRAI Program of Japan Science and Technology Corporation (http://www.jst.go.jp/mirai/jp/about/index.html)
- Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project. (http://www.jst.go.jp/inte/english/sicorp/index.html)
- Impulsing Paradigm Change through Disruptive Technologies (iPACT), (http://www.jst.go.jp/ipact/en/index.html)

Figure 36c: Expression of an F1 gene from the AcF1 and AcF1 promotors is sufficient for flowering in noninductive conditions in transgenic proAcF1:AcF1 Arabidopsis in SD.

New Zealand

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University of Otago, Department of Biochemistry, Dunedin

Use of Arabidopsis

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

Conferences, Workshops and Outreach events

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

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

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

Selected Publications


Major Funding Sources

- The Marsden Fund administered by the Royal Society of New Zealand (http://www.royalsociety.org.nz/programmes/funding/marsden)
- Ministry for Business, Innovation and Employment (MBIE; http://www.mbie.govt.nz/) through:
  - Core funding to Crown Research Institutes
  - The Agricultural and Marketing Research and Development Trust (AAMARDT; http://agmardt.org.nz/)


Use of Arabidopsis

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

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

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

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

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

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

Saudi Arabia

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

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

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


Conferences, Workshops and Outreach events

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

Selected Publications


Major Funding Sources

King Abdullah University of Science and Technology.
Use of Arabidopsis

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

Plant research community in Singapore also includes researchers working on rice and leafy vegetables to which knowledge gained in Arabidopsis research is actively being transferred and vice versa. Despite being small in an urban setting, research community in Singapore embraces big challenges in environmental sustainability and food security by advancing our basic understanding on plants using Arabidopsis as a major model system. Our areas of research is diverse with complementary strengths, ranging from developmental biology, plant immunity, stress biology, evolutionary genetics, and stem cell biology.

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

Conferences, Workshops and Outreach events

<table>
<thead>
<tr>
<th>Event</th>
<th>Date</th>
<th>Website</th>
</tr>
</thead>
<tbody>
<tr>
<td>10th Anniversary Conference, Mechanobiology Institute</td>
<td>November 7-10, 2018</td>
<td><a href="https://mbi.nus.edu.sg/mbi-10th-anniversary-conference/">https://mbi.nus.edu.sg/mbi-10th-anniversary-conference/</a></td>
</tr>
</tbody>
</table>

Molecular mechanisms of developmental and regenerative biology (November 11-13, 2018)

http://meetings.embo.org/event/18-devandregeneration

Selected Publications


Major Funding Sources

- National Research Foundation Singapore (Prime Minister’s Office Singapore) https://www.nrf.gov.sg/
- Agri-Food and Veterinary Authority of Singapore (AVA) https://www.ava.gov.sg/
- Temasek Foundation Innovates http://www.temasekfoundation-innovates.org.sg/


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

- Figure 42. Discovered a novel regulatory mechanism for acclimation of plants to cold

Spain

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Universidad Miguel Hernández, Elche, Spain

Conferences, Workshops and Outreach events

- The “XIV Meeting on Plant Molecular Biology” was organized by plant biologists lead by Prof. Oscar Lorenzo in Salamanca (July 4-6, 2018).
- The “III Workshop on New Frontiers in Plant Biology” was organized by members of the Center of Plant Biotechnology and Genomics lead by Prof Antonio Molina in Madrid (May 30-June 1, 2018).
- The “At the Forefront of Plant Research 2019” workshop was organized by members of the Centre for Research in Agricultural Genomics lead by Prof José Luis Riechmann in Barcelona (May 6-8, 2019).


Selected Publications


- Major Funding Sources

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

- About 100 laboratories.

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

Some software packages were made available to the community, including:

“Easymap: a program that eases mapping-by-sequencing of large insertions and point mutations.”, developed by D. Wilson-Sánchez, S.D. Lup, S. Andreu-Sánchez and J.L. Micol. Available at http://genetics.edu.umh.es/resources/easymap


- About 100 laboratories.

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- About 100 laboratories.


Major Funding Sources

About 80 grants from the State Research Agency of Spain (Ministry of Science, Innovation and Universities) fund Arabidopsis research projects at individual laboratories.

