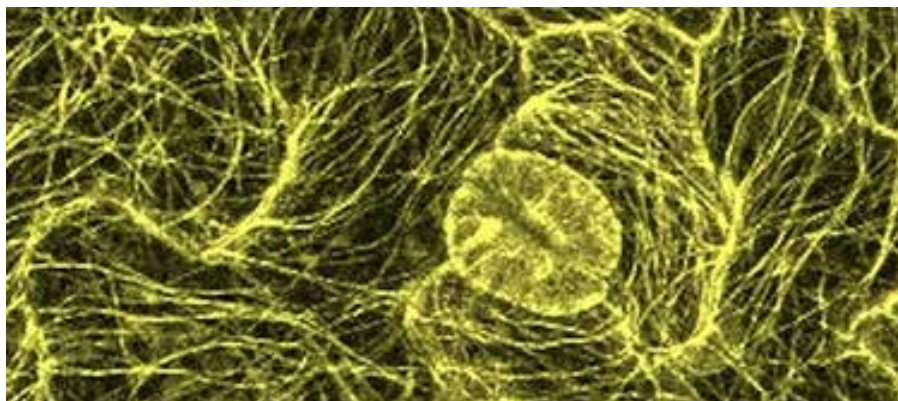
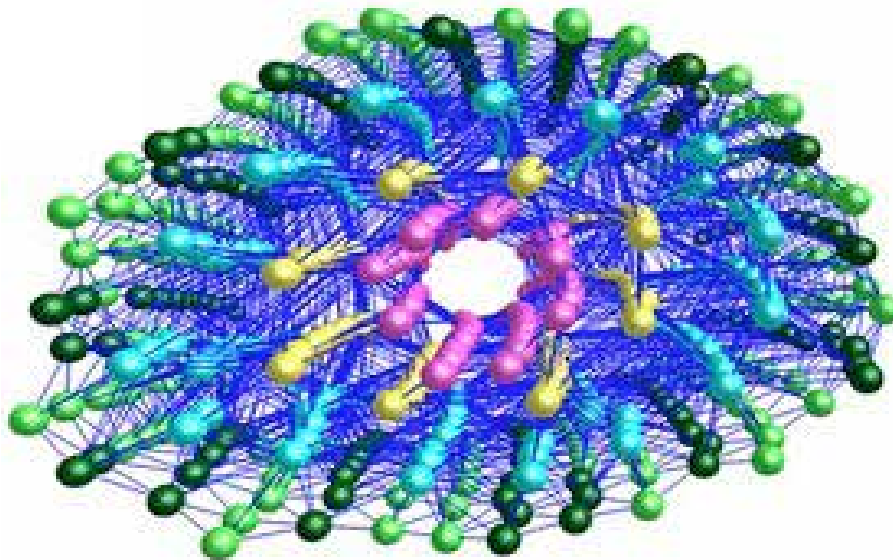


From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee
(MASC)

Annual Report 2017/2018



The Multinational Arabidopsis Steering Committee

Annual Report 2017/2018

Nicholas Provart
nicholas.provart@utoronto.ca
MASC Inc President

Siobhan Brady
sbrady@ucdavis.edu
MASC Inc Treasurer

Geraint Parry
geraint@garnetcommunity.org.uk
MASC Inc Secretary

MASC Directors

Rodrigo A. Gutiérrez	rgutierrez@bio.puc.cl
Elizabeth Haswell	ehaswell@wustl.edu
Masatomo Kobayashi	kobayasi@rtc.riken.jp
Sean May	sean@Arabidopsis.org.uk
Blake Meyers	BMeyers@danforthcenter.org
Barry Pogson	Barry.Pogson@anu.edu.au
Xuelu Wang	xlwang@mail.hzau.edu.cn
Michael Wrzaczek	michael.wrzaczek@helsinki.fi

MASC Subcommittee Chairs and Co-Chairs

Malcolm Bennett	Malcolm.Bennett@nottingham.ac.uk
Siobhan Brady	sbrady@ucdavis.edu
Joe Ecker	ecker@salk.edu
Fabio Fiorani	f.fiorani@fz-juelich.de
Joshua Heazlewood	jheazlewood@unimelb.edu.au
J. Chris Pires	piresjc@missouri.edu
Nicholas Provart	nicholas.provart@utoronto.ca
Kazuki Saito	kazuki.saito@riken.jp
Robert Schmitz	schmitz@uga.edu
Motoaki Seki	motoaki.seki@riken.jp
Wolfram Weckwerth	wolfram.weckwerth@univie.ac.at
Xuehua Zhong	xuehua.zhong@wisc.edu



MASC Country Representatives

Wagner Araújo	wlaraujo@ufv.br
María Francisca Blanco	mfblanco@unab.cl
Dario Bonetta	dario.bonetta@uoit.ca
Lynette Brownfield	lynette.brownfield@otago.ac.nz
Ana I. Caño-Delgado	ana.cano@cragenomica.es
Maura Cardarelli	maura.cardarelli@uniroma1.it
Sacco De Vries	sacco.devries@wur.nl
Maria E. Eriksson	maria.eriksson@plantphys.umu.se
Joanna D. Friesner	jdfriesner@ucdavis.edu
Thorsten Hamann	thorsten.hamann@ntnu.no
Klaus Harter	klaus.harther@zmbp.uni-tuebingen.de
Polydefkia Hatzopoulos	phat@aua.gr
Marie-Theres Hauser	marie-theres.hauser@boku.ac.at
Inhwan Hwang	ihhwang@postech.ac.kr
Yuling Jiao	ylijiao@genetics.ac.cn
Masatomo Kobayashi	kobayasi@rtc.riken.jp
Jitendra P. Khurana	khuranaj@genomeindia.org
Loic Lepiniec	Loic.Lepiniec@versailles.inra.fr
Minami Matsui	minami@riken.jp
José Luis Micol	jimicol@umh.es
Monika Murcha	monika.murcha@uwa.edu.au
Moritz K. Nowack	moritz.nowack@vib.be
Adriano Nunes-Nesi	nunesnesi@ufv.br
Michael Palmgren	palmgren@plen.ku.dk
Catherine Perrot-Rechenmann	catherine.rechenmann@cncrs-dir.fr
Nicholas Provart	nicholas.provart@utoronto.ca
Sigal Savaldi-Goldstein	sigal@technion.ac.il
Motoaki Seki	motoaki.seki@riken.jp
Charles Spillane	charles.spillane@nuigalway.ie
Kentaro K. Shimizu	kentaro.shimizu@ieu.uzh.ch
Ramamurthy Srinivasan	srinivasan53@gmail.com
László Szabados	szabados@brc.hu
Marcelo J. Yanovsky	mjyanovsky@gmail.com
Viktor Žárský	viktor@natur.cuni.cz

Cover design and editing

Geraint Parry MASC Secretary, GARNet, Cardiff University, UK
geraint@garnetcommunity.org.uk

Cover images taken from Open Access publications

Top Image: <http://dx.doi.org/10.7554/eLife.26023>
Middle Image: <http://dx.doi.org/10.7554/eLife.23625>
Bottom Image: <http://dx.doi.org/10.7554/eLife.34064>

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

The MASC report 2017/18 and previous reports are available online at:

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

Published by the Multinational Arabidopsis Steering Committee (MASC) June, 2018

MASC Inc is registered as a not-for-profit corporation in Canada under Corporation Number 960778-1, subject to the regulations of the Canada Not-for-profit Corporations Act

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

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 Hanne Kvalheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turkey.

MASC especially thanks *Science des Plantes de Saclay* who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.

Table of Contents

Table of Contents	4	Czech Republic	59
Foreword and Executive Summary	6	Denmark	61
Progress and Activities of MASC	8	Finland	62
Analysis and Recommendations by MASC	10	France	63
Reports of the MASC Subcommittees	12	Germany	64
Bioinformatics	12	India	66
Clone-Based Functional Genomics Resources (ORFeomics)	15	Israel	69
Epigenetics and Epigenomes	15	Italy	70
Metabolomics	18	Japan	73
Proteomics	19	New Zealand	77
Systems and Synthetic Biology	20	Norway	78
Arabidopsis Community Projects and Resources	23	South Korea	79
Resource and Stock Centers	24	Spain	80
Arabidopsis Informatics and Data Sharing Resources	26	Sweden	81
Plant Projects and Resources with Strong Participation of <i>Arabidopsis</i> Community	29	Switzerland	83
Summary Page	34	United Kingdom	85
Analysis of Arabidopsis Publications	35	United States	87
Research Highlights in 2017/18	36	Members of the MASC Subcommittees	90
Country Highlights	41		
Argentina	42		
Australia	43		
Austria	45		
Belgium	48		
Brazil	50		
Canada	52		
Chile	54		
China	57		

Forward and Executive Summary

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). Although you will read within these pages that it has been a successful year for Arabidopsis research there is always the challenge to ensure that support is maintained for research conducted with this important model organism. To this end the report includes discussion on the future possibilities within the field, in particular to support the bioinformatics tools that are critical for the analysis of the enormous amount of data that can be generated through 'omic technologies.

MASC started in the early 1990's, when scientists from several countries formed an *ad hoc* committee to promote large-scale research with Arabidopsis. The ultimate goal was the understanding of physiological, biochemical and developmental processes of flowering plants at the molecular level, employing Arabidopsis as a model system. In order to reach this long-term goal, a commitment from the global Arabidopsis community was essential. Therefore, actively engaged researchers developed 'The Multinational Coordinated Arabidopsis - Genome Research Project' in 1990. Over time this changed through different versions of MASC, which in the current and hopefully long lasting version is registered in Canada as a charitable 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 2017/2018 annual MASC report is the 6th 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.

During 2017 MASC evolved into the not-for-profit MASC Inc. that includes non-paid positions for the President, Treasurer and Secretary. These officers are supported by a Board of eight Directors, The previous Country, Resource and Subcommittee representatives of MASC have become members of MASC Inc.

Over the past year MASC Inc (hereafter MASC) has selected a set of eight directors whose remit is to broadly oversee MASC activities. The permanent board members of MASC are Nicholas Provart as President, Siobhan Brady as Treasurer, and Geraint Parry as Secretary.

After 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. We are extremely grateful that the organisers of ICAR2018 in Turku will contribute a small donation from each meeting attendee toward MASC activities.

We hope that in the future MASC will be able to provide seed funding for ICAR meetings or associated workshops. The precise mechanisms for this interaction will be discussed at the MASC annual meeting which takes place at ICAR2018 in Turku.

MASC Subcommittees

Currently eight MASC Subcommittees monitor progress and important activities as well as discuss future directions of each of their respective fields of Arabidopsis research. Members of each subcommittee are in positions to stay in close contact with the community and promote international cooperation (pages 12-21).

In the lead up to the MASC annual meeting that takes place at ICAR2018, there have been questions tabled about the future directions of these subcommittees. Therefore this will be a topic of conversation at the annual meeting.

Six of the subcommittees have contributed to the 2017-2018 annual MASC report and the activities of the Phenomics subcommittee are included in the report of international phenotyping.

Contributing subcommittees are:

Bioinformatics (page 12)

ORFeomics (page 15)

Epigenetics and Epigenomes (page 15)

Metabolomics (page 18)

Proteomics (page 19)

Systems and Synthetic Biology (page 20)

MASC is open to discuss the evolution of the current subcommittees and community members are welcome to suggest if there is a community need for a new subcommittee. In this case please contact the permanent members of MASC (Nick 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 possible organisation of subcommittee-related 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 centers and bioinformatic resources enable researchers to fully integrate their research from its initial phenotypic description through to full multi-omic characterisation.

Information on the progress and activities of the range of community resources can be found on pages 23-33.

Country Highlights

MASC is supported by individual countries through the selection of representatives that report each year on the progress that their colleagues have made. In addition, they provide an important commentary on the prospects for Arabidopsis research in their individual countries. The country reports highlight the exceptional numbers of research tools that have been developed for the benefit of the global Arabidopsis community as well as highlighting where future issues might emerge that could be tackled on a global level.

In this report we are delighted to include an inaugural report from Norway whose contribution means that 25 of the 29 current member countries have reported to MASC this year (page 41-89).

We encourage researchers from other countries who are not featured in this MASC report to become involved with this process by contacting a member of the MASC Board of Directors. Providing an update for the global community not only highlights the outstanding work that is occurring in their home country but also provides an easy reference point that can be important in discussions with potential funders and other interested parties.

Arabidopsis Scientific Highlights in 2017/2018

According to an NCBI search, Arabidopsis researchers published over 4100 peer-reviewed papers in 2017, which is a decline from the highest numbers from 2013 and 2014. This number is buoyed by continued increase in publications from Chinese researchers. As also shown in figure 2 this reflects a plateauing in papers from many other countries.

In this report we highlight ten papers that demonstrate the breadth of research in which Arabidopsis is involved. The papers include those that tackle challenges in basic research as well as those that provide community resources as a intentional side-effect of their research.

> Towards financially viable phytoextraction and production of plant-based palladium catalysts. *Environ Sci Technol*. <http://dx.doi.org/10.1021/acs.est.6b04821>

> Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis. *EMBO J* <http://dx.doi.org/10.15252/embj.201694983>

> Topological analysis of multicellular complexity in the plant hypocotyl. *Elife*. <http://dx.doi.org/10.7554/eLife.26023>

> WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. *PLoS Genet*. <http://dx.doi.org/e1007177>

> The AraGWAS Catalog: a curated and standardized *Arabidopsis thaliana* GWAS catalog. *Nucleic Acids Res*. 46: D1150–D1156 <http://dx.doi.org/10.1093/nar/gkx954>

> CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nature Methods* <http://dx.doi.org/10.1038/nmeth.4343>.

> Genome-wide characterization of differential transcript usage in *Arabidopsis thaliana*. *Plant J*. 92: 1218–1231. <https://doi.org/10.1111/tbj.13746>

> Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. *Mol Plant* <http://dx.doi.org/10.1016/j.molp.2017.08.012>

> N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. *New Phytol*. <http://dx.doi.org/10.1111/nph.14909>

> A small peptide modulates stomatal control via abscisic acid *Nature* <https://doi.org/10.1038/s41586-018-0009>

MASC thanks Michael Wrazcek and the local organisers of ICAR2018 in Turku for their organisational and financial support for our activities and to all MASC members who contributed to this report.

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



Progress and Activities of MASC

MASC web page: www.Arabidopsisresearch.org

Previously the chairmanship of MASC rotated between the lead organisers of successive International Conference on Arabidopsis Research (ICAR). However the incorporation of not-for-profit MASC Inc in Canada required a change in organisational structure. This includes 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 MASC directors officially take up their positions at the ICAR2018 meeting and to ensure that only two directors rotate off the board the initial term lengths will be less than 4 years. This is a list of the inaugural board of directors and the length of their terms:

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

2018-2021: Xuelu Wang (China), Elizabeth Haswell (United States of America)

2018-2022: Blake Meyers (United States of America), Sean May (United Kingdom)

2018-2023: Rodrigo Gutierrez (Chile), Masatomo Kobayashi (Japan)

From 2020 two new directors will be elected for four term years. Primarily appointments these will aim to improve the gender balance on the board of directors as well as maintaining geographical diversity.

Previous members of MASC have been asked to become members of MASC Inc by providing some limited information about their areas of expertise. MASC are happy to welcome other members who wish to be involved in activities to benefit the global Arabidopsis community.

The 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. It is hoped that this role will continue for the foreseeable future, taking advantage of the full time funding provided to the UK plant science community by the Biotechnology and Biological Sciences Research Council (BBSRC).

The MASC coordinator/secretary position was established in 2002 and has been previously supported by the NSF

(USA), the DFG (Germany) and by the BBSRC. The MASC coordinator provides help and coordination to MASC and the larger Arabidopsis research community.

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

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

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

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from six of the eight current subcommittees: Bioinformatics, Epigenetics and Epigenomes, ORFeomics, Metabolomics, Proteomics and Systems and Synthetic Biology.

The requirements for a subcommittee to be considered active were formulated in 2009 and remain relevant during the transition to MASC:

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

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

The three resource and stock centers, the Arabidopsis Biological Resource Center (ABRC, US), the Nottingham Arabidopsis Stock Centre (uNASc, UK) and the RIKEN BioResource Center (RIKEN BRC, Japan), continue to encourage donations to keep their stocks up-to-date following the newest technologies. In order to ensure

a broader and more efficient distribution of resources within the community, the stock centers operate coordinately with each other, as well as with Arabidopsis online portals.

Progress of Arabidopsis informatics and data sharing resources is also highlighted in this year's report, including updates from the International Arabidopsis Informatics Consortium (IAIC) and The Arabidopsis Information Resource (TAIR).

Efforts of two other community projects (BAR, Gramene) with strong participation of the Arabidopsis community are also presented in the report as well as a summary from the International Plant Phenotyping Community (page 31).

Country representatives attend the MASC annual meeting held during ICARs and contribute to the annual MASC report by submitting country reports. MASC is delighted to welcome Thorsten Hamann as the country representative from Norway and thanks the other 24 country representatives for their valuable contributions this year.

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

International Conference on Arabidopsis Research (ICAR)

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

- 29th ICAR, Turku, Finland: June 25th-29th 2018
- 30th ICAR, Wuhan China: June 16th-21st 2019.
- 31st ICAR, Seattle, USA June 22nd-26th 2020
- 32nd ICAR, Europe, June 2021.

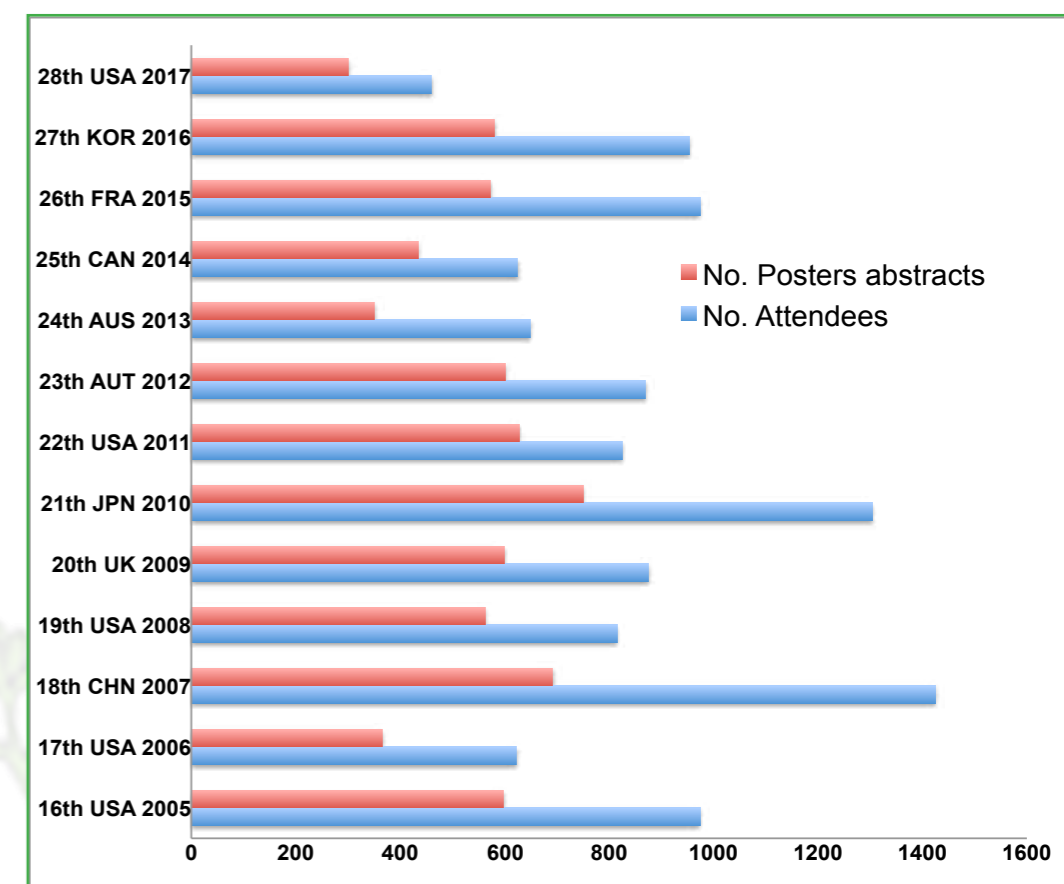


Figure 1. Number of attendees (blue) and number of posters presented (red) at the International Conference on Arabidopsis Research since 2005, when information about posters became available.

The 28th International Conference on Arabidopsis Research (ICAR) was held in St Louis, Missouri between 19th-23rd June 2017 where the organising committee was led by Joanna Friesner. The number of attendees was less than usual, likely due to competition from the ASPB meeting in Hawaii, yet it included the usual variety of outstanding scientific sessions arguably highlighted by presentations of unpublished data from Niko Geldner and Keiko Torii.

460 people attended the 28th ICAR with and 65% of the attendees (300) submitting a poster abstract (Figure 1). On average 63% of the attendees have presented a poster during the ICARs over the last 10 years.

One strong feature of ICAR2017 were the independently organised workshops that remain an important part of the schedule. Members of MASC were involved in the organisation of workshops on Careers (Joanna Friesner, NAASC), Science Communication (Ruth Bastow, GPC), Chemical Biology (David Gifford, Minami Matsui, RIKEN) and Bioinformatics (Eva Huala, TAIR-Phoenix Bioinformatics and Chris Town Araport).

It is great to learn that these workshop sessions have been further extended for ICAR2018 and that MASC members are contributing to these sessions.

Analysis and Recommendations by MASC

Prepared by Geraint Parry with input from Nicholas Provart.

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

In global terms, research that uses Arabidopsis as a model organism is still in good shape. In most countries the number of publications that feature Arabidopsis remains stable or is increasing that means the total productivity is not declining. As there is an increase in applied research that uses crops such as rice, maize or wheat, research funding diverted into those areas might negatively impact the amount of funding available to Arabidopsis research. However it is clear that much applied research relies on initial findings made using model organisms so it is important to maintain support at the early phase of the discovery pipeline.

Despite many years of research, 14,717 of 27,655 Araport 11 genes lack a Gene Ontology Biological Process annotation and 10,035 lack a Gene Ontology Molecular Function annotation. Clearly there is still a lot to learn and within this report the MASC ORFeomics subcommittee proposes that the community should be aiming to establish an Arabidopsis ORFeome project to capture information about each of the 28K ORFs in order to provide a complete picture of protein coding genes in a single plant system. This strategy would link well with improved informatics tools for the analysis of co-expressed gene sets as well as improvements in GO annotation, highlighted by the new Gene Ontology (GO) Term Enrichment tool developed at TAIR. https://www.arabidopsis.org/tools/go_term_enrichment.jsp

The germplasm and bioinformatics resources available to Arabidopsis researchers are far in advance of those available to other plant systems. There are a well-known set of core community tools such as TAIR, BAR, the SIGnAL T-DNA resources and the Arabidopsis stock centres that have been developed over the past twenty years. In addition, this report highlights numerous less well known but important software tools for interrogation

of Arabidopsis data. In particular the country reports from China, Japan, Australia, USA and the UK provide information about many such tools but most countries are developing their own resources that are available for use by the global community. We urge potential users to investigate these resources and to utilize those that fit their research needs.