Additional Information

Authors from laboratories studying Arabidopsis in Spain published about 400 papers in the last year. Prof. Crisanto Gutiérrez was awarded a European Research Council Advanced Grant (“Exploiting genome replication to design improved plant growth strategies”).

Prof. José Luís Micó was elected President of the Genetics Society of Spain.


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Prof. José Luís Micó was elected President of the Genetics Society of Spain.
AT1G64660-GFP × WT

WT × AT1G64660-GFP

Figure 43. Reporter lines for AT1G64660 confirm imprinted expression. Representative images of seeds derived after reciprocal crosses of the AT1G64660 reporter line (fusion with green fluorescent protein (GFP)) with wild-type (WT) plants. GFP fluorescence was detected in the seed coat when the AT1G64660 reporter was maternally inherited, but endosperm-specific expression was only detected when the AT1G64660 reporter was paternally inherited. Seeds at 2 DAP were used for imaging. Red stain is propidium iodide. Scale bars correspond to 50 μm.

Major Funding Sources
- The Swedish Research Council (VR; http://www.vr.se) a core funder of researcher-initiated basic research.
- The Swedish Foundation for Strategic Research (http://www.strategiresearch.se) supports strategic research in natural science, engineering and medicine.
- The Kempe Foundations (http://www.kempe.com) private foundations devoted to support scientific research in all natural sciences, 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) supports strategic research in the areas Environment, Agricultural Sciences and Spatial Planning.
- The Wallenberg Foundations (http://www.wallerbang.org/se) private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.

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Use of Arabidopsis
c.a. 12 institutions and c.a. 100 labs.

2019 Highlights
- Trinational Arabidopsis meeting will be held in Zurich in April 2019.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019
- Software tools
  - Homeolog expression quantification methods for allopolyploids
- Resources
  - Rapid extraction of living primary veins from the leaves of Arabidopsis thaliana.

Conferences, Workshops and Outreach events

Workshops
- Plant Science at School Continuing Education Program in Plant Sciences for Secondary School Teachers
- Plant Receptor Kinases and Related Pathways, 30 Oct 2018, Zurich

Selected Publications
Figure 44: Measuring wound-induced electrical signals in a 5 week-old Arabidopsis rosette. (By courtesy of Prof. Edward Elliston Farmer, University of Lausanne.)
Use of Arabidopsis

The United Kingdom has approximately 45 academic departments and research institutes that are actively conducting Arabidopsis research.

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

- The Eurasiang Arabidopsis Stock Centre (uNASC) is based at the University of Nottingham. http://nasccentre.org
- The PhenomUK: The UK Plant Phenomics Network is a technology touching life network grant that provides phenotyping opportunities for UK researchers to use the core facilities situated around the country. https://www.phenomuk.net/
- Ara-BOX-cis database allows interrogation on how bHLHs and bZIPs (which are expressed in seedlings) regulate genes downstream of perfect G-boxes (CACGTG). http://araboxcis.org/
- The DNA BioFoundry at the Earlham Institute. This synthetic biology hub allows facile preparation of golden gate cloners for use by plant scientists. http://earlham.biofoundry.org
- Community Wheat Transformation resource allows UK Arabidopsis researchers to propose for their gene of interest to be introduced into wheat. https://www.niab.com/transgenic
- Visit the GARNet Resources Page for a categorised list of software tools available for the analysis of this widely used source of data. https://www.garnetcommunity.org.uk/resources
- Advice for Gene Editing in Arabidopsis from Jonathan Jones’ lab at the Sainsbury Lab, Norwich.
- The Hidden Hill at the University of Nottingham is an outstanding scientific and science communication project that uses X-ray computed tomography to visualise plant roots. https://www.nottingham.ac.uk/hiddenhill/home.aspx

Conferences, Workshops and Outreach events

- GARNet-CyverseUK RNAseq Analysis Workshop. December 10th-12th 2016. This event held at the Earlham Institute provides software tools available for the analysis of this widely used source of data. http://www.earlham.ac.uk/cyverse-uk-maseq-workshop-2016

Major Funding Sources

Ministry of Science and Technology, Taiwan https://www.most.gov.tw/fi-em
Academia Sinica https://www.sinica.edu.tw/en/

Selected Publications

The majority set of UK publications that feature Arabidopsis are documented on the GARNet blog.

http://blog.garnetcommunity.org.uk/Arabidopsis-research-roundups/


Major Funding Sources

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

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


Natural Environment Research Council http://www.nerc.ac.uk/
Use of Arabidopsis

It’s not straightforward to get accurate numbers of Arabidopsis users in the United States. However, according to two major resources, The Arabidopsis Information Resource (TAIR) and the Arabidopsis Biological Resource Center (ABRC), estimates are that there are approximately 4,700 labs that use Arabidopsis resources registered in the US, and 12,500 people.

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

1. DiversifyPlantSci Resource: NAASC is committed to promoting a global plant sciences community that reflects the true diversity of all its members. To further this mission the NAASC Diversity and Inclusion Task Force have created the DiversifyPlantSci online resource, a list of plant biology researchers from under-represented categories and groups* to reference for consideration when inviting speakers, reviewers, and participants for career or mentorship opportunities. This list is intended to highlight the diversity within the global plant science community. We hope to increase diversity and inclusion by making it easy to expand invitations past one’s personal networks. *List includes plant scientists who identify in 1 or more of these under-represented categories as defined by NSF: Women; persons with disabilities; and three racial and ethnic groups—blacks, Hispanics, and American Indians or Alaska Natives—are underrepresented in US STEM; we also include Filipino.

2. MASC Country Reports

United States of America

Joanna Friesner
jdriesner@ucdavis.edu
University of California, Davis, with input from the North American Arabidopsis Steering Committee (NAASC)
https://www.araport.org/community/group/naasc

Figure 47. Microtubule alignment and cell elastic asymmetry additively regulate anisotropic growth in silicic. (A) Template for finite element method simulation of a growing hypocotyl epidermis, alongside predicted strain anisotropy (growth) with no anisotropism and with or without 100x elastic asymmetry added. White lines indicate the maximal stress direction. (B) Pre-growth and after-growth simulation results for a case with matched anisotropy (irregularly shaped) and organized by the internal seedling geometry. Growth is enhanced by the addition of 2-fold elastic asymmetry, resulting in increased growth of the template. (C) Simulation output as percent growth in time from the simulation in (B) showing the increased relative growth achieved by addition of 2-fold elastic asymmetry. https://elifesciences.org/articles/38161

2. November 2018: “Broadening the Impact of Plant Science Through Community-Based Innovation, Evaluation, and Sharing of Outreach Programs” Workshop*: José Dinneny, Liz Haswell, Roger Innes and Joanna Friesner of NAASC led the workshop at UC Davis (Davis, CA, USA); the workshop’s overarching objective was to “re-envision how plant science outreach programs are funded, evaluated, acknowledged and shared within the plant science community” with specific focus on being more Innovative, Inclusive, and Integrative in how plant scientists engage with students, the broader public, and leverage the power of plants to improve our world now and in the future. A white paper generated by workshop participants is in development.


3. November, 2018: “Broadening the Impact of Plant Science Through Community-Based Innovation, Evaluation, and Sharing of Outreach Programs” Workshop*: José Dinneny, Liz Haswell, Roger Innes and Joanna Friesner of NAASC led the workshop at UC Davis (Davis, CA, USA); the workshop’s overarching objective was to “re-envision how plant science outreach programs are funded, evaluated, acknowledged and shared within the plant science community” with specific focus on being more Innovative, Inclusive, and Integrative in how plant scientists engage with students, the broader public, and leverage the power of plants to improve our world now and in the future. A white paper generated by workshop participants is in development.


5. May 2018: “The Future of Arabidopsis Bioinformatics” Workshop: The International Arabidopsis Informatics Consortium (IAIC), initiated in 2010 by NAASC and led by former NAASC member Blake Meyers (Danforth Center) held this NSF supported workshop in St. Louis, Missouri, USA, to evaluate the current status of Arabidopsis informatics and chart a course for future research and development (for more details please see the IAIC report in the MASC Inc Annual Report section on Community resources). The workshop participants published a white paper outlining the current state, challenges, and priorities
MASC Country Reports

for the future of Arabidopsis bioinformatics resources (https://doi.org/10.1002/pld3.109). This workshop was based upon work supported by the National Science Foundation under Grant No. 11062348. Any opinions, findings, and conclusions or recommendations expressed in this event, or in resulting work, are those of the participants and do not necessarily reflect the views of the NSF.