MASC President Nicholas Provart recently conducted a survey on the future of plant-focused bioinformatic resources. The results of this can be downloaded here: (arabidopsisresearch.org/images/publications/documents_articles/2018_MASC_BioinfoSurvey.pdf). A quarter of 320 respondents would like to see a centralised website that lists all of these resources although the option favoured by almost 50% of respondents was for individual sites to be more tightly linked to other appropriate tools. This would allow a step-wise progression of data analysis and increase usage of multiple sites.

Although there are lots of available resources the community is entering a new phase regarding the future of these resources and how they can be funded over the longer term. The MASC bioinformatics survey asked about funding for community bioinformatics resources. The two favoured options were the 'Freemium' option currently operated by TAIR as well as the 'Surcharge model' where an extra cost was added to seed stocks ordered from the three Arabidopsis stock centres. Slightly less favoured but still popular where the 'Sugar daddy model' where large research centres supported resources for all and the

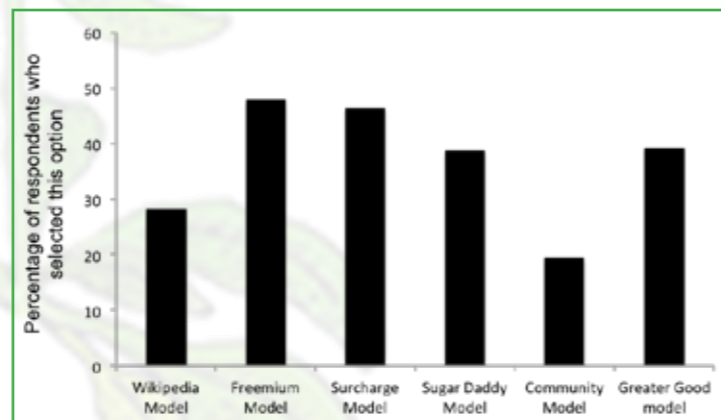


Figure 2: Results from survey question 'Ongoing funding is an issue for many bioinformatic resources. Would you be willing to support the following options (select more than one if needed)? 323 respondents. Full report: arabidopsisresearch.org/images/publications/documents_articles/2018_MASC_BioinfoSurvey.pdf

'Greater Good model' wherein resources are supported by funding agencies to ensure the research community and that users did not have directly contribute for their use (Figure 2).

Maintaining funding for community resources is clearly a challenging puzzle but hopefully discussions amongst international collaborators can develop a system that can ensure the long-term viability of the most useful resources. The pressing need to solve this challenge is highlighted by uncertainty over the future of Araport and how that resource will be maintained and whether a more international source of funding can be leveraged to support this global resource. A possible option is to consider an "OpenPlant" model whereby data sets, code, and expertise are deposited in open repositories, similar to the OpenWorm.org initiative, which is becoming widely used in the *C. elegans* research community.

Research in Arabidopsis spans all topics and the International Conference on Arabidopsis Research (ICAR) serves to bring together researchers from across scientific disciplines to fertilise the development of new ideas. Since 2007 ICAR has been hosted on a three-year cycle between Asia, North America and Europe. The 2016 ICAR in South Korea has almost 1000 attendees yet the ICAR2017 meeting had the lowest recent number of attendees with 420 travelling to St Louis. The reasons for this decline are complex and include competition from the ASPB meeting in Hawaii and any perceived issues regarding travel to the US from many countries. Regardless of the reduced numbers of delegates, the meeting hosted an outstanding selection of scientific sessions, workshops and posters.

To understand what people would like from future ICAR meetings the North American Arabidopsis Steering Committee (NAASC) conducted a survey where almost 700 respondents answered questions about location, content and cost.

Interestingly the most important consideration for delegates was to have the opportunity to present a research talk (unlike North American or Europeans, Asian respondents also highly valued the chance to give a poster presentation) closely followed by the wish for a diverse topic and speaker list that does not just focus on 'big names'. This provides both food for thought for future organisers and evidence that there is an important role for large general conferences despite the increase of smaller research-topic specific meetings.

Hopefully this report can provide a unique global perspective that gives important information that can reduce any unnecessary repetition of effort. We demonstrate that Arabidopsis research remains very

active, efficient and innovative with thriving research communities in many countries. Many countries are developing their own community tools so the global challenge is to bring together these tools to maximise their usage and usefulness.

No doubt that as these tools are generated, federated and shared MASC will continue to promote and support these exciting resources.

Reports of the MASC Subcommittees

Bioinformatics

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



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

Araport.org: From not existing a couple of years ago, Araport has become one of the most popular sources for Arabidopsis researchers according to a survey on Arabidopsis bioinformatics conducted by MASC in April 2018. It offers a multitude of ways to query various genomic data sets from Arabidopsis, both for researchers accessing it via its detailed web pages and programmatically. It is seeking renewed funding this year through the U.S. National Science Foundation.

TAIR: TAIR staff have continued updating Arabidopsis gene data in TAIR from published literature over the past year. Between March 2017 and February 2018, TAIR added 662 new gene symbols to TAIR and added or updated 701 gene summaries. A total of 7376 new GO and PO annotations, generated by TAIR curators, TAIR community, UniProt and the GO consortium, were added to 1907 loci, incorporating experiment-based data from 943 research articles. TAIR linked 2571 articles to 4261 loci, added or updated descriptions for 147 alleles, and added or updated 146 phenotypes from the literature. In 2017 TAIR processed 607 GO/PO annotations contributed by 86 community members covering 99 publications. The recently updated TAIR user guide (<http://bit.ly/2Go2wuP>) has detailed protocols for using TAIR's search, browse and analysis capabilities to access these data. Finally, TAIR continues to release year old data with no restrictions to the public. The 14th public release from TAIR contains recent annotation data up to March 31, 2017. Educators can continue to request access to the "full" version of TAIR for teaching purposes.

DNA and RNA resources: The Bailey-Serres Lab and collaborators used a combination of mRNA-seq and ribo-seq to identify vast and selective translational regulation in Arabidopsis in response to phosphate starvation (Bazin *et al.*, 2017). Dolf Weijer's Lab published an "atlas" of early embryo development based on the INTACT method for isolating cell-type-specific nuclear RNA, hybridized to Arabidopsis Gene 1.1 ST microarrays (Palovaara *et al.*, 2017). The Searle Lab reported a transcriptome-wide study mapping of RNA 5-methylcytosine in Arabidopsis mRNAs and ncRNAs (David *et al.*, 2017). The Yamamoto Lab used pair-end sequencing of transcription start site tags

(TSS tags) to identify 324,461 promoters in Arabidopsis, including many not associated with existing gene models (Tokizawa *et al.*, 2017). The Vandepoele Lab reported differential transcript usage events – related to alternative splicing – for 8,148 Arabidopsis genes across 206 public RNA-seq data sets, with protein sequences being changed in 22% of the cases (Vanechoutte *et al.*, 2017). The Van de Peer Lab used gene pairs resulting from whole genome duplication events to show a "remarkable" 92 homoeologous gene pairs with similar patterns of tissue-specific gene expression where one homoeolog exhibits more expression in aerial tissues and the other homoeolog exhibits more expression in tip-growth tissues (Smet *et al.*, 2017).

Gene regulatory networks/codes: Roger Deal's group used ATAC-seq to interrogate chromatin accessibility in stem cells and mesophyll cells to help delineate cell-type-specific gene regulatory networks acting in each (Sijacic *et al.*, 2018). The Muday Lab identified transcriptional and receptor networks controlling root responses to ethylene (Harkey *et al.*, 2018). Several groups published methods for inferring or exploring gene regulatory networks in Arabidopsis including GRACE (Banf and Rhee, 2017), GENIST (Balaguer *et al.*, 2017), TF2Network (Kulkarni *et al.*, 2018), Expresso (Aghamirzaie *et al.*, 2017), and SeqEnrich (Becker *et al.*, 2017). The Wigge Lab published a paper describing the G-box regulatory code in Arabidopsis to identify the set of bZIP and bHLH transcription factors that bind to G-boxes (CACGTG) that are most predictive of expression of genes with G-boxes in their promoters (Ezer *et al.*, 2017).

Other "big data": The 1001 (Arabidopsis) Genomes Consortium continues to make leveraging the power of natural variation for elucidating gene function easier than ever. The recent paper describing the global pattern of polymorphisms across 1,135 Arabidopsis accessions (1001 Genomes Consortium, 2016) provides the underlying data, while useful tools like AraGWAS – a "major new resource" that contains hundreds of thousands of linkages between phenotypes and polymorphisms (Togninalli *et al.*, 2018) – and easyGWAS, published last year (Grimm *et al.*, 2017), enable easy identification of potentially causal SNPs. Text mining: the Sternberg lab at the California Institute of Technology published Textpresso Central, which contains many new associations for Arabidopsis genes (Müller *et al.*, 2018), while eGenPub selects articles that are about specific plant proteins (from 8 species) in the UniProt database (Ding *et al.*, 2017). The Ecker lab published 8,577 interactions among Arabidopsis transcription factors (AtTFIN-1) using a next-gen sequencing-based Y2H assay (CrY2H-seq) method they developed (Trigg *et al.*, 2017).

Integrative tools: The ePlant tool for exploring Arabidopsis data from the kilometre- to nanometre-scale in an integrative manner was published by the Provart Lab and collaborators (Waese *et al.*, 2017), and is available at <http://bar.utoronto.ca/eplant> or as an "app" on Araport. A 2018 update to ePlant includes Klepikova *et al.*'s (2016) RNA-seq-based developmental atlas for Arabidopsis and O'Malley *et al.*'s DAP-Seq effort (2016) to map the binding specificity of 529 TFs from Arabidopsis – more than 2.8 million protein-DNA interactions are now viewable in ePlant's Interaction Viewer.

GENIUS is a user-friendly web server that uses a novel machine learning algorithm to infer functional gene networks focused on specific genes and experimental conditions that are relevant to biological functions of interest, developed by the Gutiérrez Lab. Try it for 8 species, including Arabidopsis at <http://networks.bio.puc.cl/genius>.

Overviews/collections: To reiterate from last year's report, a good overview of several plant genomic databases is provided in volume 1533 of Methods in Molecular Biology (Plant Genomics Databases, edited by Aalt-Jan van Dijk, 2016), including chapters on ENSEMBL Plants, the BAR, PLAZA, Plant Promoter DB and many others. A similar collection providing a good overview of plant bioinformatic resources is available in the open-access Current Plant Biology special edition on genomic resources and databases (Naithani and Van de Peer - eds., 2016). The 2018 Nucleic Acids Research database issue (Rigden and Fernández, 2018) contains updates or reports on several plant databases. Of note here: Plant Chromatin State Database (Liu *et al.*, 2018), Planteome – a portal for plant ontologies (Cooper *et al.*, 2018), updates to PLAZA (Van Bel *et al.*, 2018) and Gramene (Tello-Ruiz *et al.*, 2018), and the aforementioned AraGWAS. AgriGO for Gene Ontology enrichment analyses in several plant species was also updated to version 2.0 by the Su Lab at the Chinese Agricultural University (Tian *et al.*, 2017).

References

1001 Genomes Consortium (2016). 1,135 Genomes Reveal the Global Pattern of Polymorphism in *Arabidopsis thaliana*. *Cell* 166: 481–491.

Aghamirzaie, D., Raja Velmurugan, K., Wu, S., Altarawy, D., Heath, L.S., and Grene, R. (2017). Expresso: A database and web server for exploring the interaction of transcription factors and their target genes in *Arabidopsis thaliana* using ChIP-Seq peak data. *F1000Research* 6: 372.

Balaguer, M.A. de L., Fisher, A.P., Clark, N.M., Fernandez-Espinosa, M.G., Möller, B.K., Weijers, D., Lohmann, J.U., Williams, C., Lorenzo, O., and Sozzani, R. (2017). Predicting gene regulatory networks by combining spatial and temporal gene expression data in Arabidopsis root stem cells. *Proc. Natl. Acad. Sci.*: 201707566.

Banf, M. and Rhee, S.Y. (2017). Enhancing gene regulatory network inference through data integration with markov random fields. *Sci. Rep.* 7.

Bazin, J., Baerenfaller, K., Gosai, S.J., Gregory, B.D., Crespi, M., and Bailey-Serres, J. (2017). Global analysis of ribosome-associated noncoding RNAs unveils new modes of translational regulation. *Proc. Natl. Acad. Sci. U. S. A.* 114: E10018–E10027.

Becker, M.G., Walker, P.L., Pulgar-Vidal, N.C., and Belmonte, M.F. (2017). SeqEnrich: A tool to predict transcription factor networks from co-expressed Arabidopsis and Brassica napus gene sets. *PLoS One* 12: e0178256.

Cooper, L. *et al.* (2018). The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. *Nucleic Acids Res.* 46: D1168–D1180.

David, R., Burgess, A., Parker, B., Li, J., Pulsford, K., Sibbritt, T., Preiss, T., and Searle, I.R. (2017). Transcriptome-Wide Mapping of RNA 5-Methylcytosine in Arabidopsis mRNAs and Noncoding RNAs. *Plant Cell* 29: 445–460.

Ding, R., Boutet, E., Lieberherr, D., Schneider, M., Tognolli, M., Wu, C.H., Vijay-Shanker, K., and Arighi, C.N. (2017). eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. *Database* 2017.

Ezer, D., Shepherd, S.J., Brestovitsky, A., Dickinson, P., Cortijo, S., Charoensawan, V., Box, M.S., Biswas, S., Jaeger, K., and Wigge, P.A. (2017). The G-box transcriptional regulatory code in Arabidopsis. *Plant Physiol.*: pp.01086.2017.

Grimm, D.G., Roqueiro, D., Salomé, P.A., Kleeberger, S., Greshake, B., Zhu, W., Liu, C., Lippert, C., Stegle, O., Schölkopf, B., Weigel, D., and Borgwardt, K.M. (2017). easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies[OPEN]. *Plant Cell* 29: 5–19.

Harkey, A.F., Watkins, J.M., Olex, A.L., DiNapoli, K.T., Lewis, D.R., Fetrow, J.S., Binder, B.M., and Muday, G.K. (2018). Identification of Transcriptional and Receptor Networks That Control Root Responses to Ethylene. *Plant Physiol.* 176: 2095–2118.

Klepikova, A.V., Kasianov, A.S., Gerasimov, E.S., Logacheva, M.D., and Penin, A.A. (2016). A high resolution map of the *Arabidopsis thaliana* developmental transcriptome based on RNA-seq profiling. *Plant J.* 88: 1058–1070.

Kulkarni, S.R., Vanechoutte, D., Van de Velde, J., and Vandepoele, K. (2018). TF2Network: predicting transcription factor regulators and gene regulatory networks in Arabidopsis using publicly available binding site information. *Nucleic Acids Res.* 46: e31.

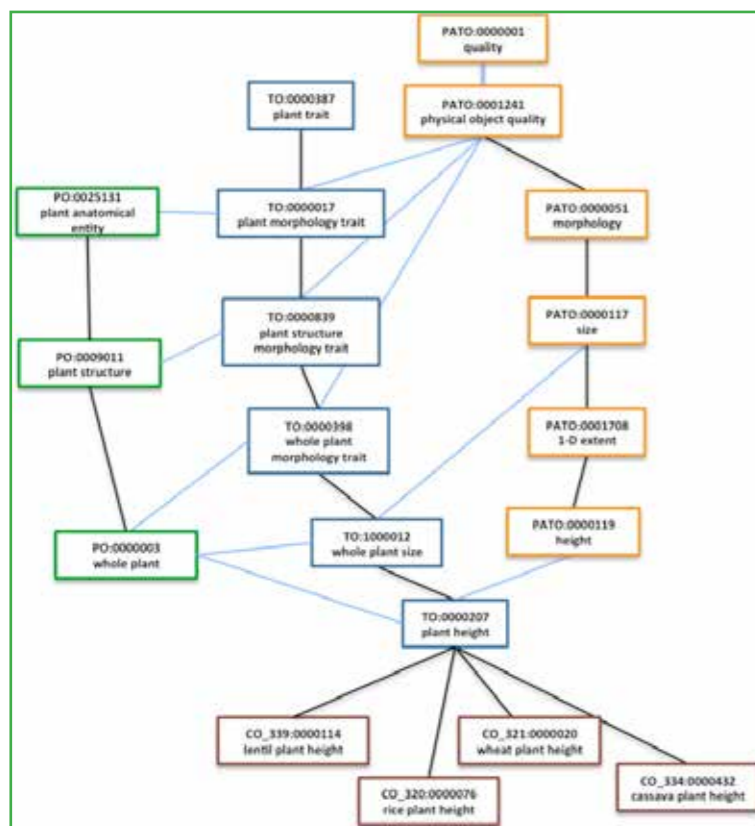


Figure 3: A view of the ontology hierarchy around Trait Ontology term plant height (TO:0000207). Crop Ontology (CO) terms for plant height from the lentil, wheat, rice and cassava ontologies are mapped to the Trait Ontology term for data integration.

Rigden, D.J. and Fernández, X.M. (2018). The 2018 Nucleic Acids Research database issue and the online molecular biology database collection. *Nucleic Acids Res.* 46: D1–D7.

Sijacic, P., Bajic, M., McKinney, E.C., Meagher, R.B., and Deal, R.B. (2018). Changes in chromatin accessibility between *Arabidopsis* stem cells and mesophyll cells illuminate cell type-specific transcription factor networks. *Plant J.* 94: 215–231.

Smet, R.D., Sabaghian, E., Li, Z., Saeys, Y., and Peer, Y.V. de (2017). Coordinated Functional Divergence of Genes after Genome Duplication in *Arabidopsis thaliana*. *Plant Cell: tpc.00531.2017.*

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

Tian, T., Liu, Y., Yan, H., You, Q., Yi, X., Du, Z., Xu, W., and Su, Z. (2017). agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. *Nucleic Acids Res.* 45: W122–W129.

Togninalli, M., Seren, Ü., Meng, D., Fitz, J., Nordborg, M., Weigel, D., Borgwardt, K., Korte, A., and Grimm, D.G. (2018). The AraGWAS Catalog: a curated and standardized *Arabidopsis thaliana* GWAS catalog. *Nucleic Acids Res.* 46: D1150–D1156.

Tokizawa, M., Kusunoki, K., Koyama, H., Kurotani, A., Sakurai, T., Suzuki, Y., Sakamoto, T., Kurata, T., and Yamamoto, Y.Y. (2017). Identification of *Arabidopsis* genic and non-genic promoters by paired-end sequencing of TSS tags. *Plant J.* 90: 587–605.

Trigg SA, Garza RM, MacWilliams A, Nery JR, Bartlett A, Castanon R, Goubil A, Feeney J, O'Malley R, Huang SC, Zhang ZZ, Galli M and Ecker JR (2017) CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nature Methods* 14(8):819-825. doi: 10.1038/nmeth.4343

Van Bel, M., Diels, T., Vancaester, E., Kreft, L., Botzki, A., Van de Peer, Y., Coppens, F., and Vandepoele, K. (2018). PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. *Nucleic Acids Res.* 46: D1190–D1196.

Vanechoutte, D., Estrada, A.R., Lin, Y.-C., Loraine, A.E., and Vandepoele, K. (2017). Genome-wide characterization of differential transcript usage in *Arabidopsis thaliana*. *Plant J.* 92: 1218–1231.

Waese, J. *et al.* (2017). ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. *Plant Cell* 29: 1806–1821.

Liu, Y., Tian, T., Zhang, K., You, Q., Yan, H., Zhao, N., Yi, X., Xu, W., and Su, Z. (2018). PCSD: a plant chromatin state database. *Nucleic Acids Res.* 46: D1157–D1167.

Müller, H.-M., Van Auken, K.M., Li, Y., and Sternberg, P.W. (2018). Textpresso Central: a customizable platform for searching, text mining, viewing, and curating biomedical literature. *BMC Bioinformatics* 19: 94.
Naithani, S. and Van de Peer, Y. (2016). Genomic resources and databases for plant research community. *Curr. Plant Biol.* 7–8: 1.

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

Palovaara, J., Saiga, S., Wendrich, J.R., Hofland, N. van 't W., Schayck, J.P. van, Hater, F., Mutte, S., Sjollem, J., Boekschoten, M., Hooiveld, G.J., and Weijers, D. (2017). Transcriptome dynamics revealed by a gene expression atlas of the early *Arabidopsis* embryo. *Nat. Plants* 3: 894–904.

Plant Genomics Databases - Methods and Protocols | Aalt-Jan van Dijk | Springer.

Puelma T, Araus V, Canales J, Vidal EA, Cabello JM, Soto A, Gutiérrez RA (2017) GENIUS: web server to predict local gene networks and key genes for biological functions. *Bioinformatics*. doi: 10.1093/bioinformatics/btw702

Clone-Based Functional Genomics Resources (ORFeomics)

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

Motoaki Seki (Chair), motoaki.seki@riken.jp, RIKEN CSRS
Joe Ecker (Co-Chair), ecker@salk.edu, Salk Institute
Pascal Braun (Subcommittee Member), pascal.falterbraun@helmholtz-muenchen.de, Helmholtz Zentrum München (HMGU)
Satoshi Iuchi (Subcommittee Member), satoshi.iuchi@riken.jp, RIKEN BRC
Debbie Christ, crist.30@osu.edu, ABRC

Open Tools and Resources for Arabidopsis Researchers

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

Recent activities of Subcommittee members.

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

Future Activities of the Subcommittee.

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

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

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

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

Publication

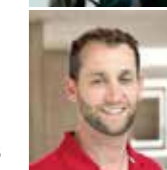
Trigg SA, Garza RM, MacWilliams A, Nery JR, Bartlett A, Castanon R, Goubil A, Feeney J, O'Malley R, Huang SC, Zhang ZZ, Galli M and Ecker JR (2017) CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nature Methods* 14(8):819-825. doi: 10.1038/nmeth.4343.

Epigenetics and Epigenomics

Xuehua Zhong
xuehua.zhong@wisc.edu
University of Wisconsin-Madison



Robert Schmitz
schmitz@uga.edu
University of Georgia



Open Tools and Resources for Arabidopsis Researchers

Enhanced Jbrowse Plug-ins for Epigenomic Data Visualization.