Selected Publications


Major Funding Sources

US Arabidopsis Research is primarily supported by funding through the Federal Government via the National Science Foundation (NSF): http://www.nsf.gov Additional support has come from these sources: US Department of Agriculture (USDA): http://www.usda.gov
Private Sources: Howard Hughes Medical Institute (HHMI)- alone and partnered with several other organizations, support a number of prominent US Arabidopsis researchers and educators: (1) HHMI Faculty Scholars; e.g. Siobhan Brady, Jose Dinney, Elizabeth Haswell, Jennifer Nemhauser, Elizabeth Sattely (2) HHMI Investigators; Phil Benley, Dominique Bergmann, Xuemei Chen, Joanne Chory, Jeff Deng, Xinxian Dong, Joe Ecker, Mark Estelle, Sheng Yang He, Steve Jacobsen, Zach Lippmann, Rob Martienssen, Elliot Meyerowitz, Craig Pikaard, Elizabeth Sattely, Keiko Torii and Ning Zheng (the next anticipated competition opens in 2020)

Additional Information

1. In fall 2018, Federica Brandizzi (MSU-DOE Plant Research Laboratory, Michigan State University) and Anna Stepanova (North Carolina State University) were elected by the North American Arabidopsis community to serve a five-year term. They replaced Sally Assmann (Penn State University) and Erich Grotewold (Michigan State University) who had concluded their five-year term of service.

a. Federica and Anna join these NAASC members, in order of longest to shortest elected service on NAASC: Elizabeth Haswell (Washington University in St. Louis), Jose R. Dinneny (Stanford University), Peter McCourt (University of Toronto), Roger Innes (Indiana University), Sean Cutler (UC Riverside), and Jennifer Nemhauser (University of Washington-Seattle).

b. Current and former NAASC members, and NAASC information, can be found at: https://www.araport.org/community/group/naasc

3. TapRoot Podcast (https://plantae.org/podcast/the-taproot) by Elizabeth Haswell, NAASC member: One challenge with outreach and retention activities is reaching geographically, ideologically, or intellectually isolated individuals. Podcasting provides an alternative source of support and community for plant science trainees, with low barriers to access, production, and distribution, and a highly diverse audience. While podcasts are rapidly growing in popularity they are underutilized as a mechanism for science outreach. Of the over half a million active podcast listeners, less than 1000 are related to science.

In 2017, Ivan Baxter and I started The Taproot Podcast (tagline: “We tell the story behind the science”): with support from ASPB and Plantae. In each episode, we discuss the publication of a plant biology paper with one of its authors, addressing the narratives that aren’t represented in a final manuscript—such as technology development, work-life balance, career gaps, gender discrimination, and student mental health. About half of our podcast guests work on Arabidopsis specifically.

We also maintain an active @taprootpodcast Twitter account (>1200 followers) to foster discussion and solicit feedback, and to reach as broad an audience as possible. Ultimately, we aim to foster a sense of belonging, agency and community among plant biology trainees, thereby improving diversity and inclusion. We have released 17 episodes over two seasons with over 34,000 downloads to date.

According to a survey in the summer of 2018, 46% of our listeners identify as female, over 50% are Ph.D students and postdocs, and 85% are in North America or Europe. Future efforts will aim to continue to seek guests with diverse ethnicity, career level, geographical location, and research area, in part by crowdsourcing suggestions via Twitter. In addition, we will engage with a more global audience and have identified several young plant biology leaders in South America and Africa to serve as ambassadors for the podcast in their countries.
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ICAR 2020: Seattle, Washington, USA
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We are soliciting proposals for concurrent session organizers. If your proposal is selected, you will have the opportunity to organize your own mini symposium on the topic of your choice, and select the session speakers for short talks. Timely research topics and proposals by early career scientists are particularly encouraged. Submit by July 31st, 2019 for full consideration.


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