<https://github.com/bhofmei/bhofmei-jbplugins>

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

Conferences and Workshops

2017
International Conference on Arabidopsis Research, St. Louis, MO, June 2017 (Session on Epigenetics).

Gordon Research Conference, Epigenetics. Holderness, NH, August 2017

Plant & Animal Genomes Conference, San Diego, CA, January 2017 (Session on Epigenomics of Plants International Consortium)

40th New Phytologist Symposium – Plant Epigenetics, Vienna, Austria, June 2017

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

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)

Reports from MASC Subcommittees

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14,398	signal.salk.edu/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	http://interactome.dfci.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/ RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC

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

American Society for Plant Biologist, Montreal, Canada, July 2018 (Session on Plant Epigenetics)

28th International Conference on Arabidopsis Research, Turku Finland, June 2018 (Session on Epigenetics)

2019

Impact of Nuclear Domains On Gene Expression and Plant Traits, France, December 2019
Plant Epigenetics, Vienna, Austria, (hosted by Magnus Nordborg) Date:TBD, 2019

2020

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

Training

EpiDiverse Research & Training Network, Wageningen, Netherlands, June 5-8, 2018

Reports from MASC Subcommittees

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
					sheenweb/category_genes.html	
Steve Clouse	Gateway expression	N-terminal Flag/His tagged kinases		855	http://www4.ncsu.edu/~sclouse/Clouse2010.htm	ABRC
Frommer et al.	Gateway entry, no stop	Membrane and signaling proteins	5' and 3' end seq.	2,712	http://associomics.org	ABRC
Frommer et al.	Gateway Expression (mbSUS clones)	Membrane and signaling proteins	5' and 3' end seq.	5,414	http://associomics.org	ABRC
AIST/RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	1,998		BRC
RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	399		BRC
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	PIX-HALO vector			12,069		ABRC
O'Malley et al.	PIX-HALO vector	Transcription factor	Full sequence	1,315		ABRC
Guillaume Pilot	pDONRZEO vector	Membrane protein	5' and 3' end seq.	192		ABRC
Pruneda-Paz et al.	Gateway Entry, no stop	Transcription factor	Full sequence	1,956		ABRC
Pruneda-Paz et al.	Gateway Destination, no stop, pDEST22	Transcription factor	Full sequence	1,956		ABRC
Lao et al.	Gateway DONR, no stop, pDONR223	glycosyltransferases	Full sequence	429	http://gt.jbei.org/	ABRC
Amita Kaundal et al.	Gateway DONR, no stop, pDONR201			26		ABRC
cDNA clones						
RIKEN/SSP/	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	22,671	www.brc.riken.go.jp/lab/	BRC
Salk Insitute					epd/Eng/order/order.shtml	
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LT I	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/Arabidopsis	CNRGV

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

Selected Publications

Biochimica et Biophysica Acta Special issue on Plant Gene Regulatory Mechanisms and Networks included 16 articles edited by Nathan Springer and Erich Grotewold.

<https://www.sciencedirect.com/journal/biochimica-et-biophysica-acta-bba-gene-regulatory-mechanisms/vol/1860/issue/1>

Genome Biology Special issue on Plant Epigenomics included 30 articles edited by Claudia Kohler and Nathan Springer

<https://www.biomedcentral.com/collections/plantepigenomics>

Metabolomics

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

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



Open Tools and Resources for Arabidopsis Researchers

www.masc-metabolomics.org
Metabolomics subcommittee website

<https://www.arabidopsis.org/portals/metabolome/index.jsp>
TAIR metabolomics Resources

<http://prime.psc.riken.jp/>
PRIME, a web-based service for metabolomics, containing computational metabolomics toolbox (MS-DIAL, MS-FINDER, etc), metabolomic datasets (DROP Met), metabolic modeling system (PASMet), metabolomic characterization of 50 Arabidopsis mutants and the database as a functional genomics tool (MeKO), standard compounds (MetBoard), Arabidopsis metabolome expression databases (AtMetExpress development, AtMetExpress 20 ecotypes) and a collection of literature and in-house MS spectra data (ReSpect for Phytochemicals).

<http://gmd.mpimp-golm.mpg.de/>
Golm Metabolome Database facilitates the search for and dissemination of reference mass spectra from biologically active metabolites quantified using gas chromatography (GC) coupled to mass spectrometry (MS).
www.plantmetabolomics.org A web portal of Arabidopsis Metabolomics Consortium that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants. <http://mmcd.nmrfam.wisc.edu/>
The Madison-Qingdao metabolomics consortium database has emphasis on Arabidopsis and contains both NMR and MS data of metabolites.

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

Recent activities of Subcommittee members.

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

Future Activities of the Subcommittee.

To realize the goals, we aimed to establish the subcommittee website www.masc-metabolomics.org for more efficient exchange of information and dissemination of the subcommittee's activity. The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where the subcommittee members can join. The webinterface 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

2017/6/26-29 Metabolomics 2017, Brisbane, Australia
2017/7/9-14 Gordon Research Conference, Plant Metabolic Engineering, Waterville Valley, NH, US
2017/7/16-20 The 4th International Conference on Plant Metabolism (ICPM 2017), Dalian, China
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

Proteomics

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

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

Joshua Heazlewood (chair)

Open Tools and Resources for Arabidopsis Researchers

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

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

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

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

SUBA - subcellular database
<http://suba.live/>
by Millar

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

AT_CHLORO - plastid proteomic resource
http://at-chloro.prabi.fr/at_chloro/
by Rolland and Ferro

Plant PTS1 Protein Prediction-
<http://ppp.gobics.de/>
by Reumann

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

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

MASCP Gator - proteomics aggregation portal
<http://gator.masc-proteomics.org/>
by MASCP

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



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

Multiple Marker Abundance Profiling
<http://suba.live/toolbox-app.html>
 by Heazlewood and Millar

Recent activities of Subcommittee members.

- A) The subcommittee members maintain an array of Arabidopsis specific proteomic repositories. These resources currently contribute to information in the Arabidopsis Information Portal (AIP).
- B) The 1001 Proteomes portal provides pre-computed nsSNP data from the sequenced accessions. Data from this portal are now available in ePlant.
- C) Members have ongoing interests in applying proteomic approaches in Arabidopsis to important crop species. A number of the on-line proteomic resources also provide proteomic datasets for agricultural relevant species.
- D) Subcommittee members maintain extensive resources in the area of protein function in Arabidopsis, and it is expected that this information will be coordinated with the IAIC.

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

Future Activities of the Subcommittee.

- (A) Maintain and develop new resources for Arabidopsis focusing on protein function and proteomics.
- (B) Demonstrate applicability of 1001 proteome data to the research community. Update the data for the recently released accessions.
- (D) Continue to develop proteomic Apps for the Arabidopsis Information Portal.
- (E) Ensure attendance and involvement in future INPPO and HUPO activities.
- (F) Maintain an active Arabidopsis proteomics subcommittee (<http://www.masc-proteomics.org/>)

Publications

Hooper CM, Stevens TJ, Saukkonen A, Castleden IR, Singh P, Mann GW, Fabre B, Ito J, Deery MJ, Lilley KS, Petzold CJ, Millar AH, Heazlewood JL, Parsons HT (2017) Multiple

marker abundance profiling: combining selected reaction monitoring and data-dependent acquisition for rapid estimation of organelle abundance in subcellular samples. *Plant J* 92: 1202-1217

Kraner ME, Muller C, Sonnewald U (2017) Comparative proteomic profiling of the choline transporter-like1 (CHER1) mutant provides insights into plasmodesmata composition of fully developed *Arabidopsis thaliana* leaves. *Plant J* 92: 696-709

Willems P, Ndah E, Jonckheere V, Stael S, Sticker A, Martens L, Van Breusegem F, Gevaert K, Van Damme P (2017) N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in *Arabidopsis thaliana*. *Mol Cell Proteomics* 16: 1064-1080

Rantala M, Tikkanen M, Aro EM (2017) Proteomic characterization of hierarchical megacomplex formation in Arabidopsis thylakoid membrane. *Plant J* 92: 951-962

Carrera DA, Oddsson S, Grossmann J, Trachsel C, Streb S (2018) Comparative Proteomic Analysis of Plant Acclimation to Six Different Long-Term Environmental Changes. *Plant Cell Physiol* 59: 510-526

Systems and Synthetic Biology

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

Siobhan Brady, UC Davis
sbrady@ucdavis.edu
 Malcolm Bennett, University of Nottingham
Malcolm.Bennett@nottingham.ac.uk,
 Gabriel Krouk, CNRS
gabriel.krouk@cnrs.fr
 Nicola Patron, Earlham Institute
Nicola.Patron@earlham.ac.uk,
 Rodrigo Gutierrez, P. Universidad Catolica de Chile
rgutierrez@bio.uc.cl
 Pascal Falter-Braun, Hemholtz Zentrum Munchen
pascal.falter-braun@helmholtz-muenchen.de



Open Tools and Resources for Arabidopsis Researchers

GB3.0 A Digital Toolbox for Plant Synthetic Biology
<https://gbcloning.upv.es>
 LOOP A simple, open-source system for recursive fabrication of DNA circuits
<https://www.biorxiv.org/content/early/2018/01/15/247593>

OpenMTA. A simple, standardized legal tool that enables individuals and organizations to share their materials on an open basis. Developed as a collaborative effort between the BioBricks Foundation and the OpenPlant Initiative, with input from researchers, technology transfer professionals,

social scientists, lawyers, and other stakeholders from across the globe, the OpenMTA reflects the values of open communities and the practical realities of technology transfer.
<https://www.openplant.org/openmta/>

OpenSimRoot - Postma, J.A., Kuppe, C., Owen, M.R., Mellor, N., Griffiths, M., Bennett, M.J., Lynch J.P., Watt, M. (2017) OpenSimRoot: Widening the scope and application of root architectural models *New Phytologist* 215 (3) 1274-1286. This paper describes how researchers from 3 centres in the US, UK and Germany worked together to create an open source version of SimRoot, termed OpenSimRoot, to make this FSPM (functional-structural plant model) available to the wider scientific community

Conferences, Workshops and Training events

- Conferences and Workshops
 Practical Synthetic Biology. Pretoria, South Africa, February 2017
- Synthetic Biology for Natural Products. Cancun, Mexico, May 2017
- SB7.0 Singapore, June 2017
- Synthetic Biology: Engineering, Evolution & Design (SEED). Vancouver, July 2017
- Gordon Research Conference, Plant Metabolic Engineering – Plant Engineering in the Synthetic Biology Era. Waterville Valley, NH, July 2017
- Open Plant. Cambridge, UK, July 2017
- Genome Science/Genome10K. Norwich, UK, August 2017
- Natural Products and Synthetic Biology: Parts and Pathways. Olympic Valley, California USA, January 2018
- Molecular Biosystems, Puerto Varas, Chile, September 23-26, 2017
- 1st Latin American Workshop and Conference on Systems Biology, Mexico City, Mexico, May 2-5, 2017
- Systems Biology: Networks, Cold Spring Harbor, New York, USA, March 14-18, 2017
- International Conference on Arabidopsis Research, St. Louis, Missouri, USA, June 19-23, 2017, session on Modeling, Gene Regulation, Systems, Quantitative and Computational Biology.
- Synbiosys Summer School, Copenhagen Plant Sciences Centre, Denmark, August 2017
- The Synthetic and Systems Biology Summer School (SSBSS) Robinson College, University of Cambridge, UK, July 2017
- Second International Plant Biology Course (Santiago, Chile), 2017.

Future Conferences or Workshops:

- EMBO Workshop: Integrating Systems Biology, April 15-17, 2018; with prominent plant talks and Sorina Popescu and as organizers Pascal Falter-Braun, Luis Serrano and Sandra Orchard.
- iPSB - First International Plant Systems Biology Meeting; September 10-14, 2018; organized by Gabriel Krouk, Pascal Falter-Braun, Siobhan Brady, Gloria Coruzzi and Rodrigo Gutierrez
- SEB Interdisciplinary Sessions: The 2018 Annual Meeting of the Society for Experimental Biology will be held in Florence on the 3rd-6th July 2018. This will feature many parallel sessions including interdisciplinary sessions on "Shaping root architecture - from nutrient sensing and tropisms to systemic signals and decision making" organised by Stefan Kepinski and Julia Davis,
- Systems analyses of multicellularity complexity and organ biology organised by George Bassel, Leah Band and Mark Fricker,
- Quantitative synthetic biology organised by Christian Fleck, Mustafa Khamash and Robert Smith.

Selected Publications

- Robaina-Estévez S, Daloso DM, Zhang Y, Fernie AR, Nikoloski Z.; Resolving the central metabolism of Arabidopsis guard cells. *Sci Rep.* 2017 Aug 16;7(1):8307. doi: 10.1038/s41598-017-07132-9.
- Kautsar SA, Suarez Duran HG, Blin K, Osbourn A, Medema MH (2017) plantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters *Nucleic Acids Research.* 45(W1):W55-W63. doi: 10.1093/nar/gkx305.
- Di Mambro R, De Ruvo M, Pacific E, Salvi, E, Sozzani R, Benfey PN, Busch W, Novak O, Ljung K, Di Paola L, Maree AFM, Costantino P, Grieneisen VA, Sabatini S. Auxin minimum triggers the developmental switch from cell division to cell differentiation in the Arabidopsis root. *PNAS.* (2017) 114(36):E7641-E7649.
- Li B, Tang M, Nelson A, Caligagan H, Zhou X, Clark-Wiest C, Ngo R, Brady SM, Kliebenstein, DJ. Network-Guided Discovery of Extensive Epistasis between Transcription Factors Involved in Aliphatic Glucosinolate Biosynthesis. *Plant Cell.* 2018 Jan;30(1):178-195. doi: 10.1105/tpc.17.00805. Epub 2018 Jan 9.
- Jackson MD, Xu H, Duran-Nebreda S, Stamm P, Bassel GW. Topological analysis of multicellular complexity in the plant hypocotyl. *Elife.* 2017. pii: e26023. doi: 10.7554/eLife.26023

Additional Information

iPSB was a direct result of activities and leadership efforts on behalf of the Systems and Synthetic Biology Subcommittee.

Arabidopsis Community Projects and Resources

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

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

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

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

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

Resource and Stock Centers

Arabidopsis Biological Resource Center (ABRC) (page 24)

Nottingham Arabidopsis Stock Centre (uNASC) (page 25)

RIKEN BioResource Center (BRC) (page 26)

The Arabidopsis Information Resource (TAIR) (page 26)

International Arabidopsis Informatics Consortium (IAIC) (page 28)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

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

International Plant Phenotyping Resources (page 31)

Gramene (page 32)

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

-The 1001 Arabidopsis Genomes Project
www.1001genomes.org

-The Epigenomics of Plants International Consortium EPIC;
www.plant-epigenome.org

- The Plant and Microbial Metabolomics Resource
<http://metnetdb.org/PMR/>

- The SUBA4: The SubCellular Proteomic Database
<http://suba.plantenergy.uwa.edu.au/>

- 1001 Proteomes
<http://1001proteomes.masc-proteomics.org/>

- AraGWAS
<https://aragwas.1001genomes.org/>

- GENIUS machine learning algorithm to infer functional gene networks
<http://networks.bio.puc.cl/genius>

, Arabidopsis hormone database 2.0
<http://ahd.cbi.pku.edu.cn/>

- PlantGSEA: a gene set enrichment analysis
<http://structuralbiology.cau.edu.cn/PlantGSEA/>

- Arabidopsis Protein Phosphorylation Site Database
<http://phosphat.uni-hohenheim.de/index.html>

- 3DCellAtlas
<http://www.georgebassellab.com/3d-cell-atlas/>



Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC)

www.abrc.osu.edu

David Somers, somers.24@osu.edu, ABRC Director (since April 2018)
 Jelena Brkljacic, brkljacic.1@osu.edu, ABRC Associate Director
 Keith Slotkin, slotkin.2@osu.edu, ABRC Director (until April 2018)



Open Tools and Resources for Arabidopsis Researchers

ABRC provides seed, clones, vectors, host strains, antibodies, cell lines and education resources for species ranging from *Arabidopsis thaliana* and other Brassica species to maize and other crops.

Recent activities of your project or resource.

We are pleased to announce that we secured additional support for our operation in 2017 through an NSF RAPID funding program, adding to the current CSBR NSF support (April 2016 – March 2019).

Last year we expanded and diversified the ABRC's collection. Within Arabidopsis, we acquired a number of cutting-edge resources such as a set of HALO-tagged transcription factors (TFs) for identification of DNA binding regions, CrY2H vectors and host strains for high-throughput yeast two hybrid assays by deep sequencing, and a comprehensive toolkit comprising 162 vectors for advanced genome engineering via CRISPR/Cas9 mutagenesis.

In addition to Arabidopsis resources, the ABRC has continued to diversify our collection through the acquisition of a soybean TF clone set, seeds from diverse Brassica species, and a comprehensive toolkit for CRISPR/Cas9 across monocots and dicots.

The ABRC has continued to expand and enhance our education and outreach program, reaching out to larger and more diverse audiences. Our education kits using Arabidopsis continue to be highly ordered and most of the kits are available free of charge. Two education papers were published (see Additional Information) and a revamped education website is about to be released (see Future Activities), making this a very good year for our education and outreach program.

Planned future activities of your project or resource.

For the past 17 years, The Arabidopsis Information Resource (TAIR) has provided services for searching and ordering ABRC stocks. For the past two years, the ABRC has been collaborating with the College of Arts and Sciences Technology Services (ASC Tech) at Ohio State to design an independent ABRC database and ordering system. The ABRC database provides superior searching capabilities and access to complete stock information, including quality control (QC) and additional features. In addition, the new system is much more flexible and provides full access to a growing number of the ABRC's non-Arabidopsis resources. The ABRC database will be released for testing in the spring of 2018. The ABRC stock ordering will still be available through TAIR during the testing stage. After successful testing of the new database, ABRC stocks will only be available for ordering through our system, and no longer through TAIR.

We have recently received a donation of Brassica species as part of a collection of "Top 20 Brassicales" sequenced through the Brassicales Map Alignment Project (BMAP) sponsored by the U.S. Department of Energy Joint Genome Institute (DOE JGI). The propagation and distribution of this resource is planned for 2018.

More bioenergy-related and other Brassica species, including 100 *Brassica rapa* stocks and a GWAS population of ~500 sequenced accessions of *Boechera stricta*, are expected in the near future. The ABRC plans to continue serving a wide Brassica community by providing stock propagation, maintenance and QC. In addition, our new database with a user-friendly online search tool will allow users to search exclusively for Brassica stocks, making these resources much easier to find and order.

Conferences, Workshops and Training events

The ABRC shared a booth with The Nottingham Arabidopsis Stock Centre (NASC) and participated in the bioinformatics resources workshop at the International Conference on Arabidopsis Research (ICAR) in St. Louis in 2017. The ABRC also had a booth at the annual Plant Biology meeting of the American Society of Plant Biologists (ASPB) in Hawaii. In 2018, ABRC participated in the Plant and Animal Genome conference in San Diego, by presenting a talk focused on the ABRC education program and by promoting donation and distribution of other species' resources. Current conference plans include ICAR, ASPB and the International Plant Molecular Biology (IPMB) meeting in the summer of 2018.

Additional Information

The ABRC published a methods paper (Lindsey B, Rivero L, Calhoun C, Grotewold E, and Brkljacic J (2017) Standardized Method for High-throughput Sterilization of Arabidopsis Seeds. *J Vis Exp* E56587, doi:10.3791/56587) and an education paper (Mann J, Larson J, Pomeranz M, Knee E, Shin D, Miller J, Price C, Crist D, Grotewold E, and Brkljacic J (2017) Life in Bloom: Using Arabidopsis Mutants to Study Plant Development. Course Source, <https://www.coursesource.org>) last year and one this year (Price C, Knee E, Miller J, Shin D, Mann J, Crist D, Grotewold E, and Brkljacic J (2018) Following Phenotypes: An Exploration of Mendelian Genetics Using Arabidopsis Plants. *American Biology Teacher*, doi: 10.1525/abt.2018.80.4.291).

We are very grateful to Dr. Keith Slotkin for his service as an ABRC Director and welcome Dr. David Somers, an esteemed OSU Professor, as our new Director.



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



Another productive year sending over 150,000 tubes of seed to the worldwide plant community sees a slight change in the international profile of our users. Out of a total of 43 countries ordering from NASC during 2017, the top five countries (in order by individual stock numbers) are China (No.1 for the third year in a row), the UK, Australia (first time in the top 5), Germany, and France.

For entertainment purposes, we shared (@NascArabidopsis - Jan 2018) a map of locations in China and the UK (by institute) that had ordered seed from us in 2017.

Of course, our broader catalogue access maps for all countries can always be found at <http://clustrmaps.com/map/Arabidopsis.info>.

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

If we (NASC and ABRC) can save you time, effort and promote your research impact by distributing seed on your behalf to the wider plant community then please do holler (or email) - don't wait for us to come to you.

See you in Turku!



RIKEN BioResource Center (RIKEN BRC)

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

Masatomo Kobayashi
(RIKEN coordinator)



Open Tools and Resources for Arabidopsis Researchers

Seeds of Arabidopsis (natural accessions, mutants, and transgenic lines)
Plant DNA materials including Arabidopsis
Plant cultured cell lines including Arabidopsis T87 cell
<http://epd.brc.riken.jp/en/>

Recent activities

The Japanese government launched the fourth term of the five-year National BioResource Project (NBRP) in April 2017 (<http://www.nbrp.jp/index.jsp>). RIKEN BRC was selected as the core facility of Arabidopsis, cultured plant cells and genes. We are reconstructing the web catalog and accumulating useful information for research communities.

Planned future activities

RIKEN starts the fourth 7-year term plan from April 2018. During this period, RIKEN BRC enriches biological materials, technologies and information which are crucial requirements for both basic and advanced researches. Revision of the Bioresource Frontier Programs contributes the global issues such as human health, food supply and environmental protection. In the revised Program, Plant-Microbe Symbiosis Research and Development Team engages in the isolation, characterization and utilization of rhizosphere microbes to innovate agricultural technologies.

Conferences, Workshops and Training events

The 29th International Conference on Arabidopsis Research (ICAR2018), June 25-29, 2018, Turku, Finland
The 9th International Meeting of Asian Network of Research Resource Centers (ANRRC), Sept. 20-22, 2017, Beijing, China
The 10th International Meeting of Asian Network of Research Resource Centers (ANRRC), Sept. 5-7, 2018, Seoul, Korea

Additional Information

RIKEN BioResource Center is renamed to RIKEN BioResource Research Center to increase the R & D activities on biological resources.



Arabidopsis Informatics and Data Sharing Resources

The Arabidopsis Information Resource (TAIR)

www.Arabidopsis.org

Leonore Reiser (TAIR curator)
Eva Huala (Director)



Activities

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

These activities are made possible by support from the international Arabidopsis and plant research community whose contributions ensure that TAIR remains available and an up to date resource for plant biologists around the world.

New Tool: Gene Ontology (GO) Term Enrichment

One of the most common applications of the Gene Ontology is for term enrichment; finding groups of terms that are over or under-represented in a gene set. The accuracy of enrichment results is, to a large extent, dependent upon the underlying data sets; specifically, the annotations and ontologies. Changes to the Arabidopsis annotations are frequent; new annotations are added on a weekly basis and occasionally annotations are deleted. Changes to ontologies include addition of new terms or pruning of nodes. It is therefore critical that term enrichment tools use current annotation and ontology datasets to produce the most reliable results. To assist the Arabidopsis community in performing term enrichment, we have added the GO Term Enrichment tool developed by PANTHER (http://www.arabidopsis.org/tools/go_term_enrichment.jsp). The tool takes a list of gene IDs (e.g. AGI locus codes, UniProt or GenBank IDs) and sends the data to the PANTHER Classification System (www.pantherdb.org). PANTHER GO term enrichment data sources are updated monthly.

In addition to performing term enrichment for Arabidopsis, the tool can also be used to perform enrichment on 9 other species included in the PANTHER database: Brachypodium, Chlamydomonas, soybean, rice, Physcomitrella, poplar, tomato, sorghum and grape.

Genome and Gene Function Curation

A major goal of TAIR curation is to present the most up to date and accurate picture of the Arabidopsis genome. All gene models, assignments, computational descriptions and sequences in TAIR have been updated to Araport11. In addition, we have updated and added thousands of T-DNA polymorphisms using genome coordinates and locus assignments provided by the Ecker Lab. Many TAIR tools (e.g. gene descriptions, sequences, locus history) now use Araport11 as the underlying data source and the remaining tools will follow. The addition of new gene models has increased the pool of 'unknown' or 'unannotated' genes slightly, as reflected in the updated genome snapshot (http://www.arabidopsis.org/portals/genAnnotation/genome_snapshot.jsp). Identifying and extracting knowledge about these two classes of gene products continues to be a major activity at TAIR.

TAIR continuously updates information about Arabidopsis gene function, expression and mutant phenotypes using data extracted from recent literature. When choosing articles TAIR curators prioritize those that allow us to add functional information about genes that had not previously been described in the literature ('unknown' genes) thus increasing the breadth of functional annotation. We capture this experimentally derived knowledge in the form of GO and Plant Ontology (PO) annotations, individually composed gene summaries and phenotype descriptions, and new links between articles and genes, which are added to TAIR on a weekly basis.

Between March 2017 and February 2018, we added 662 new gene symbols to TAIR and added or updated 701 gene summaries. We added 7376 new GO and PO annotations, generated by TAIR curators, TAIR community, UniProt and the GO consortium, to 1907 loci, incorporating experiment-based data from 943 research articles. We linked 2571 articles to 4261 loci, added or updated descriptions for 147 alleles, and added or updated 146 phenotypes from the literature. In 2017 we processed 607 GO/PO annotations contributed by 86 community members covering 99 publications.

Subscriptions and Complementary Access

TAIR is supported by a global community of researchers from over 37 countries. As of March 2018, subscribers include: 2 countries (China and Switzerland), 5 academic consortia, 208 academic institutions (list at <http://bit.ly/1RPlaau>), 10 companies and 324 individuals. We continue to provide complementary access for teaching

to instructors who request access using our simple form (<http://bit.ly/2fA5WR1>) and to low GDP countries upon request.

Data Releases

In accordance with our data sharing policy, TAIR continues to publish year-old data in the form of quarterly data releases (http://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases). These data are freely available and distributed for reuse under the CC-BY4.0 license. They include all GO and PO annotations, gene symbols and names, links between genes and publications, and updated gene descriptions added to TAIR through 12/31/2016. The most current data and tools are available through the website, which is updated on a weekly basis. Anyone can access a limited number of pages per month; unlimited access requires a subscription. Subscribers can also access current data in the form of quarterly releases (http://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Subscriber_Data_Releases) and can request custom data sets via our helpdesk (curator@arabidopsis.org).

Outreach: Workshops, Conferences, Presentations and Social Media

In the past year, TAIR has pioneered efforts aimed at increasing community engagement with curation, and training in data management. We organized the first annual 'Annotation Jamboree' at the 2018 Plant and Animal Genome meeting, that focused on gene function annotation using ontologies. Slides from the presentation are available (<http://bit.ly/phoenix-pag-2018>).

To promote Findable, Accessible, Interoperable, and Reusable (FAIR) data publication in plant sciences, we co-presented a seminar on Data Management and Publishing at UC Berkeley with curators from MaizeGDB. Slides from that presentation are available at <http://bit.ly/2pkrlj5>. TAIR is also a member of the newly formed AgBioData consortium of Agricultural Databases (www.agbiodata.org), which aims to develop and promote standards and best practices for the acquisition, display and retrieval of genetic, genomic and breeding data. We plan to continue to offer similar workshops and seminars in the coming year. TAIR staff presented posters, gave talks, and were available for one-on-one interactions at exhibit booths at the following meetings: ICAR 2017 (St. Louis, MO, USA), ASPB 2017 (Honolulu, HI, USA), and PAG 2018 (San Diego, CA, USA). TAIR curators will attend ICAR 2018 in Turku, Finland and ASPB 2018 in Montreal, Canada.

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

New User Guide

We published the first major revision of our chapter in Current Protocols in Bioinformatics since 2010. Many sections received significant updates and new protocols were added including: GO Term Enrichment, Gene List Analysis with Bulk Tools, How to submit GO/PO annotations using TAIR's Online Annotation Submission Tool, and Using the Recently Added Literature Browser. The guide is available on line from Current Protocols (doi: 10.1002/cpbi.36; subscription required) or in draft form from TAIR (<http://bit.ly/2Go2wuP>)

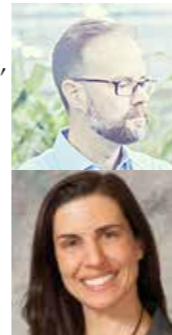
Publications

Reiser, L., Subramaniam, S., Li, D., & Huala, E. (2017). Using the Arabidopsis information resource (TAIR) to find information about Arabidopsis genes. *Current Protocols in Bioinformatics*, 60, 1.11.1–1.11.45. doi: 10.1002/cpbi.36



International Arabidopsis Informatics Consortium (IAIC)

Blake C. Meyers
IAIC Director, BMeyers@danforthcenter.org,
The Donald Danforth Plant Science Center
Joanna D. Friesner
IAIC Assistant, jdfriesner@ucdavis.edu,
North American Arabidopsis Steering
Committee



Open Tools and Resources for Arabidopsis Researchers

The IAIC was formed in 2010 to facilitate a coordinated global Arabidopsis informatics effort to maintain the continuity of key Arabidopsis resources while simultaneously expanding their breadth and depth. Key aims were to include in the IAIC new technologies, resources, and participants on a global scale and advance plant biology while creating novel opportunities for research and education and strengthening international collaborations. The primary accomplishment of IAIC with respect to globally-available resources was to facilitate the collaborative effort to establish and fund a new web-based portal, 'Araport', for Arabidopsis information and digital resources for the global plant biology community via NSF

Award #1262414: ABI Development: The Arabidopsis Information Portal. (www.nsf.gov/awardsearch/showAward?AWD_ID=1262414)

Araport enables biologists to navigate from the *Arabidopsis thaliana* Col-0 reference genome sequence to its associated annotation including gene structure, gene expression, protein function, and interaction networks. Araport offers a single interface through which to access a wide range of Arabidopsis information. Araport will grow through contributions of other labs in the form of modules: data, computation, and visualization tools. (<https://www.araport.org/about>)

Recent activities of your project or resource.

Recent IAIC efforts have focused convening relevant attendees in a workshop that will assess the current status of Arabidopsis informatics and the needs and wishes of the Arabidopsis community, looking forward to the next 5-10 years. The 'Future of Arabidopsis Bioinformatics' workshop will build on the project's previous success in enabling the establishment of 'Araport', the Arabidopsis community information resource funded by NSF, which has developed into a well-established portal with a broad range of data sets and functionalities. During the 4+ years since Araport went online the research community continued to generate increasing amounts of data that are challenging to store, manipulate and disseminate.

Plant Projects and Resources with Strong Participation of Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR)



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

Open Tools and Resources for Arabidopsis Researchers

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

- * 150 million gene expression measurements (75 million from A.th.), plus "expressologs" (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.
- * 70,944 predicted protein-protein interactions plus 36,352 documented PPIs (rice interologs also available!) and ~2.8 million protein-DNA interactions.
- * 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 9.3k 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.

Work was completed on a "mega-app" from the BAR for Araport.org, ePlant, and a publication came out in the *Plant Cell* describing it (Waese *et al.*, 2017). ePlant is a zoomable user interface for exploring data across 12 orders of magnitude, from the kilometre scale down to the nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested, open source tool. ePlant is accessible from the Araport.org homepage, and from the Bio-Analytic Resource at <http://bar.utoronto.ca/eplant>.

The broad objectives of the May 2018 IAIC workshop include to: discuss and make plans/recommendations on the directions and sustainability of Arabidopsis Informatics in the coming decade; present new resources inspired by design principles developed at the first project workshop (Dec. 2011); identify informatics challenges that impede discovery and possible community-based solutions for these challenges; brainstorm a list of new tools the community would like to have or existing tools we would like to see expanded; identify stable central data and tool platforms within the community, evaluate how to promote their long-term stability with funding entities, and identify new platforms to facilitate the ever-broadening scope of genome-wide approach data.

Workshop organizers plan to collaboratively develop a white paper publication with outcomes, analysis, and recommendations to disseminate broadly.

Conferences, Workshops and Training events

The project's PI and Araport/AIP PI gave a presentation on aspects of Araport and IAIC efforts entitled "Arabidopsis Informatics" at the 2018 Plant and Animal Genome (PAG) conference.

The first major update to ePlant was released in January 2018, and included a new Plant eFP view for Klepikova *et al.*'s (2016) RNA-seq-based developmental atlas, updated subcellular localization data using SUBA4 data, an ePlant Navigator to easily view expression patterns of homologs in other species, and the highlighting of gene parts in the Gene view.

We also released an "eFP-Seq Browser" for exploring the 113 RNA-seq data sets used to reannotate the Arabidopsis genome for the Araport11 build, or the RNA-seq data sets generated for Klepikova *et al.*'s (2016) developmental atlas, both as read maps and pictographs summarizing the expression levels in various tissues, easily sortable by any desired column: http://bar.utoronto.ca/eFP-Seq_Browser/. In addition to simply sorting the table by expression level, an "eFP overview" provides a table of pictographs to get a feeling for where expression is the strongest or weakest.

We released hundreds of new protein-protein interactions for the extra-cellular domains of leucine-rich repeat receptor kinases into our ePlant and Arabidopsis Interaction Viewer tools (Smakowska-Luzan *et al.*, 2018).

For translational researchers, publications came out for eFP Browser views announced last year: a Developmental Map for Brachypodium distachyon from Marek Mutwil and colleagues (Sibout *et al.*, 2017; http://bar.utoronto.ca/efp_brachypodium/), a Maize Root view, part of the Maize eFP Browser, from Stefan Hey and colleagues (Hey *et al.*, 2017; http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi), and a Classification SuperViewer for Medicago truncatula genomics (Herrbach *et al.*, 2017; http://bar.utoronto.ca/ntools/cgi-bin/ntools_classification_superviewer_medicago.cgi).

BAR Publications

Herrbach V, Chirinos X, Rengel D, Agbevenou K, Vincent R, Pateyron S, Huguet S, Balzergue S, Pasha A, Provart NJ, Gough C, Bensmihen S (2017). Nod factors potentiate auxin signaling for transcriptional regulation and lateral root formation in Medicago truncatula. *Journal of Experimental Botany* 68: 569-583.

Hey S, Baldauf J, Opitz N, Lithio A, Pasha A, Provart NJ, Nettleton D, Hochholdinger F (2017). Complexity and specificity of the maize (*Zea mays* L.) root hair transcriptome. *Journal of Experimental Botany* 68: 2175-2185.

Sibout R, Proost S, Oest Hansen B, Vaid N, Giorgi FM, Ho-Yue-Kuang S, Legée F, Cézart L, Bouchabké-Coussa O, Soulhat C, Provart N, Pasha A, Le Bris P, Roujol D, Hofte H, Jamet E, Lapierre C, Persson S, Mutwil M (2017). Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in Brachypodium distachyon. *New Phytologist* 215: 1009-1025.

Smakowska-Luzan E, Mott GA, Parys K, Stegmann M, Howton TC, Layeghifard M, Neuhold J, Lehner A, Kong J, Grünwald K, Weinberger N, Satbhai SB, Mayer D, Busch W, Madalinski M, Stolt-Bergner P, Provart NJ, Mukhtar MS, Zipfel C, Desveaux D, Guttman DS, Belkhadir Y (2018). An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. *Nature* 553: 342-346. doi:10.1038/nature25184.

Waese J, Fan J, Pasha A, Yu H, Fucile G, Shi R, Cumming M, Kelley LA, Sternberg MJ, Krishnakumar V, Ferlanti E, Miller J, Town C, Stuerzlinger W, Provart NJ (2017). ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. *Plant Cell* 29: 1806-1821. doi: 10.1105/tpc.17.00073.

Waese J, Provart NJ (2017). The Bio-Analytic Resource for Plant Biology. Book chapter in *Plant Genomics Databases*, Humana Press, pp. 119-148.

Planned future activities of your project or resource.

A custom eFP view in ePlant for researcher's own RNA-seq data is planned, as part of a new application to Genome Canada. Stay tuned!

Conferences, Workshops and Training 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.

International Plant Phenotyping Resources

Roland Pieruschka
Julich Plant Phenotyping Centre
r.pieruschka@fz-juelich.de



International Plant Phenotyping Network

IPPN <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. Within the last year, IPPN has established its basic operation by setting up a number of working groups on relevant topics, organizing workshops, meetings, and international symposia.

The next IPPN Symposium will be held in October 2-5th in Adelaide Australia (<http://www.ipps2018.com.au/>).

With the increasing development of a global plant phenotyping community it is also essential to extend the IPPN membership base by implementing and fostering close interaction between academia and industry partners to drive and develop innovation that delivers to academic and industry users. Thus, the IPPN General Assembly has decided to include members from industry and by mid-2018, members from industry can join the association.

EMPHASIS

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

The European Strategy Forum for Research Infrastructure (ESFRI) has identified "Plant Phenotyping" as a priority for the European research area and the project EMPHASIS has been listed on the ESFRI Roadmap as an infrastructure project to develop and implement a pan-European plant phenotyping infrastructure.

The EMPHASIS project (European Infrastructure for Multi-Scale Plant Phenotyping And Simulation for Food Security in a Changing Climate) coordinated by the Institute of Bio- and Geosciences, IBG-2: Plant Sciences at the Forschungszentrum Jülich. In 2017 EMPHASIS has started the Preparatory Phase which is a 4 year H2020 funded project. Within the Preparatory Phase, EMPHASIS will develop a business plan embedded in a sound legal framework for a long term operation of EMPHASIS. One of the major activities in preparation of the business plan consisted in a mapping of the plant phenotyping landscape in Europe to foster the information exchange about infrastructures, major



stakeholders, main projects and networks. Additionally, close interaction between national plant phenotyping communities was established and about 23 national communities have already 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 AnaEE (<https://www.anaee.com/>) which offers access to experimental and modelling platforms as well as data on terrestrial and aquatic ecosystems. The activities of both projects and areas of cooperation have been outlined in a recent publication by: Roy *et al* (2017) European infrastructures for sustainable agriculture, *Nature Plants* 3, 756-758.

European Plant Phenotyping Network 2020

EPPN2020, <https://eppn2020.plant-phenotyping.eu/>

The EPPN2020 is a H2020 funded research infrastructure project that will provide 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.

Specifically EPPN2020 includes:

- i) access to 31 key plant phenotyping installations;
- ii) Joint research activities to develop: novel technologies and methods for environmental and plant measurements, tools for statistical analysis and a European plant phenotyping information systems;
- iii) networking activities to increase integration between phenotyping facilities and users within and outside of EPPN2020.

Within the first year, EPPN2020 initiated a first call for access, which resulted in 33 application. The second call for access was issued in early February 2018 with an application deadline in June 2018. New calls will be released every 6 months.

Gramene: A comparative genomics and pathways resource for plants

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



Open Tools and Resources for Arabidopsis Researchers



Gramene provides open access to comparative genomics and pathways data, and analysis tools. We host 53 reference genomes including *Arabidopsis thaliana*, *A. lyrata*, Brassicas, sugar beet, Solanaceae, cereals, fruits, and basal plants, each displaying functional gene annotations, genetic and structural variation, gene expression, gene trees with orthologous and paralogous gene classification, whole-genome alignments, and synteny maps. In addition, we host 264 pathways curated in rice and inferred in 74 additional plant species (including the above) by orthology projection. Its integrated search capabilities and interactive views facilitate visualizing gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, pathways, and cross-references. Our tools support comparative analyses of our data as well as data brought in by our users, and include a BLAST/BLAT sequence aligner, a sequence assembly converter, a genetic variant effect predictor, an advanced BioMart-based query interface, data analysis and visualization of OMICS data, and multi-species pathway comparisons. Together these comparative data and resources enable powerful cross-species comparisons.

Recent activities of your project or resource.

BACKGROUND - The Gramene database (<http://www.gramene.org>) is an integrated resource for comparative genome and functional analysis in plants. The database provides the Arabidopsis community, agricultural researchers, and plant breeders access to reference genomes, comparative resources including whole-genome DNA alignments and protein-based gene trees for 53 crops and model species including *A. thaliana*, *A. lyrata*, Brassicas, sugar beet, Solanaceae, cereals, fruits, and lower plants. In addition to 264 pathways curated in rice and inferred in 74 additional plant species (including the above), thus enabling powerful cross-species comparisons.]

The Gramene project has had five data releases since January 2017. Of significance for the Arabidopsis community are 7 new dicot genomes: jute (*Corchorus capsularis*), cucumber (*Cucumis sativus*), cotton (*Gossypium raimondii*), common sunflower (*Helianthus annuus*), blue lupin (*Lupinus angustifolius*), cassava

(*Manihot esculenta*), coyote tobacco (*Nicotiana attenuata*), and common bean (*Phaseolus vulgaris*), as well as one monocot genome: white Guinea yam (*Dioscorea rotundata*). We also released significant updates to the genome assemblies of three major crops: sorghum (V3), soybean (V3), and peach (V2), and updated gene models for maize, barley, and Japonica rice.

BACKGROUND - Our phylogenetic gene trees classifying orthologous and paralogous relationships, provide evolutionary history and insights into speciation and duplication events. These gene trees provide the basis that informs synteny maps, which enable inter-species browsing across ancestral regions. In addition to the protein-based gene trees, our WGA mappings provide a valuable resource to characterize non-coding conservation. The analyses for multiple species can be viewed simultaneously with links showing homologous genes and WGA mappings.

Our existing whole-genome DNA alignments (WGA) collection was built against *A. thaliana* (dicot model crop; 34 alignments) and *Oryza sativa Japonica* (monocot staple food crop; 44 alignments). Currently, our synteny collection includes synteny maps for *A. thaliana* against 14 species: *A. lyrata*, cucumber, soybean, cotton, sunflower, lupin, cassava, tobacco, Japonica rice, common bean, poplar, peach, sorghum, and grape. SNP and structural diversity data, including individual genotypes, are available for *A. thaliana*, and another 11 species. The SNPs are displayed in the context of gene annotation and protein domain structure, along with predicted functional consequences (e.g. missense variant). Gramene hosts several variation data sets for Arabidopsis.

In the past year, we included the full data set (12.9 M SNPs) from the 1001 Arabidopsis Genomes Project, and linked the variants in 95 inbred lines to 107 existing phenotypes from the GWAS study by Atwell *et al* (2010). Genotypes from 1,179 strains from the 2012 study by Horton and collaborators using the Affymetrix 250k Arabidopsis SNP chip, and an updated data set produced through a BBSRC funded multi-institutional collaboration involving resequencing 18 Arabidopsis lines published by Clark *et al* in 2007 were obsoleted and archived.

For supporting Arabidopsis researchers, the annotation data hosted at Gramene was integrated with the automated GWAS workflow provided by SciApps (collaboration with the CyVerse project), a ready-to-use workflow platfor, where a list of nearby genes can be automatically retrieved for the most significant associated loci.

In collaboration with the Expression Atlas project (EMBL-EBI), we provide experimental baseline expression data for 23 plant species including *A. thaliana* (185 experiments in various ecotypes, tissues and developmental stages) and *A. lyrata* (3 experiments in 3 tissues), through our Ensembl genome browser and Plant Reactome pathways interfaces.

In addition, we provide direct links to differential gene expression data on the Atlas website for 519 experiments in *A. thaliana*, and 1 in *A. lyrata*, among a total of 720 experiments in 26 plant species. Through Gramene's Plant Reactome, we now offer 264 curated rice pathways, as well as orthology-based pathway projections to 74 plant species including both, *A. thaliana* and *A. lyrata*.

In the past year, our integrated search database and modern user interface (<http://search.gramene.org>) were greatly enhanced to leverage the diverse annotations above described to facilitate finding genes through selecting auto-suggested filters with interactive views of the results. We now offer detailed views for search results featuring genomic location, gene trees and homologs lists, gene expression, and cross-references, while a pathways view is in development.

Our Blast and BioMart interfaces enable complex queries of sequence, annotation, homology, and variation data. The genomes portal of the Gramene project is developed on the Ensembl infrastructure and in collaboration with the Ensembl Genomes project (EMBL-EBI). The pathways portal of the project is the Plant Reactome (<http://plantreactome.gramene.org>). The project supports application programming interfaces to access the data, in addition to the graphical user interface, which supports visual displays, and download of the data in standardized formats for the genome and pathway data, as well as high-resolution, publication-ready, image files.

As we aim to reach out to a larger audience, we continue our monthly webinar series and invite the arab-gen@net.bio.net mailing list whenever topics relevant to the Arabidopsis community are covered. Recorded webinars are available for public view from Gramene's YouTube channel <https://www.youtube.com/channel/UCMtmq20XMccsNUaACuqQJ-w>

Planned future activities

We will continue with activities similar as those described above, and which aim 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 16 scientific conferences to present talks, posters, training workshops, hand out brochures and other educational materials. We organized community outreach booths for members of the AgBioData consortium at the Plant and Animal Genomes and Plant Biology conferences. Continued to broadcasted live webinars, and made the video-

recordings available in Gramene's YouTube channel. In collaboration with CyVerse, we organized a bioinformatics workshop at the CSHL Plant Genomes and Biotechnology meeting and together with the MaizeCode project, organized a maize annotation jamboree. Other plant education activities geared to K-12 students and faculty included a STEM summer camp, a DNA workshop for Science Olympics participants, and hands-on activities to celebrate Fascination of Plants Day. We plan on continuing our outreach, education and training activities in the next year.



Multinational Arabidopsis Steering Committee

MASC Annual Report 2017/18



Download Full MASC Report: <http://arabidopsisresearch.org/index.php/en/publications>

Country Highlights

- > **Argentina:** Mecchia *et al* (2017) RALF4/19 peptides interact with LRX proteins to control pollen tube growth in Arabidopsis. Science doi: 10.1126/science.aao5467
- > **Australia:** SUBA4: The SubCellular Proteomic Database <http://suba.live/>
- > **Austria:** AraGWAS: manually curated database for standardised GWAS results for Arabidopsis: <https://aragwas.1001genomes.org/>
- > **Belgium:** PLAZA is an access point for plant comparative genomics centralizing genomic data: <https://bioinformatics.psb.ugent.be/plaza/>
- > **Brazil:** Dressano *et al* (2017) BAK1 is involved in AtRALF1-induced inhibition of root cell expansion. PLoS Genet. doi: 10.1371/journal.pgen.1007053
- > **Canada:** Continued development of BAR resource <http://bar.utoronto.ca>
- > **Chile:** GENIUS is a user-friendly web server that uses a novel machine learning algorithm to infer functional gene networks <http://networks.bio.puc.cl/genius>
- > **China:** Hosting ICAR2019 in Wuhan, June 16-21 2019
- > **Czech Republic:** Prasad *et al* (2017) Lipoxygenase in singlet oxygen generation as a response to wounding: in vivo imaging in Arabidopsis thaliana. Sci Rep doi: 10.1038/s41598-017-09758-1.
- > **Denmark:** Nielsen *et al* (2017) VPS9a Activates the Rab5 GTPase ARA7 to Confer Distinct Pre- and Postinvasive Plant Innate Immunity. Plant Cell. doi : 0.1105/tpc.16.00859
- > **Finland:** Hosting 29th ICAR in Turku <http://icar2018.arabidopsisresearch.org/>
- > **France:** The Versailles Arabidopsis Stock Center provides seeds useful to the international research community: <http://publiclines.versailles.inra.fr/>
- > **Germany:** 1001 Genomes Project <http://1001genomes.org/>
- > **India:** Pratibhaet *et al* (2017) Gametophyte development needs mitochondrial coproporphyrinogen III oxidase function in Arabidopsis. Plant Physiol. doi: 10.1104/pp.16.01482

- > **Israel:** Center for simulating and analyzing effects of climate change on whole plant functional phenotyping: <http://www.plant-ditech.com/>
- > **Italy:** Di Mambro *et al* (2017) Auxin minimum triggers the developmental switch from cell division to cell differentiation in the Arabidopsis root. PNAS doi: 10.1073/pnas.1705833114
- > **Japan:** Plant Promoter Database <http://ppdb.agr.gifu-u.ac.jp/ppdb/cgi-bin/index.cgi>
- > **New Zealand:** Cabout *et al* (2017) The meiotic regulator JASON utilizes alternative translation initiation sites to produce differentially localized forms. Journal of Experimental Botany doi: 10.1093/jxb/erx222
- > **Norway:** Lafon-Placette *et al* (2017) Endosperm-based hybridization barriers explain the pattern of gene flow between Arabidopsis lyrata and Arabidopsis arenosa in Central Europe 10.1073/pnas.1615123114
- > **South Korea:** Cha *et al* (2017) GIGANTEA is a co-chaperone which facilitates maturation of ZEITLUPE in the Arabidopsis circadian clock. Nat Commun doi: 10.1038/s41467-016-0014-9.
- > **Spain:** 80 grants to support Arabidopsis research from the Spanish Ministry of Economy, Industry and Competitiveness
- > **Sweden:** PlantGenIE platform: portal for indepth exploration of poplar, spruce, and Arabidopsis: <http://plantgenie.org/>
- > **Switzerland:** 5.5-year joint project for Japan and Switzerland on polyploid Arabidopsis and crop species funded by Japan Science and Technology Agency
- > **United Kingdom:** Eurasian Arabidopsis Stock Centre (uNASC) is based at the University of Nottingham: <http://arabidopsis.info/>
- > **United States:** Friesner *et al* (2017) The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. Plant Physiol doi: 10.1104/pp.17.01490.

Analysis of Arabidopsis Publications

Research Outlook 2017/18

The number of publications featured in PubMed that include Arabidopsis in the 'Title' or 'Abstract' continues to be the most commonly mentioned plant (Figure 3). However it is likely that 2017 is the final year that this will be the case as published research that includes rice/oryza continues to grow. The growth in this area is likely driven by support for rice research in Asian countries. This mimics the continued increase in the number of Arabidopsis publications, albeit at a slower rate, from Chinese researchers and represents continued excellent support for plant science research in that area of the world (figure 5). Other growing economies such as India and Brazil show slight increases in Arabidopsis publications (Figure 4).

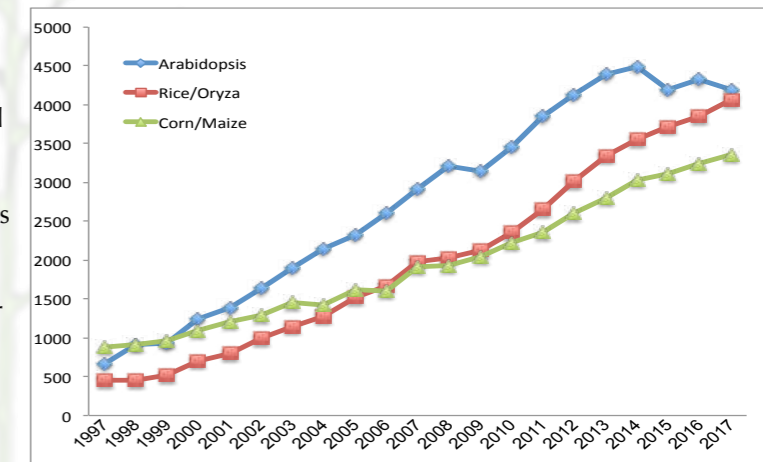


Figure 3. Papers published globally with Arabidopsis, rice/oryza or corn/maize in the Title/Abstract.

Elsewhere countries that historically were in the vanguard of support for Arabidopsis research have shown a variety of trends over the past 5 years. The USA has the second

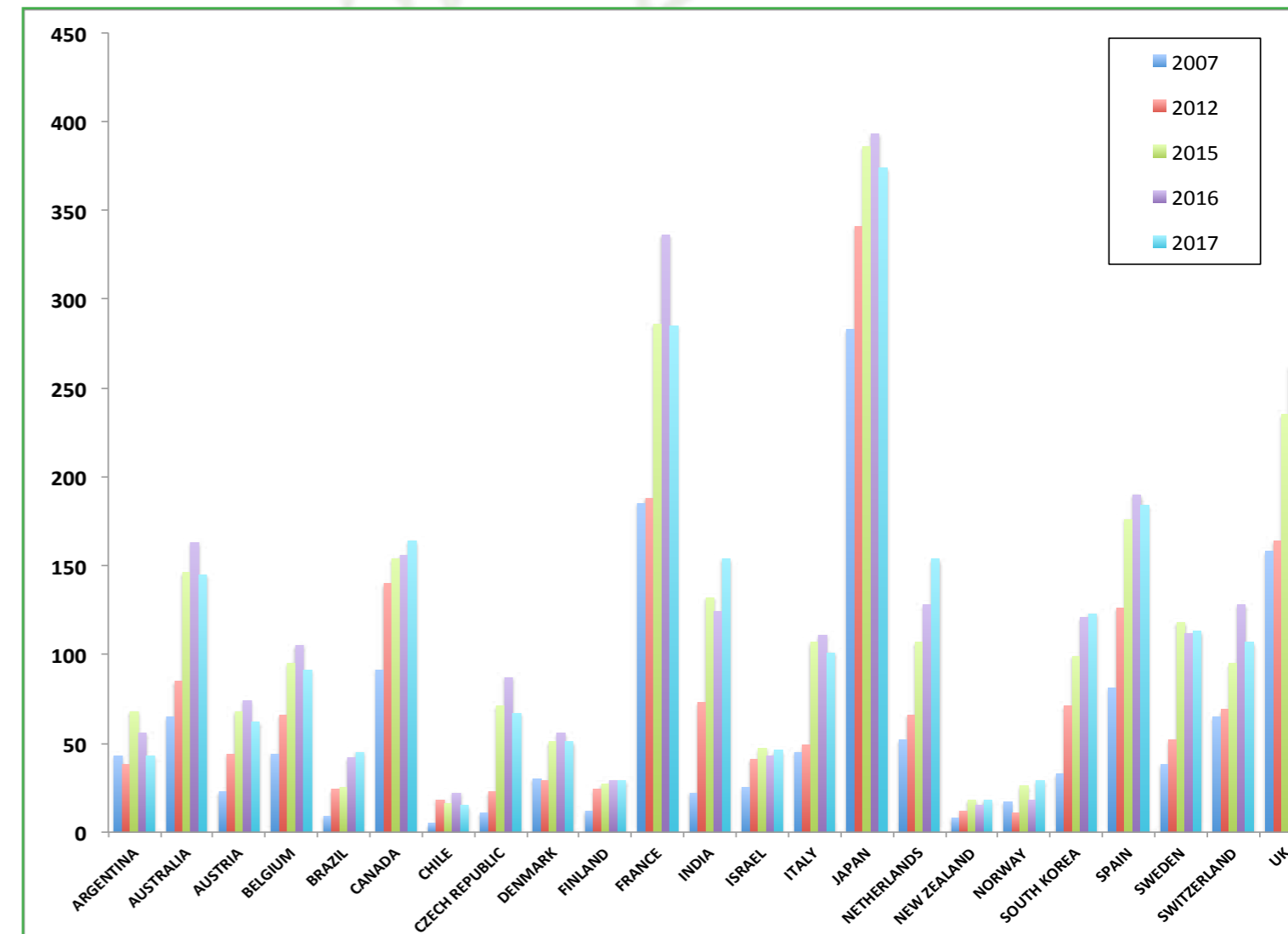
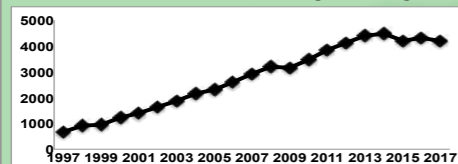


Figure 4. Number of Arabidopsis publications in a variety of MASC countries. We acknowledge that using this metric to measure research productivity is not perfect but remains a useful proxy.

Annual Global Arabidopsis Papers

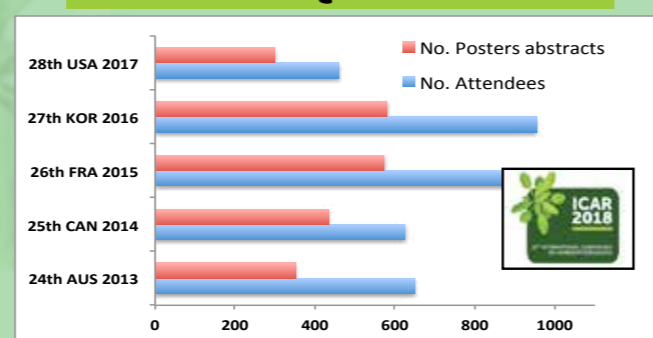


2017 Arabidopsis publications

4189



International Conference on Arabidopsis Research



ICAR2019: Wuhan, China
June 16th-21st 2019

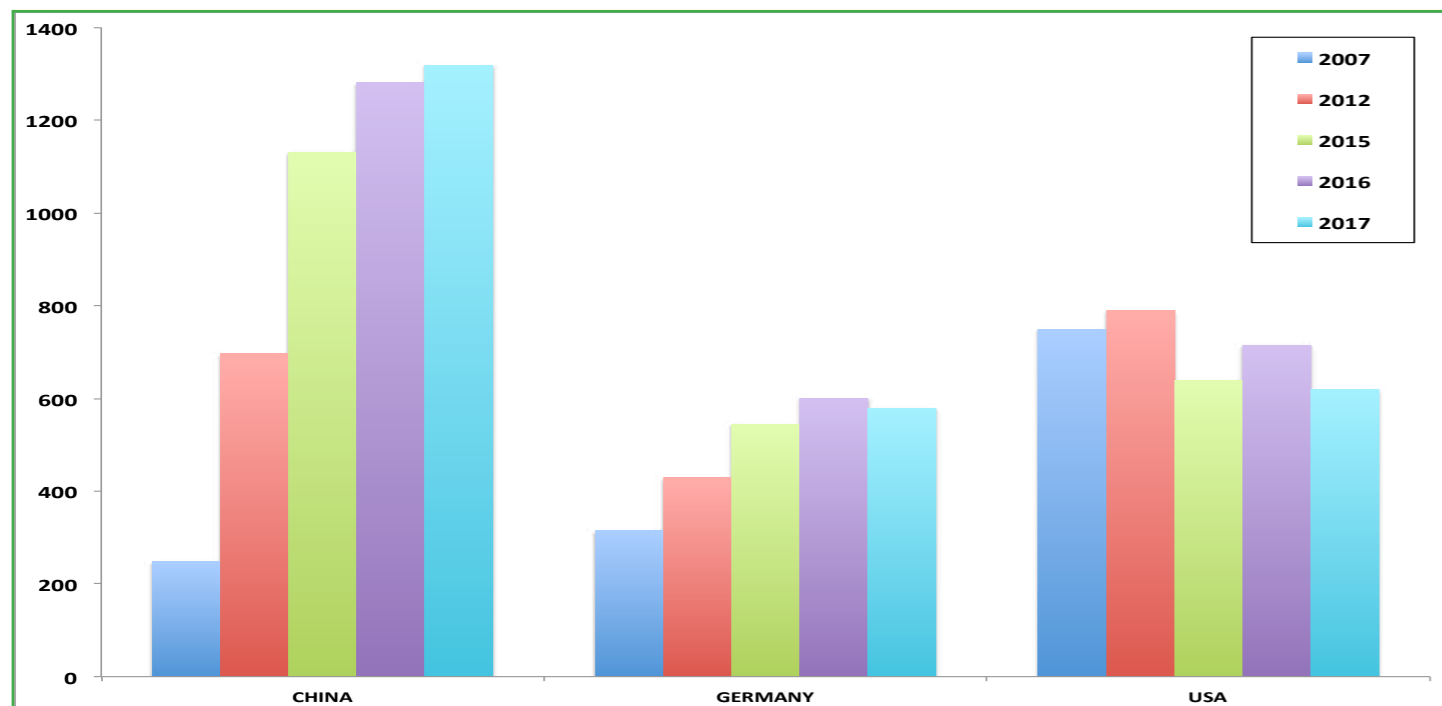


Figure 5. Number of Arabidopsis publications in China, Germany and the USA over the past decade

highest number of publications which reflects the early adoption of Arabidopsis research in this country. A slowing in the number of publications over the past 10 years might be explained by a variety of reasons not investigated here in any detail but intuitively may include a saturation on the number of articles or changes in faculty recruitment and/or grant funding policies. However the number of publication remains encouragingly high.

After 10 years of growth the number of German publications shows a very small decline over the past year and perhaps indicates that they are on a similar trajectory to the USA. Although the majority of MASC countries show a plateau in the number of publications, it is encouraging that some places, such as the Netherlands and Canada show an increase. Over the next 5-10 years we will discover whether countries with currently growing publication rates will follow the trend observed in the USA and Germany.

Overall the following Country Reports suggest a positive opinion as to the value of using Arabidopsis for discovery-led science and in the pathway to translation. The breadth of available resources places the community in an excellent position to maintain high levels of outputs.

Research Highlights

Over the following pages we feature a selection of outstanding Arabidopsis research that has been conducted by the global community of researchers. These manuscripts include some that use the power of Arabidopsis tools for molecular and cell biology.

In addition we highlight papers that have developed resources that are available for community use. These type of studies not only demonstrate outstanding science but facilitate the continued building of the global community of resources

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

Towards financially viable phytoextraction and production of plant-based palladium catalysts.

Harumain ZA, Parker HL, Muñoz García A, Austin MJ, McElroy CR, Hunt AJ, Clark JH, Meech JA, Anderson CW, Ciacci L, Graedel TE, Bruce NC, Rylott EL (2017) Environ Sci Technol. <http://dx.doi.org/10.1021/acs.est.6b04821>

Although a promising technique, phytoextraction has yet to see significant commercialization. Major limitations include metal uptake rates and subsequent processing costs. However, it has been shown that liquid-culture-grown Arabidopsis can take up and store palladium as nanoparticles. The processed plant biomass has catalytic activity comparable to that of commercially available catalysts, creating a product of higher value than extracted bulk metal. We demonstrate that the minimum level of palladium in Arabidopsis dried tissues for catalytic activity comparable to commercially available 3% palladium-on-

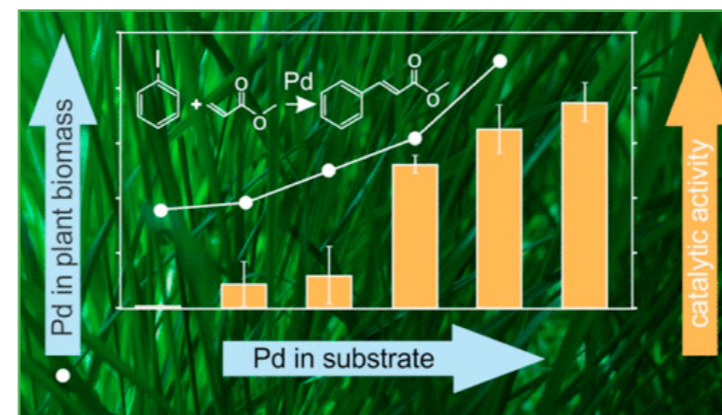


Figure 6. Towards financially viable phytoextraction and production of plant-based palladium catalysts.

<http://dx.doi.org/10.1021/acs.est.6b04821>

carbon catalysts was achieved from dried plant biomass containing between 12 and 18 g-kg⁻¹ Pd. To advance this technology, species suitable for in-the-field application; mustard, miscanthus, and 16 willow species and cultivars, were tested. These species were able to grow, and take up, palladium from both synthetic and mine-sourced tailings. Although levels of palladium accumulation in field-suitable species are below that required for commercially available 3% palladium-on-carbon catalysts, this study both sets the target, and is a step toward, the development of field-suitable species that concentrate catalytically active levels of palladium. Life cycle assessment on the phytomining approaches described here indicates that the use of plants to accumulate palladium for industrial applications has the potential to decrease the overall environmental impacts associated with extracting palladium using present-day mining processes.

Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis.

Inagaki S, Takahashi M, Hosaka A, Ito T, Toyoda A, Fujiyama A, Tarutani Y, and Kakutani T (2017) EMBO J. 36: 970-980. doi:10.15252/embj.201694983

Heterochromatin is marked by methylation of lysine 9 on histone H3 (H3K9me). A puzzling feature of H3K9me is that this modification localizes not only in promoters but also in internal regions (bodies) of silent transcription units. Despite its prevalence, the biological significance of gene-body H3K9me remains enigmatic. Here we show that H3K9me-associated removal of H3K4 monomethylation (H3K4me1) in gene bodies mediates transcriptional silencing. Mutations in an Arabidopsis H3K9 demethylase gene IBM1 induce ectopic H3K9me2 accumulation in gene bodies, with accompanying severe developmental defects. Through suppressor screening of the *ibm1* induced developmental defects, we identified the LDL2 gene, which encodes a homolog of conserved H3K4 demethylases. The *ldl2* mutation suppressed the developmental defects, without suppressing the *ibm1* induced ectopic H3K9me2. The ectopic H3K9me2 mark directed removal of gene-body H3K4me1 and caused transcriptional repression in an LDL2-dependent manner. Furthermore, mutations of H3K9 methylases increased

the level of H3K4me1 in the gene bodies of various transposable elements, and this H3K4me1 increase is a prerequisite for their transcriptional derepression. Our results uncover an unexpected role of gene-body H3K9me2/H3K4me1 dynamics as a mediator of heterochromatin silencing and epigenome differentiation.

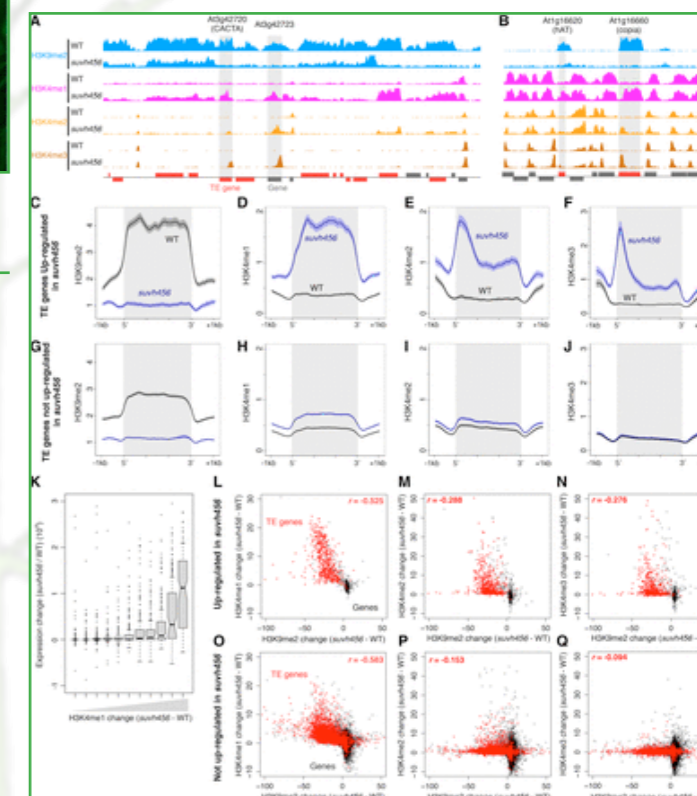


Figure 7. Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis <http://dx.doi.org/10.15252/embj.201694983>

Topological analysis of multicellular complexity in the plant hypocotyl

Jackson MD, Xu H, Duran-Nebreda S, Stamm P, Bassel GW. . Elife. 2017. pii: e26023. doi: 10.7554/eLife.26023

Multicellularity arose as a result of adaptive advantages conferred to complex cellular assemblies. The arrangement of cells within organs endows higher-order functionality through a structure-function relationship, though the organizational properties of these multicellular configurations remain poorly understood. We investigated the topological properties of complex organ architecture by digitally capturing global cellular interactions in the plant embryonic stem (hypocotyl), and analyzing these using quantitative network analysis. This revealed the presence of coherent conduits of reduced path length across epidermal atrichoblast cell files. The preferential movement of small molecules along this cell type was demonstrated using fluorescence transport assays. Both robustness and plasticity in this higher order property of atrichoblast patterning was observed across diverse genetic backgrounds, and the analysis of genetic patterning mutants identified the contribution of gene activity

towards their construction. This topological analysis of multicellular structural organization reveals higher order functions for patterning and principles of complex organ construction.

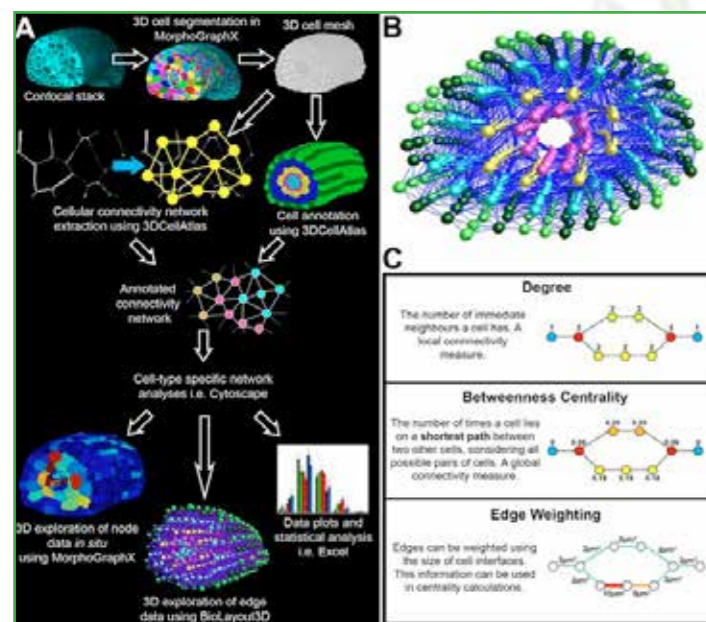


Figure 8. Topological analysis of multicellular complexity in the plant hypocotyl. <http://dx.doi.org/10.7554/eLife.26023>

WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity
Prát T, Hajný J, Grunewald W, Vasileva M, Molnár G, Tejos R, Schmid M, Sauer M, Friml J. (2018) PLoS Genet. 29;14:e1007177 doi: 10.1371/journal.pgen.1007177

Auxin is unique among plant hormones due to its directional transport that is mediated by the polarly distributed PIN auxin transporters at the plasma membrane. The canalization hypothesis proposes that the auxin feedback on its polar flow is a crucial, plant-specific mechanism mediating multiple self-organizing developmental processes. Here, we used the auxin effect on the PIN polar localization in *Arabidopsis thaliana* roots as a proxy for the auxin feedback on the PIN polarity during canalization. We performed microarray experiments to find regulators of this process that act downstream of auxin. We identified genes that were transcriptionally regulated by auxin in an AXR3/IAA17- and ARF7/ARF19-dependent manner. Besides the known components of the PIN polarity, such as PID and PIP5K kinases, a number of potential new regulators were detected, among which the WRKY23 transcription factor, which was characterized in more detail. Gain- and loss-of-function mutants confirmed a role for WRKY23 in mediating the auxin effect on the PIN polarity. Accordingly, processes requiring auxin-mediated PIN polarity rearrangements, such as vascular tissue development during leaf venation, showed a higher WRKY23 expression and required the WRKY23 activity. Our results provide initial insights into the

auxin transcriptional network acting upstream of PIN polarization and, potentially, canalization-mediated plant development.

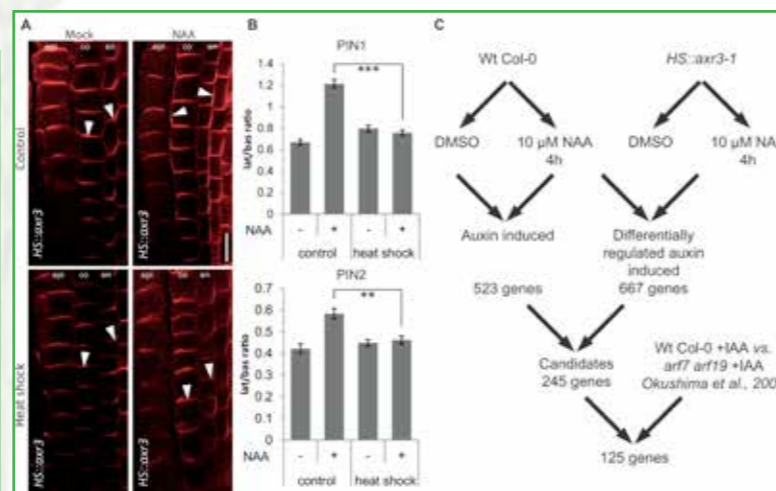


Figure 9. WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. doi: 10.1371/journal.pgen.1007177

The AraGWAS Catalog: a curated and standardized *Arabidopsis thaliana* GWAS catalog.

Togninalli, M., Seren, Ü., Meng, D., Fitz, J., Nordborg, M., Weigel, D., Borgwardt, K., Korte, A., and Grimm, D.G. (2018). Nucleic Acids Res. 46: D1150–D1156. doi: 10.1093/nar/gkx954

The abundance of high-quality genotype and phenotype data for the model organism *Arabidopsis thaliana* enables scientists to study the genetic architecture of many complex traits at an unprecedented level of detail using genome-wide association studies (GWAS). GWAS have been a great success in *A. thaliana* and many SNP-trait associations have been published. With the AraGWAS Catalog (<https://aragwas.1001genomes.org>) we provide a publicly available, manually curated and standardized GWAS catalog for all publicly available phenotypes from the central *A. thaliana* phenotype repository, AraPheno. All GWAS have been recomputed on the latest imputed



Figure 10. The AraGWAS Catalog: a curated and standardized *Arabidopsis thaliana* GWAS catalog doi: 10.1093/nar/gkx954

genotype release of the 1001 Genomes Consortium using a standardized GWAS pipeline to ensure comparability between results. The catalog includes currently 167 phenotypes and more than 222 000 SNP-trait associations with $P < 10^{-4}$, of which 3887 are significantly associated using permutation-based thresholds. The AraGWAS Catalog can be accessed via a modern web-interface and provides various features to easily access, download and visualize the results and summary statistics across GWAS.

CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping.

Trigg SA, Garza RM, MacWilliams A, Nery JR, Bartlett A, Castanon R, Goubil A, Feeney J, O'Malley R, Huang SC, Zhang ZZ, Galli M and Ecker JR (2017) Nature Methods 14(8):819-825. doi: 10.1038/nmeth.4343.

Broad-scale protein-protein interaction mapping is a major challenge given the cost, time, and sensitivity constraints of existing technologies. Here, we present a massively multiplexed yeast two-hybrid method, CrY2H-seq, which uses a Cre recombinase interaction reporter to intracellularly fuse the coding sequences of two interacting proteins and next-generation DNA sequencing to identify these interactions en masse. We applied CrY2H-seq to investigate sparsely annotated *Arabidopsis thaliana* transcription factors interactions. By performing ten independent screens testing a total of 36 million binary interaction combinations, and uncovering a network of 8,577 interactions among 1,453 transcription factors, we demonstrate CrY2H-seq's improved screening capacity, efficiency, and sensitivity over those of existing technologies. The deep-coverage network resource we call AtTFIN-1 recapitulates one-third of previously reported interactions derived from diverse methods, expands the number of known plant transcription factor interactions by three-fold, and reveals previously unknown family-specific interaction module associations with plant reproductive development, root architecture, and circadian coordination.

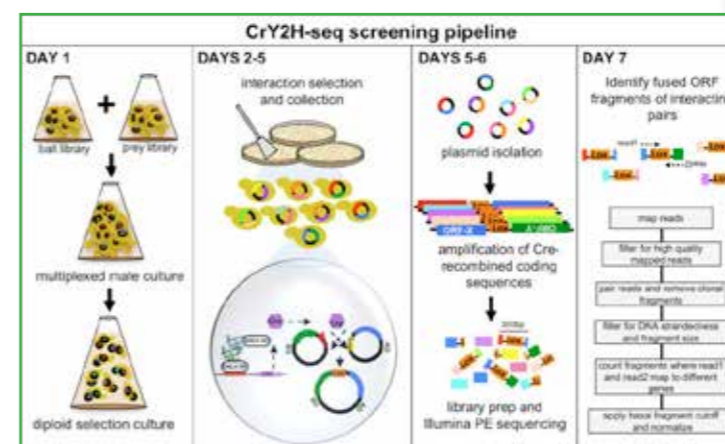


Figure 11. CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. doi: 10.1038/nmeth.4343.

Genome-wide characterization of differential transcript usage in *Arabidopsis thaliana*.

Vaneechoutte, D., Estrada, A.R., Lin, Y.-C., Loraine, A.E., and Vandepoele, K. (2017). Plant J. 92: 1218–1231. <https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.13746>

Alternative splicing and the usage of alternate transcription start or stop sites allows a single gene to produce multiple transcript isoforms. Most plant genes express certain isoforms at a significantly higher level than others, but under specific conditions this expression dominance can change, resulting in a different set of dominant isoforms. These events of differential transcript usage (DTU) have been observed for thousands of *Arabidopsis thaliana*, *Zea mays* and *Vitis vinifera* genes, and have been linked to development and stress response. However, neither the characteristics of these genes, nor the implications of DTU on their protein coding sequences or functions, are currently well understood. Here we present a dataset of isoform dominance and DTU for all genes in the AtRTD2 reference transcriptome based on a protocol that was benchmarked on simulated data and validated through comparison with a published reverse transcriptase polymerase chain reaction panel. We report DTU events for 8148 genes across 206 public RNA-Seq samples, and find that protein sequences are affected in 22% of the cases. The observed DTU events show high consistency across replicates, and reveal reproducible patterns in response to treatment and development. We also demonstrate that genes with different evolutionary ages, expression breadths and functions show large differences in the frequency at which they undergo DTU, and in the effect that these events have on their protein sequences. Finally, we showcase how the generated dataset can be used to explore DTU events for genes of interest or to find genes with specific DTU in samples of interest.

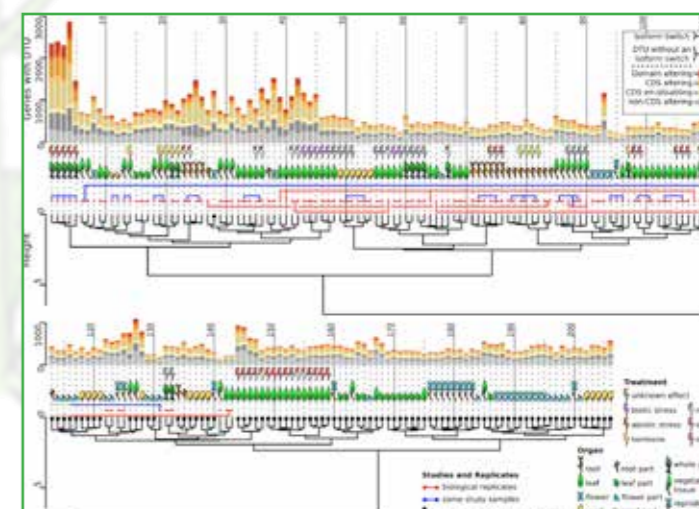


Figure 12. Genome-wide characterization of differential transcript usage in *Arabidopsis thaliana*. <https://doi.org/10.1111/tpj.13746>

Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions

Wu S, Tohge T, Cuadros-Inostroza A, Tong H, Tenenboim H, Kooke R, Méret M, Keurentjes JB, Nikoloski Z, Fernie AR, Willmitzer L, Brotman Y. . Mol Plant. 2018 Jan 8;11(1):118-134. doi: 10.1016/j.molp.2017.08.012

Metabolic genome-wide association studies (mGWAS), whereupon metabolite levels are regarded as traits, can help unravel the genetic basis of metabolic networks. A total of 309 Arabidopsis accessions were grown under two independent environmental conditions (control and stress) and subjected to untargeted LC-MS-based metabolomic profiling; levels of the obtained hydrophilic metabolites were used in GWAS. Our two-condition-based GWAS for more than 3000 semi-polar metabolites resulted in the detection of 123 highly resolved metabolite quantitative trait loci ($p \leq 1.0E-08$), 24.39% of which were environment-specific. Interestingly, differently from natural variation in Arabidopsis primary metabolites, which tends to be controlled by a large number of small-effect loci, we found several major large-effect loci alongside a vast number of small-effect loci controlling variation of secondary metabolites. The two-condition-based GWAS was followed by integration with network-derived metabolite-transcript correlations using a time-course stress experiment. Through this integrative approach, we selected 70 key candidate associations between structural genes and metabolites, and experimentally validated eight novel associations, two of them showing differential genetic regulation in the two environments studied.

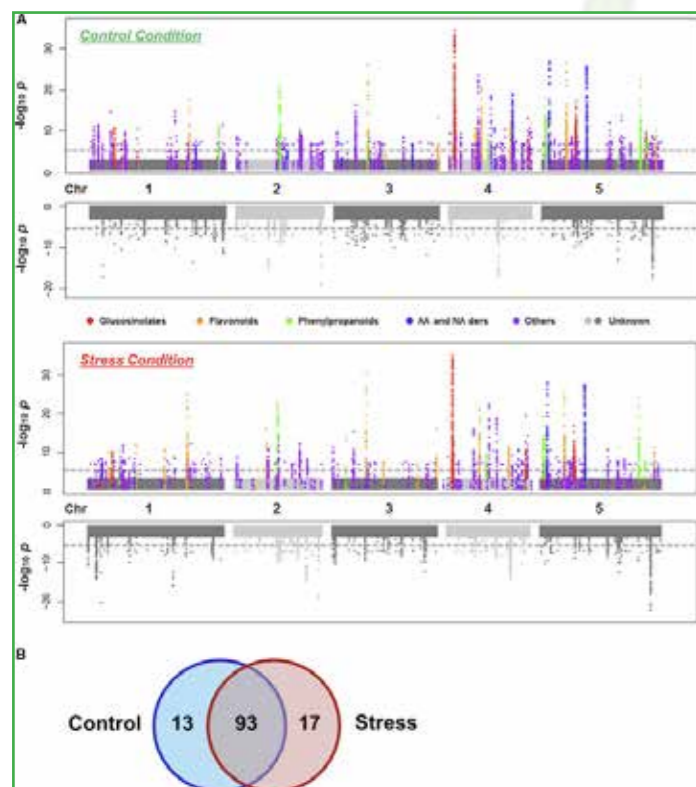


Figure 13. Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. <http://dx.doi.org/10.1016/j.molp.2017.08.012>

We demonstrate the power of combining large-scale untargeted metabolomics-based GWAS with time-course-derived networks both performed under different abiotic environments for identifying metabolite-gene associations, providing novel global insights into the metabolic landscape of Arabidopsis.

N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway.

Zhang H, Gannon L, Hassall KL, Deery MJ, Gibbs DJ, Holdsworth MJ, van der Hoorn RAL, Lilley KS, Theodoulou FL (2017) New Phytol. doi: 10.1111/nph.14909

The N-end rule pathway of targeted protein degradation is an important regulator of diverse processes in plants but detailed knowledge regarding its influence on the proteome is lacking. To investigate the impact of the Arg/N-end rule pathway on the proteome of etiolated seedlings, we used terminal amine isotopic labelling of substrates with tandem mass tags (TMT-TAILS) for relative quantification of N-terminal peptides in prt6, an Arabidopsis thaliana N-end rule mutant lacking the E3 ligase PROTEOLYSIS6 (PRT6). TMT-TAILS identified over 4000 unique N-terminal peptides representing c. 2000 protein groups. Forty-five protein groups exhibited significantly increased N-terminal peptide abundance in prt6 seedlings, including cruciferins, major seed storage proteins, which were regulated by Group VII Ethylene Response Factor (ERFVII) transcription factors, known substrates of PRT6. Mobilisation of endosperm cruciferin was delayed in prt6 seedlings. N-termini of several proteases were downregulated in prt6, including RD21A. RD21A transcript, protein and activity levels were downregulated in a largely ERFVII-dependent manner. By contrast, cathepsin B3 protein and activity were upregulated by ERFVII independent of transcript. We propose that the PRT6 branch of the pathway regulates protease activities in a complex manner and optimises storage reserve mobilisation in the transition from seed to seedling via control of ERFVII action.

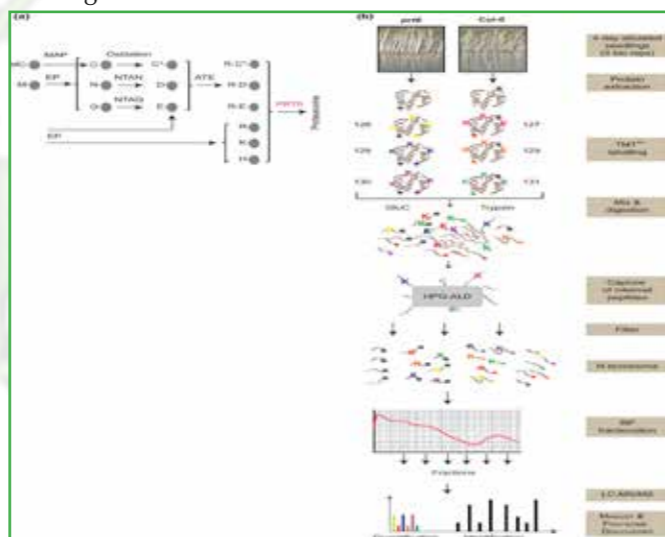


Figure 14. N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway <https://doi.org/10.1111/nph.14909>

The final paper selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modulates stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betsuyaku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuko Yamaguchi-Shinozaki, Kazuo Shinozaki. (2018) Nature <https://doi.org/10.1038/s41586-018-0009-2>

Mammalian peptide hormones propagate extracellular stimuli from sensing tissues to appropriate targets to achieve optimal growth maintenance. In land plants, root-to-shoot signalling is important to prevent water loss by transpiration and to adapt to water-deficient conditions. The phytohormone abscisic acid has a role in the regulation of stomatal movement to prevent water loss. However, no mobile signalling molecules have yet been identified that can trigger abscisic acid accumulation in leaves. Here we show that the CLAVATA3/EMBRYO-SURROUNDING REGION-RELATED 25 (CLE25) peptide transmits water-deficiency signals through vascular tissues in Arabidopsis, and affects abscisic acid biosynthesis and stomatal control of transpiration in association with BARELY ANY MERISTEM (BAM) receptors in leaves. The CLE25 gene is expressed in vascular tissues and enhanced in roots in response to dehydration stress. The root-derived CLE25 peptide moves from the roots to the leaves, where it induces stomatal closure by modulating abscisic acid accumulation and thereby enhances resistance to dehydration stress. BAM receptors are required for the CLE25 peptide-induced dehydration stress response in leaves, and the CLE25-BAM module therefore probably functions as one of the signalling molecules for long-distance signalling in the dehydration response

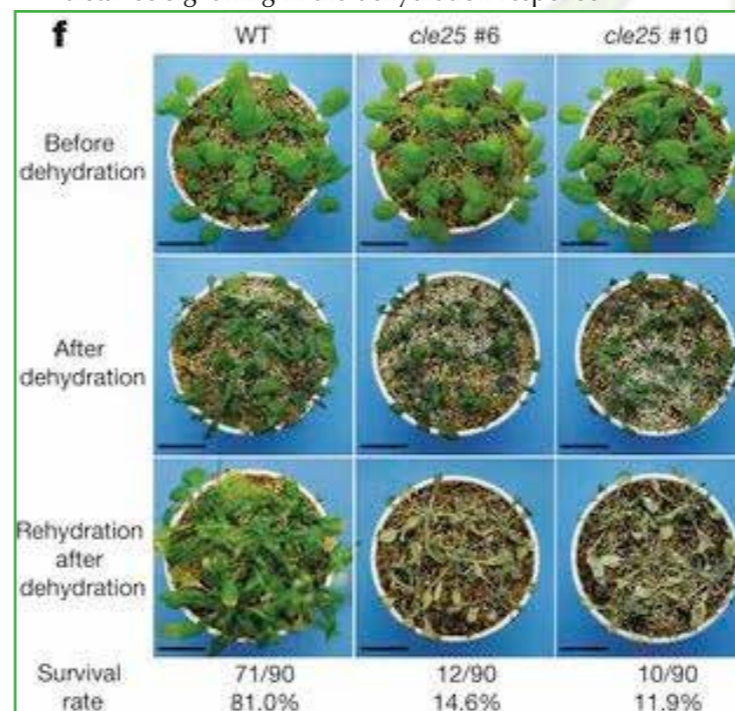


Figure 15. A small peptide modulates stomatal control via abscisic acid Nature <https://doi.org/10.1038/s41586-018-0009-2>

Country Reports

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

This includes details of the extent of Arabidopsis research, the community resources and bioinformatic tools that members of their researchers have generated for the international community.

In addition they outline outreach events and selected publications from the past year.

Country	Page
Argentina	42
Australia	43
Austria	45
Belgium	48
Brazil	50
Canada	52
Chile	54
China	57
Czech Republic	59
Denmark	61
Finland	62
France	63
Germany	64
India	66
Israel	69
Italy	70
Japan	74
New Zealand	77
Norway	78
South Korea	79
Spain	80
Sweden	81
Switzerland	83
United Kingdom	85
United States of America	87

Argentina

Marcelo J. Yanovsky
myanovsky@leloir.org.ar
 Fundación Instituto Leloir, CONICET,
 Buenos Aires, Argentina



Heat stress induces ferroptosis-like cell death in plants. Distéfano AM, Martin MV, Córdoba JP, Bellido AM, D'Ippólito S, Colman SL, Soto D, Roldán JA, Bartoli CG, Zabaleta EJ, Fiol DF, Stockwell BR, Dixon SJ, Pagnussat GC. *J Cell Biol.* 2017 Feb;216(2):463-476. doi: 10.1083/jcb.201605110. Epub 2017 Jan 18.

Heterologous expression of AtBBX21 enhances the rate of photosynthesis and alleviates photoinhibition in *Solanum tuberosum*. Crocco CD, Gomez-Ocampo G, Mantese A, Ploschuk EL, Botto JF. *Plant Physiol.* 2018 Mar 19. pii: pp.01417.2017. doi: 10.1104/pp.17.01417.

Perception of sunflecks by the UV-B photoreceptor UV RESISTANCE LOCUS 8. Moriconi V, Binkert M, Costigliolo Rojas MC, Sellaro R, Ulm R, Casal JJ. *Plant Physiol.* 2018 Mar 12. pii: pp.00048.2018. doi: 10.1104/pp.18.00048.

Hydrogen Sulfide Increases Production of NADPH Oxidase-Dependent Hydrogen Peroxide and Phospholipase D-Derived Phosphatidic Acid in Guard Cell Signaling. Scuffi D, Nietzel T, Di Fino LM, Meyer AJ, Lamattina L, Schwarzländer M, Laxalt AM, García-Mata C. *Plant Physiol.* 2018 Mar;176(3):2532-2542. doi: 10.1104/pp.17.01636.

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

A uORF Represses the Transcription Factor AtHB1 in Aerial Tissues to Avoid a Deleterious Phenotype. Ribone PA, Capella M, Arce AL, Chan RL. *Plant Physiol.* 2017 Nov;175(3):1238-1253. doi: 10.1104/pp.17.01060.

Phospholipase C2 Affects MAMP-Triggered Immunity by Modulating ROS Production. D'Ambrosio JM, Couto D, Fabro G, Scuffi D, Lamattina L, Munnik T, Andersson MX, Álvarez ME, Zipfel C, Laxalt AM. *Plant Physiol.* 2017 Oct;175(2):970-981. doi: 10.1104/pp.17.00173.

Major Funding Sources

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

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.

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

New Software Tools

ASpli, a Bioconductor package for the analysis of alternative splicing from RNA-seq data.

Selected Publications

RALF4/19 peptides interact with LRX proteins to control pollen tube growth in Arabidopsis. Mecchia MA, Santos-Fernandez G, Duss NN, Somoza SC, Boisson-Dernier A, Gagliardini V, Martínez-Bernardini A, Fabrice TN, Ringli C, Muschietti JP, Grossniklaus U. *Science.* 2017 Dec 22;358(6370):1600-1603. doi: 10.1126/science.aao5467.

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

Australia

Monika Murcha
monika.murcha@uwa.edu.au
 Australian Research Council Centre of Excellence, Plant Energy Biology, The University of Western Australia.



The Virtual Plant Cell (VPC) developed by the Centre of excellence in Plant Energy Biology allows users to become immersed in and interact with a plant cell, learn about the importance of phosphate and walk through labs and facilities such as The Plant Accelerator. Aimed at primary and senior school students. <https://www.youtube.com/channel/UCEIGuXCAGkkHgAZP9LWbXgA>

Use of Arabidopsis

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

Open Resources for Arabidopsis Researchers

The Plant Detectives Manual: teaching resource tool that focuses on using Arabidopsis for plant science research. <https://press.anu.edu.au/publications/plant-detectives-manual>

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

RICE DB: Rice DB facilitates and integrates direct comparison of rice annotations to Arabidopsis allowing parallel comparison between these two model species within one database. <http://ricedb.plantenergy.uwa.edu.au/>

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

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

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

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

Conferences, Workshops and Outreach events

COMBIO 2017 Adelaide and COMBIO 2018 Sydney; Combined Biological Sciences Annual Conference. Annual national conference that includes several symposia dedicated to plant research. This conference incorporates the annual Australian Society of Plant Biologists meeting. <https://www.asbmb.org.au>

Lorne Conferences; Annual conferences held at Lorne, Victoria dedicated to "Protein Structure and Function" and "Genome biology".

Selected Publications

Australian researchers have published over 170 articles involving Arabidopsis; Pubmed search using keyword searches Arabidopsis (Title/Abstract) and Australia (affiliation) since Jan 2017-Mar 2018). Selected publications indicating the breadth of outputs are listed below.

Lonhienne T, Garcia MD, Pierens G, Mobli M, Nouwens A, Guddat LW. Structural insights into the mechanism of inhibition of AHAS by herbicides. *Proc Natl Acad Sci U S A.* 2018 Feb 27;115(9):E1945-E1954. doi: 10.1073/pnas.1714392115.

Wen Z, Tyerman SD, Dechorgnat J, Ovchinnikova E, Dhugga KS, Kaiser BN. Maize NPF6 Proteins Are Homologs of Arabidopsis CHL1 That Are Selective for Both Nitrate and Chloride. *Plant Cell.* 2017 Oct;29(10):2581-2596. doi:10.1105/tpc.16.00724.

David R, Burgess A, Parker B, Li J, Pulsford K, Sibbritt T, Preiss T, Searle IR. Transcriptome-Wide Mapping of RNA 5-Methylcytosine in Arabidopsis mRNAs and Noncoding RNAs. *Plant Cell.* 2017 Mar;29(3):445-460. doi: 10.1105/tpc.16.00751.

Li L, Nelson CJ, Trösch J, Castleden I, Huang S, Millar AH. Protein Degradation Rate in *Arabidopsis thaliana* Leaf Growth and Development. *Plant Cell.* 2017 Feb;29(2):207-228. doi: 10.1105/tpc.16.00768.

Pornsiriwong W, Estavillo GM, Chan KX, Tee EE, Ganguly D, Crisp PA, Phua SY, Zhao C, Qiu J, Park J, Yong MT, Nisar N, Yadav AK, Schwessinger B, Rathjen J, Cazzonelli CI, Wilson PB, Gilliam M, Chen ZH, Pogson BJ. A chloroplast retrograde signal, 3'-phosphoadenosine 5'-phosphate, acts as a secondary messenger in abscisic acid signaling in stomatal closure and germination. *Elife.* 2017 Mar 21;6. pii: e23361. doi: 10.7554/eLife.23361.

Wang L, Wu LM, Greaves IK, Zhu A, Dennis ES, Peacock WJ. PIF4-controlled auxin pathway contributes to hybrid vigor in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 2017 Apr 25;114(17):E3555-E3562. doi: 10.1073/pnas.1703179114.

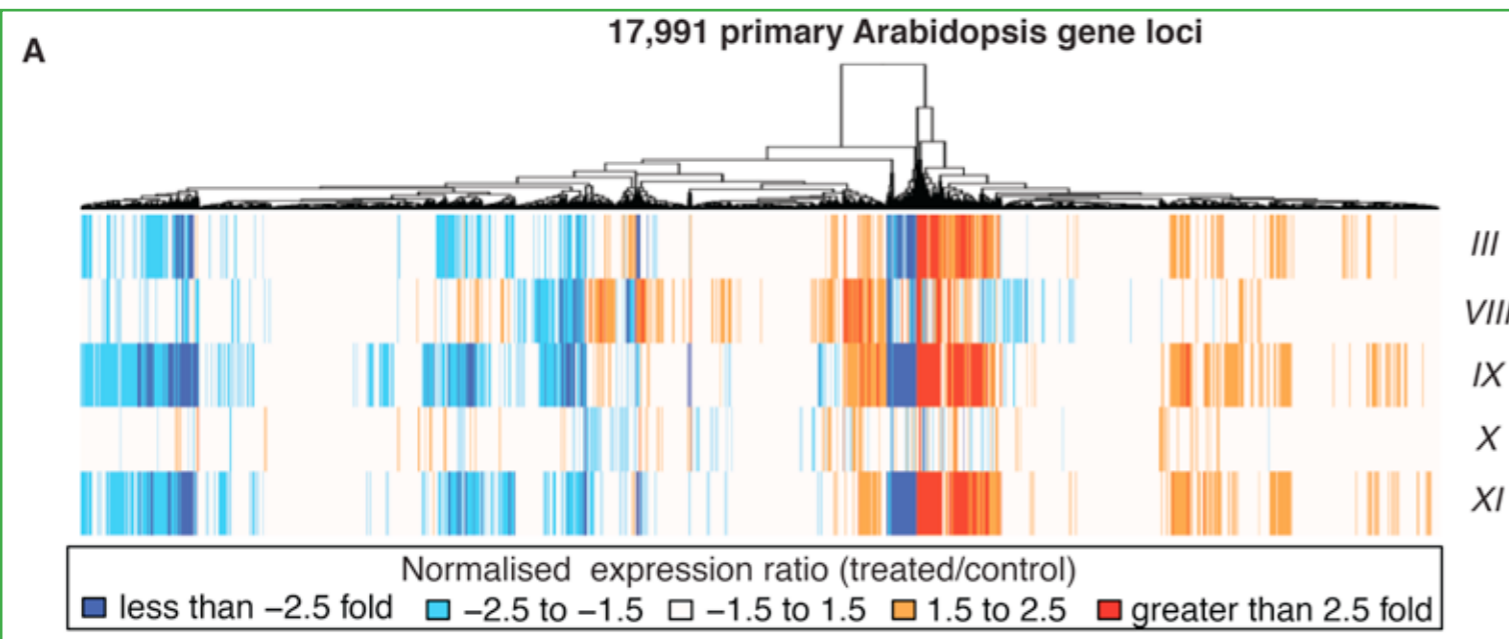


Figure 16. A Heatmap summarising the patterns of relative expression for each treatment vs the untreated control, including 60 minutes of excess light (III), recovery of 60 minutes (VIII), immediate repeat of 60 minutes of excess light (IX), 24-hour recovery (X) and further repeat excess light after the 24-hour recovery period. doi: 10.1105/tpc.16.00828

Crisp PA, Ganguly DR, Smith AB, Murray KD, Estavillo GM, Searle I, Ford E, Bogdanovic O, Lister R, Borevitz JO, Eichten SR, Pogsosn BJ. Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in Arabidopsis. *Plant Cell*. 2017 Aug;29(8):1836-1863. doi: 10.1105/tpc.16.00828.

Rautengarten C, Birdseye D, Pattathil S, McFarlane HE, Saez-Aguayo S, Orellana A, Persson S, Hahn MG, Scheller HV, Heazlewood JL, Ebert B. The elaborate route for UDP-arabinose delivery into the Golgi of plants. *Proc Natl Acad Sci U S A*. 2017 Apr 18;114(16):4261-4266.

Garcia MD, Nouwens A, Lonhienne TG, Guddat LW. Comprehensive understanding of acetohydroxyacid synthase inhibition by different herbicide families. *Proc Natl Acad Sci U S A*. 2017 Feb 14;114(7):E1091-E1100.

Schneider R, Tang L, Lampugnani ER, Barkwill S, Lathe R, Zhang Y, McFarlane HE, Pesquet E, Niittyla T, Mansfield SD, Zhou Y, Persson S. Two Complementary Mechanisms Underpin Cell Wall Patterning during Xylem Vessel Development. *Plant Cell*. 2017 Oct;29(10):2433-2449.

Major Funding Sources

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

Translational research is funded by the Grains Research Development Corporation <http://grdc.com.au>

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

Austria

Marie-Theres Hauser
marie-theres.hauser@boku.ac.at
University of Natural Resources and Life Sciences BOKU, Vienna



Use of Arabidopsis

Research Institutions:

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

Subject Areas

Population Genetics

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

Chromosome Biology

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

Epigenetics

- Frederic Berger (www.gmi.oeaw.ac.at/research-groups/frederic-berger/): Chromatin architecture and function.

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

Glycobiology

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

RNA metabolism

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

Plant pathogen interaction

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

Open Resources for Arabidopsis Researchers

CRISPR/Cas9 facility in ProTECH (www.vbcf.ac.at/facilities/protein-technologies/)
Advanced Microscopy at the VBCF (www.vbcf.ac.at/facilities/advanced-microscopy/)
Plant Sciences Facility (PlantsS) at the VBCF (www.vbcf.ac.at/facilities/plant-sciences/)

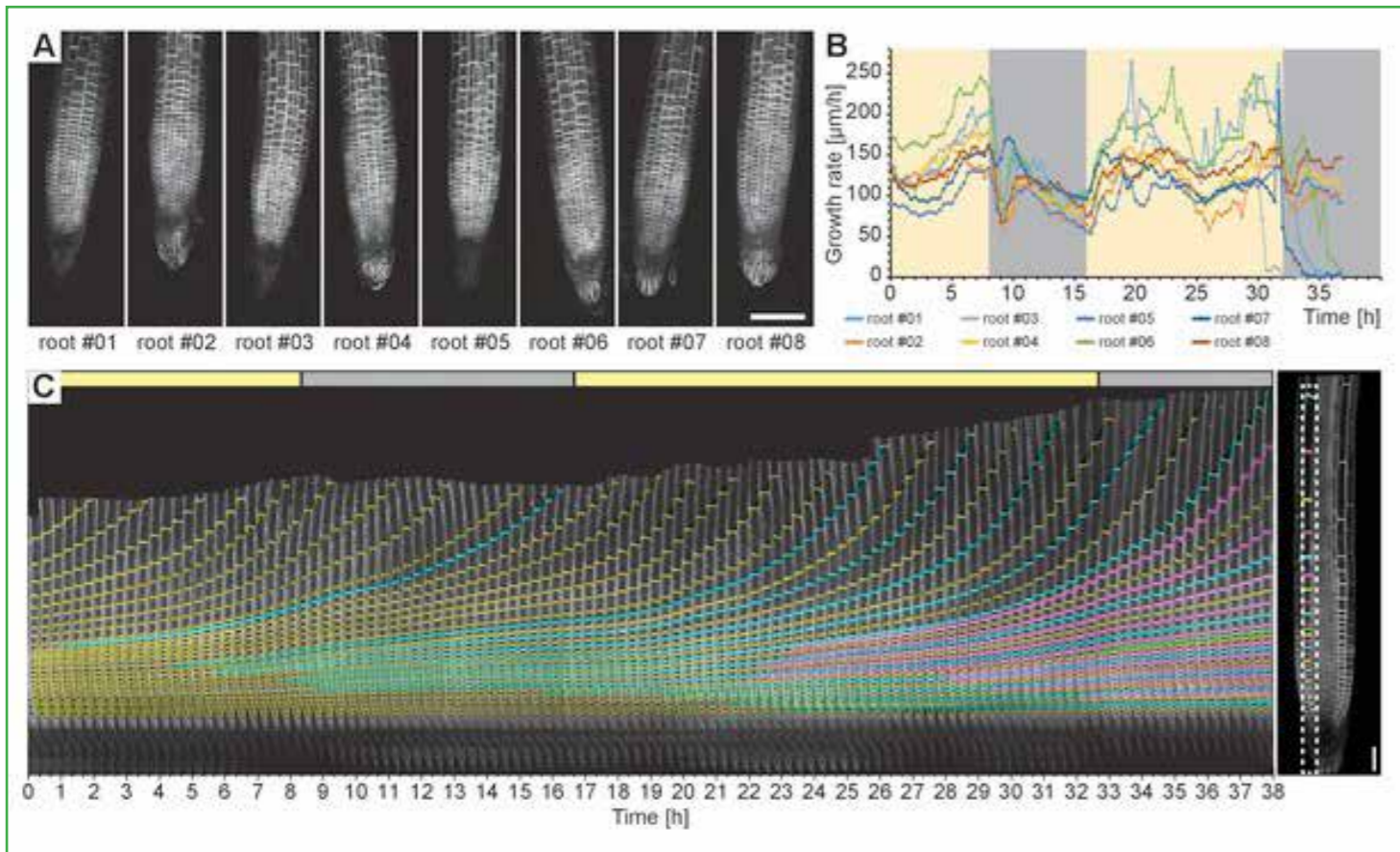


Figure 17. Time-lapse recording of eight *Arabidopsis* root tips expressing UBQ10::YFP-PIP1;4 over the course of 38 h. (A) Maximum intensity projections of a single time point for the eight roots tracked. (B) Growth rates of the root tips were calculated from the output of the TipTracker program. The yellow and grey areas indicate when the LED illumination was on or off, respectively. (C) Cell division and elongation are visualized for the root #5. Each new cell wall is highlighted so that the original cell walls are in yellow, the second generation of the walls is in cyan, the third generation is in magenta, and the fourth generation in green. The last image of the series is shown on the right side. A stack of 14 images (x/y/z: 1400 × 1400 × 14 pixels, voxelsize: 0.457 × 0.457 × 2.5 µm³) was captured every 20 min for a period of 38 h 20 min using the Plan-Apochromat 20x/0.8 air objective lens. Scale bars: (A) 100 µm, (C) 40 µm. <https://doi.org/10.7554/eLife.26792.008>

AtRTD2 -The *Arabidopsis thaliana* Reference Transcript Dataset 2 is a comprehensive, non-redundant, high quality transcript reference dataset developed for RNA-seq analysis. www.ncbi.nlm.nih.gov/pubmed/28402429

AtRTD2-QUASI – a version of AtRTD2, designed for analysis of alternative splicing. www.ncbi.nlm.nih.gov/pubmed/28402429

SPIM - Light sheet fluorescence microscopy of plant roots growing on the surface of a gel. www.ncbi.nlm.nih.gov/pubmed/28190052

Vertical confocal microscope allowing automatic tracking of the root growth www.ncbi.nlm.nih.gov/pubmed/28628006

Microfluidic-like device - “root chip” for simultaneous root treatments and confocal visualization (not published yet)

New Software Tools

AraGWAS - <https://aragwas.1001genomes.org/#/>

SNPMatch - www.ncbi.nlm.nih.gov/pubmed/29257129

Tissue Enrichment Test - www.ncbi.nlm.nih.gov/pubmed/28314828

Pipeline for transcriptome assemblies from short read data. This pipeline reduces the number of poorly supported, mis-assembled transcripts often arising from the high degree of inaccuracy of transcript assembly programs. www.ncbi.nlm.nih.gov/pubmed/28402429

Conferences, Workshops and Outreach events

5th European Workshop on Plant Chromatin, 22-24 June 2017

22nd Meeting of the Austrian Society of plant Biology (ATSPB), 5-7 April 2018

21st Meeting of the European Network for Plant Endomembrane Research (NPER), 4-7 Sep 2018

Open campus day at IST Austria presenting also *Arabidopsis* research

Selected Publications

Doblas VG, Smakowska-Luzan E, Fujita S, Alassimone J, Barberon M, Madalinski M, Belkhadir Y, Geldner N (2017) Root diffusion barrier control by a vasculature-derived peptide binding to the SGN3 receptor. *Science* 355:280-4.

Jiang D and Berger F (2017) DNA replication-coupled histone modification maintains Polycomb gene silencing in plants. *Science* 357(6356):1146-9.

Lorkovic ZJ, Park C, Goiser M, Jiang D, Kurzbauer MT, Schlögelhofer P, Berger F (2017) Compartmentalization of DNA Damage Response between Heterochromatin and Euchromatin Is Mediated by Distinct H2A Histone Variants. *Curr Biol* 27:1192-9.

Schon M and Nodine M (2017) Widespread Contamination of *Arabidopsis* Embryo and Endosperm Transcriptome Datasets. *Plant Cell* 29:608-17.

Stegmann M, Monaghan J, Smakowska-Luzan E, Rovenich H, Lehner A, Holton N, Belkhadir Y, Zipfel C (2017) The receptor kinase FER is a RALF-regulated scaffold controlling plant immune signaling. *Science* 355:287-9.

Von Wangenheim D, Hauschild R, Fendrych M, Barone V, Benková E, Friml J. (2017): Live tracking of moving samples in confocal microscopy for vertically grown roots. *Elife* 6

Kurzbauer MT, Pradillo M, Kerzendorfer C, Sims J, Ladurner R, Oliver C, Janisiw MP, Mosiolek M, Schweizer D, Copenhaver GP, Schlögelhofer P. (2018) *Arabidopsis thaliana* FANCD2 Promotes Meiotic Crossover Formation. *Plant Cell*. 30:415-428.

Tejos R, Rodriguez-Furlan C, Adamowski M, Sauer M, Norambuena L, Friml J. (2017): PATELLINS are regulators of auxin-mediated PIN1 relocation and plant development in *Arabidopsis thaliana*. *J Cell Sci*. 29;131(2).

Prát T, Hajný J, Grunewald W, Vasileva M, Molnár G, Tejos R, Schmid M, Sauer M, Friml J. (2018): WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. *PLoS Genet*. 29;14:e1007177.

Béziat C, Barbez E, Feraru MI, Lucyshyn D, Kleine-Vehn J. (2017) Light triggers PILS-dependent reduction in nuclear auxin signalling for growth transition. *Nat Plants*. 3:17105.

Major Funding Sources

Austrian Science Fund (FWF) www.fwf.ac.at/en/

OeAD www.oead.at/projects_cooperations/EN/

Austrian Academy of Sciences (ÖAW) www.oeaw.ac.at/en/fellowship-funding/stipendien-preise/nachwuchsfoerderung-der-oeaw/

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

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

European Research Council (ERC) erc.europa.eu/

Marie Skłodowska-Curie actions <http://ec.europa.eu/research/mariecurieactions/>

ERA CAPS www.ercaps.org/

DFG www.dfg.de/en/

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

Belgium

Moritz K. Nowack
moritz.nowack@vib.be
 VIB-UGent Center for Plant Systems
 Biology, Ghent, Belgium



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

Other developed resources include:

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

Conferences, Workshops and Outreach events

Conferences and Workshops:

- At the Forefront of Plant Research, 15-16 June 2017, Ghent, Belgium, <http://www.vibconferences.be/event/at-the-forefront-of-plant-research>
- 4th Plant Protease and Programmed Cell Death Symposium, 11-13 September 2018, Ghent, Belgium, <https://vibconferences.be/event/4th-plant-protease-and-pcd-symposium>
- 6th symposium on Phosphorus in Soils and Plants, 10-12 September 2018, Leuven, Belgium <https://kuleuvencongres.be/PSP6/articles>
- Agrobacterium 2018, 12-13 September 2018, Ghent, Belgium, <https://www.psb.ugent.be/agro>

Outreach events:

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

Selected Publications

Schoenaers S, Balcerowicz D, Breen G, Hill K, Zdanio M, Mouille G, Holman TJ, Oh J, Wilson MH, Nikonorova N, Vu LD, De Smet I, Swarup R, De Vos WH, Pintelon I, Adriaensen D, Grierson C, Bennett MJ, Vissenberg K. (2018) The Auxin-Regulated CrRLK1L Kinase ERULUS Controls Cell Wall Composition during Root Hair Tip Growth. *Curr Biol.* 2018 Mar 5;28(5):722-732.e6.

De Vleeschauwer D, Filipe O, Hoffman G, Seifi HS, Haeck A, Canlas P, Van Bockhaven J, De Waele E, Demeestere K, Ronald P, Hofte M. (2018) Target of rapamycin signaling orchestrates growth-defense trade-offs in plants. *New Phytol.* 2018 Jan;217(1):305-319.

Use of Arabidopsis

Research Facilities

Arabidopsis Research Centers in Belgium:

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

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

Open Resources for Arabidopsis Researchers

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

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

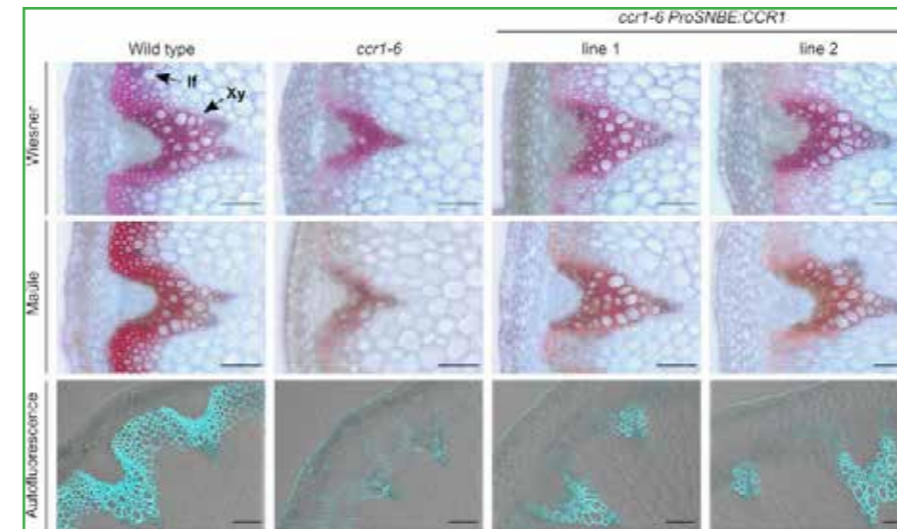


Figure 18. Lignin deposition in inflorescence stems of *ccr1-6* ProSNBE:CCR1 lines. Transverse stem sections are shown for the wild type, *ccr1-6*, and *ccr1-6* ProSNBE:CCR1 lines. Wiesner and Mäule staining and lignin autofluorescence are shown. If, Interfascicular fibers; Xy, xylem. Bars = 100 μ m [doi:10.1104/pp.17.01462](https://doi.org/10.1104/pp.17.01462)

De Meester B, de Vries L, Özparpucu M, Gierlinger N, Corneillie S, Pallidis A, Goeminne G, Morreel K, De Bruyne M, De Rycke R, Vanholme R, Boerjan W. (2018) Vessel-Specific Reintroduction of CINNAMOYL-COA REDUCTASE1 (CCR1) in Dwarfed *ccr1* Mutants Restores Vessel and Xylary Fiber Integrity and Increases Biomass. *Plant Physiol.* 2018 Jan;176(1):611-633.

De Smet R, Sabaghian E, Li Z, Saey Y, Van de Peer Y. (2017) Coordinated Functional Divergence of Genes after Genome Duplication in *Arabidopsis thaliana*. *Plant Cell.* 2017 Nov;29(11):2786-2800.

Willems P, Ndah E, Jonckheere V, Stael S, Sticker A, Martens L, Van Breusegem F, Gevaert K, Van Damme P. (2017) N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in *Arabidopsis thaliana*. *Mol Cell Proteomics.* 2017 Jun;16(6):1064-1080.

Ritter A, Iñigo S, Fernández-Calvo P, Heyndrickx KS, Dhondt S, Shi H, De Milde L, Vanden Bossche R, De Clercq R, Eeckhout D, Ron M, Somers DE, Inzé D, Gevaert K, De Jaeger G, Vandepoele K, Pauwels L, Goossens A. (2017) The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in Arabidopsis. *Nat Commun.* 2017 May 11;8:15235.

Blomme J, Van Aken O, Van Leene J, Jégu T, De Rycke R, De Bruyne M, Vercruyse J, Nolf J, Van Daele T, De Milde L, Vermeersch M, des Francs-Small CC, De Jaeger G, Benhamed M, Millar AH, Inzé D, Gonzalez N. (2017) The Mitochondrial DNA-Associated Protein SWIB5 Influences mtDNA Architecture and Homologous Recombination. *Plant Cell.* 2017 May;29(5):1137-1156.

Zhang X, Ivanova A, Vandepoele K, Radomiljac J, Van de Velde J, Berkowitz O, Willems P, Xu Y, Ng S, Van Aken O, Duncan O, Zhang B, Storme V, Chan KX, Vanechoutte D, Pogson BJ, Van Breusegem F, Whelan J, De Clercq I. (2017) The Transcription Factor MYB29 Is a Regulator of ALTERNATIVE OXIDASE1a. *Plant Physiol.* 2017 Mar;173(3):1824-1843.

Bodra N, Young D, Astolfi Rosado L, Pallo A, Wahni K, De Proft F, Huang J, Van Breusegem F, Messens J. (2017) *Arabidopsis thaliana* dehydroascorbate reductase 2: Conformational flexibility during catalysis. *Sci Rep.* 2017 Feb 14;7:42494. [doi: 10.1038/srep42494](https://doi.org/10.1038/srep42494).

Li F, De Storme N, Geelen D. (2017) Dynamics of male meiotic recombination frequency during plant development using Fluorescent Tagged Lines in *Arabidopsis thaliana*. *Sci Rep.* 2017 Feb 13;7:42535.

Major Funding Sources

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

Brazil

Wagner L. Araújo
Departamento de Biologia Vegetal
Universidade Federal de Viçosa
36570-900 Viçosa, MG, Brazil
wlaraujo@ufv.br



Adriano Nunes Nesi
Departamento de Biologia Vegetal
Universidade Federal de Viçosa
36570-900 Viçosa, MG, Brazil
nunesnesi@ufv.br

Use of Arabidopsis

In Brazil at least eight institutions use Arabidopsis in their research.

Conferences, Workshops and Outreach events

VI Simpósio Brasileiro de Genética Molecular de Plantas, Ouro Preto, Minas Gerais Brazil, from May 28 to June 02, 2017.

47th Annual Meeting of the Brazilian Society for Biochemistry and Molecular Biology (SBBq), Joinville, Santa Catarina, Brazil, May 26th to 29th, 2018

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

Selected Publications

Medeiros DB, Barros KA, Barros JAS, Omena-Garcia RP, Arrivault S, Sanglard LMVP, Detmann KC, Silva WB, Daloso DM, DaMatta FM, Nunes-Nesi A, Fernie AR, Araújo WL. Impaired Malate and Fumarate Accumulation Due to the Mutation of the Tonoplast Dicarboxylate Transporter Has Little Effects on Stomatal Behavior. *Plant Physiol.* 2017 Nov;175(3):1068-1081

Cavalcanti JHF, Quinhones CGS, Schertl P, Brito DS, Eubel H, Hildebrandt T, Nunes-Nesi A, Braun HP, Araújo WL. Differential impact of amino acids on OXPHOS system activity following carbohydrate starvation in Arabidopsis cell suspensions. *Physiol Plant.* 2017 Dec;161(4):451-467.

Barros JAS, Cavalcanti JHF, Medeiros DB, Nunes-Nesi A, Avin-Wittenberg T, Fernie AR, Araújo WL. Autophagy Deficiency Compromises Alternative Pathways of Respiration following Energy Deprivation in *Arabidopsis thaliana*. *Plant Physiol.* 2017 Sep;175(1):62-76.

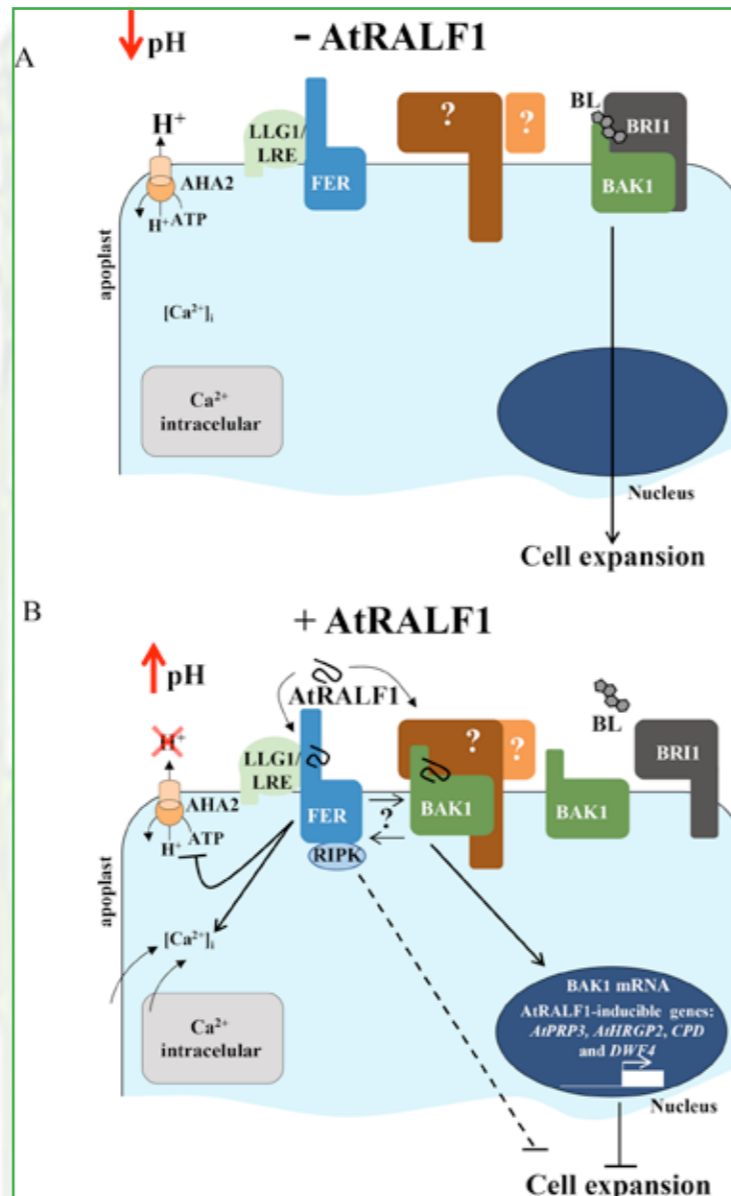


Figure 19. Proposed model for AtRALF1 perception in root cells of Arabidopsis. (A) In the absence of AtRALF1, the BRI1-BL-BAK1 complex is active in the plasma membrane and the cell expands. The apoplast is acidic as the plasma membrane proton pump AHA2 is functional and FERONIA (FER) is in the cell membrane complexed with LRE-like GPI-AP1 (LLG1)/LORELEI (LRE). (B) In the presence of AtRALF1, the peptide binds FER-LLG1/LRE complex, recruits the receptor-like cytoplasmic kinase RIPK and inactivates AHA2, leading to an increase in apoplastic pH. It is proposed that the resulted apoplastic alkalization dissociates the BRI1-BL-BAK1 complex, allows AtRALF1 to bind BAK1, disrupts BL signaling, activates AtRALF1-inducible genes and, ultimately, inhibits cell expansion. According to our model, AtRALF1/BAK1-dependent responses are downstream of intracellular Ca²⁺ mobilization and apoplastic alkalization. Both FER and BAK1 may interact, and an apoplastic factor, and at least another receptor is expected to play a role in AtRALF1 perception (question marks). The intersecting line indicates incomplete insensitivity to inhibition of cell expansion caused by AtRALF1; solid lines depict direct actions (with bars at the end = inhibition or arrowed = activation).
<https://doi.org/10.1371/journal.pgen.1007053>

Moro CF, Gaspar M, da Silva FR, Pattathil S, Hahn MG, Salgado I, Braga MR. S-nitrosoglutathione promotes cell wall remodelling, alters the transcriptional profile and induces root hair formation in the hairless root hair defective 6 (rhd6) mutant of *Arabidopsis thaliana*. *New Phytol.* 2017 Mar;213(4):1771-1786.

Dressano K, Ceciliato PHO, Silva AL, Guerrero-Abad JC, Bergonci T, Ortiz-Moreira FA, Bürger M, Silva-Filho MC, Moura DS. BAK1 is involved in AtRALF1-induced inhibition of root cell expansion. *PLoS Genet.* 2017 Oct 13;13(10):e1007053

Marcolino-Gomes J, Nakayama TJ, Molinari HBC, Basso MF, Henning LMM, Fuganti-Pagliarini R, Harmon FG and Nepomuceno AL (2017) Functional Characterization of a Putative Glycine max ELF4 in Transgenic Arabidopsis and Its Role during Flowering Control. *Front. Plant Sci.* 8:618. doi: 10.3389/fpls.2017.00618

Rodrigues NF, Christoff AP, da Fonseca GC, Kulcheski FR and Margis R (2017) Unveiling Chloroplast RNA Editing Events Using Next Generation Small RNA Sequencing Data. *Front. Plant Sci.* 8:1686. doi: 10.3389/fpls.2017.01686

Lima MF, Eloy NB, Siqueira JAB, Inzé D, Hemery AS, Ferreira PCG (2017) Molecular mechanisms of biomass increase in plants. *Biotechnology Research and Innovation*, v. 1, p. 14-27, 2017. doi: 10.1016/j.biori.2017.08.001.

Major Funding Sources

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

It is important to mention that research in Brazil is only starting to use Arabidopsis and other species are usually employed, particularly crop species. There is a gradual increase in the usage of Arabidopsis as a model plant to molecular and genetic studies due to its power.

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

Dario Bonetta
dario.bonetta@uoit.ca
 University of Ontario - Institute of
 Technology, Ontario

Nicholas Provart
nicholas.provart@utoronto.ca
 University of Toronto, Canada



open source tool. ePlant is accessible from the Araport.org homepage, and from the Bio-Analytic Resource at <http://bar.utoronto.ca/eplant>.

The first major update to ePlant was released in January 2018, and included a new Plant eFP view for Klepikova *et al.*'s (2016) RNA-seq-based developmental atlas, updated subcellular localization data using SUBA4 data, an ePlant Navigator to easily view expression patterns of homologs in other species, and the highlighting of gene parts in the Gene view.

"eFP-Seq Browser" was released for exploring the 113 RNA-seq data sets used to reannotate the Arabidopsis genome for the Araport11 build, or the RNA-seq data sets generated for Klepikova *et al.*'s (2016) developmental atlas, both as read maps and pictographs summarizing the expression levels in various tissues, easily sortable by any desired column: http://bar.utoronto.ca/eFP-Seq_Browser/.

In addition to simply sorting the table by expression level, an "eFP overview" provides a table of pictographs to get a feeling for where expression is the strongest or weakest. Released hundreds of new protein-protein interactions for the extra-cellular domains of leucine-rich repeat receptor kinases into our ePlant and Arabidopsis Interaction Viewer tools (Smakowska-Luzan *et al.*, 2018).

For translational researchers, publications came out for eFP Browser views announced last year: a Developmental Map for *Brachypodium distachyon* from Marek Mutwil and colleagues (Sibout *et al.*, 2017; http://bar.utoronto.ca/efp_brachypodium/), a Maize Root view, part of the Maize eFP Browser, from Stefan Hey and colleagues (Hey *et al.*, 2017; http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi), and a Classification SuperViewer for *Medicago truncatula* genomics (Herrbach *et al.*, 2017; http://bar.utoronto.ca/ntools/cgi-bin/ntools_classification_superviewer_medicago.cgi).

Outlook on Arabidopsis Research

Funding for Arabidopsis research is largely from NSERC, one of the three federal funding agencies in Canada. The federal government has recently committed additional funding to support basic research through the NSERC Discover Grant program.

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.

Use of Arabidopsis

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

Open Resources for Arabidopsis Researchers

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

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 new ePlant tool.

* 70,944 predicted protein-protein interactions plus 36,352 documented PPIs (rice interologs also available!) and ~2.8 million protein-DNA interactions.

* 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 9.3k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Work was completed on a "mega-app" from the BAR for Araport.org, ePlant, and a publication came out in the Plant Cell describing it (Waese *et al.*, 2017). ePlant is a zoomable user interface for exploring data across 12 orders of magnitude, from the kilometre scale down to the nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested,

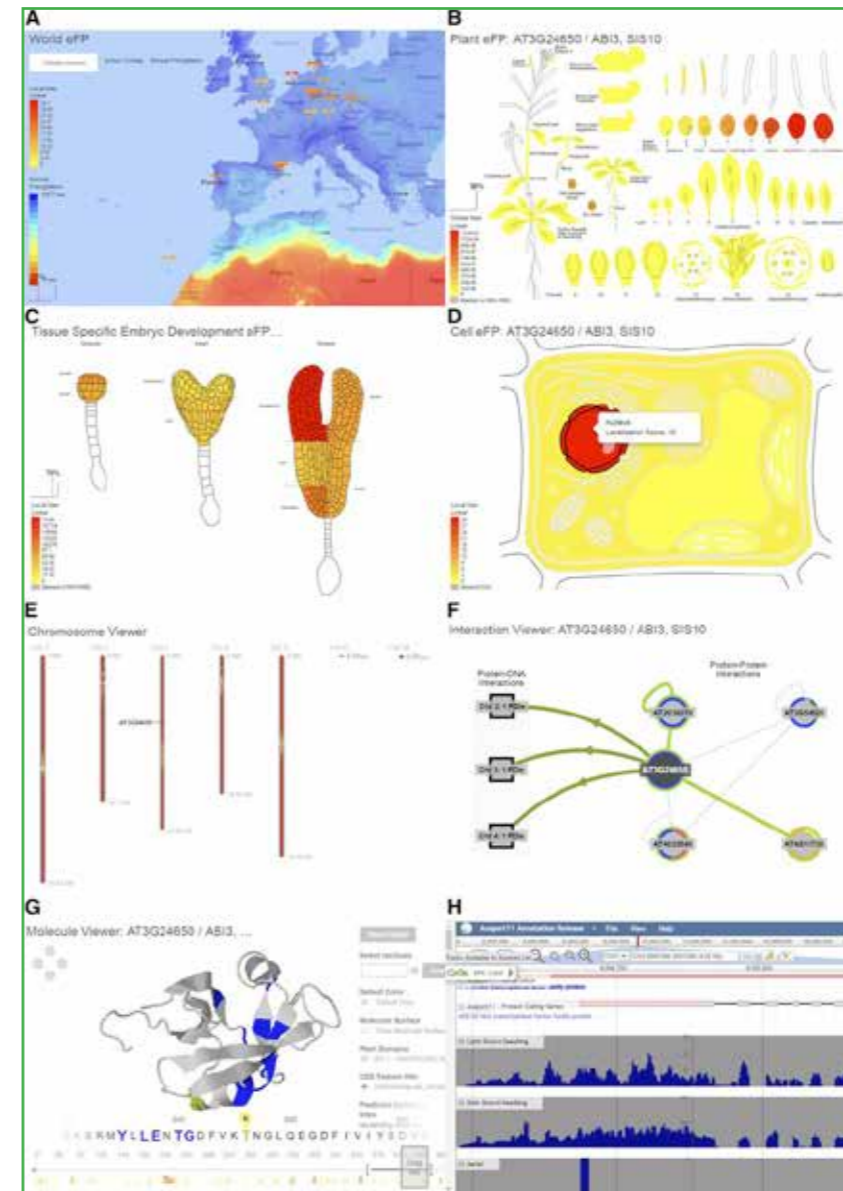


Figure 20. ePlant's Module Viewers (Each Displaying Data for ABI3), Illustrating ePlant's Hierarchy of Scale. World eFP Viewer (A), Plant eFP Viewer (B), Tissue and Experiment eFP Viewer (C), Subcellular eFP Viewer (D), Chromosome Viewer (E), Interaction Viewer (F), Molecule Viewer (G), and Sequence Viewer (H). ePlant outputs are freely usable via an "open" license. <http://dx.doi.org/10.1105/tpc.17.00073>

Selected Publications

Herrbach V, Chirinos X, Rengel D, Agbevenou K, Vincent R, Pateyron S, Huguet S, Balzergue S, Pasha A, Provart NJ, Gough C, Bensmihen S (2017). Nod factors potentiate auxin signaling for transcriptional regulation and lateral root formation in *Medicago truncatula*. *Journal of Experimental Botany* 68: 569-583.

Hey S, Baldauf J, Opitz N, Lithio A, Pasha A, Provart NJ, Nettleton D, Hochholdinger F (2017). Complexity and specificity of the maize (*Zea mays* L.) root hair transcriptome. *Journal of Experimental Botany* 68: 2175-2185.

Sibout R, Proost S, Oest Hansen B, Vaid N, Giorgi FM, Ho-Yue-Kuang S, Legée F, Cézart L, Bouchabké-Coussa O, Soulhat C, Provart N, Pasha A, Le Bris P, Roujol D, Hofte H, Jamet E, Lapierre C, Persson S, Mutwil M (2017). Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in *Brachypodium distachyon*. *New Phytologist* 215: 1009-1025.

Smakowska-Luzan E, Mott GA, Parys K, Stegmann M, Howton TC, Layeghifard M, Neuhold J, Lehner A, Kong J, Grünwald K, Weinberger N, Satbhai SB, Mayer D, Busch W, Madalinski M, Stolt-Bergner P, Provart NJ, Mukhtar MS, Zipfel C, Desveaux D, Guttman DS, Belkadir Y (2018). An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. *Nature* 553: 342-346. doi:10.1038/nature25184.

Waese J, Fan J, Pasha A, Yu H, Fucile G, Shi R, Cumming M, Kelley LA, Sternberg MJ, Krishnakumar V, Ferlanti E, Miller J, Town C, Stuerzlinger W, Provart NJ (2017). ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. *Plant Cell* 29: 1806-1821. doi: 10.1105/tpc.17.00073

Major Funding Sources

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

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

Chile

Francisca Blanco-Herrera
mblanco@unab.cl
 Centro de Biotecnología Vegetal,
 Universidad Andres Bello, Chile.



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

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

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

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

Loreto Holuigue's lab research goal is to contribute to understanding plant defense mechanism in response to stress. They study the mechanism of Salicylic Acid (SA) function using *Arabidopsis thaliana*. They could identify and perform functional characterization of SA induced defense genes and study the mechanism how SA induce their expression. Lorena Norambuena's laboratory integrates cell biology aspect of protein trafficking on plant development using mainly *Arabidopsis thaliana*. Her lab uses cell biology, molecular biology and chemical genomic approaches.

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

Use of Arabidopsis

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

Open Resources for Arabidopsis Researchers

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

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

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

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

Hannetz Roschttardt's laboratory focusses on the mechanisms of iron uptake in plant roots, and mainly how does govern the distribution to organs, cells and organelles targets. The development of methods allowing iron visualization in plant tissues has been key in the significant progress observed in last years. Recently, a histochemical iron staining method (Perls/DAB) has been used on plant tissues. using this approach, it has been possible to identify new pools of iron in plants. Our results open new questions about the mechanisms of iron distribution and accumulation in seeds, and could be used as a basis for the development of novel biotechnological strategies to increasing total iron content in seeds for human consumption.

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

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

New Software Tools

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

GENIUS: web server to predict local gene networks and key genes for biological functions. Puelma T, Araus V, Canales J, Vidal EA, Cabello JM, Soto A, Gutiérrez RA. *Bioinformatics*. 2017 Mar 1;33(5):760-761. doi: 10.1093/bioinformatics/btw702.

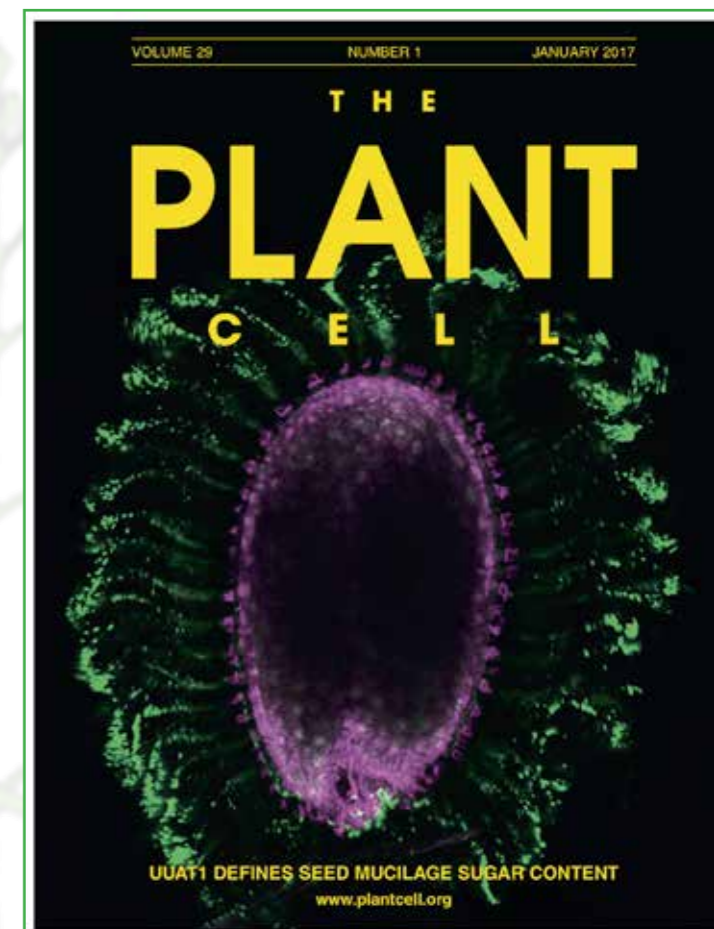


Figure 21. Labeling of highly methylesterified HG in the adherent mucilage from seeds of the *uuat1-2* mutant line imaged using confocal microscopy optical section reconstruction of adherent mucilage released from imbibed seeds. The LM20 antibody (green) was used to label HG domains, and propidium iodide was used to stain the seed coat surface (pink).

doi: 10.1105/tpc.16.00465

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

Conferences, Workshops and Outreach events

Thursday November 30th, 2017.
 Workshop: "Applied Plant Biology II: Expression of gene regulation in plant development and fruit ripening"
 Organizers: Universidad de Talca

November 30th to December 2nd, 2017
 Signat Workshop on Environmental Regulation of Plant Development. This workshop will be held at P. Universidad Católica de Chile in Santiago from Organizers: SIGNAT, Horizon 2020 European Union funding for Research & Innovation

December 4th to 7th, 2017- XII Chilean Plant Biology Meeting. The meeting was held at the Hotel Villarrica Park Lake in Villarrica, Chile.

As it is now a tradition, the last year conference consisting of sessions ranging across plant sciences: Plant Genome Regulation, Cell and Developmental Biology, Metabolism and Natural Products, Biotic/Abiotic Stress, Genetic Resources and Plant Breeding. Attendees at our conference are primarily students, young scientists and faculty from major Universities and research institutes in Chile. The last year, the XII ReBiVe, have around 200 attendees. The scientific program featured a list of 17 international speakers, covering almost all the disciplines of plant biology research. Nearly 250 abstracts have been submitted to the Meeting. Nearly 180 research M.Sc. or Ph.D. students are among the participants who with their great enthusiasm and hard work will be the future world leaders of our research field. Organizers: Chilean Society of Plant Biologist

Selected Publications

Saez-Aguayo S, Rautengarten C, Temple H, Sanhueza D, Ejsmentewicz T, Sandoval-Ibañez O, Doñas D, Parra-Rojas JP, Ebert B, Lehner A, Mollet JC, Dupree P, Scheller HV, Heazlewood JL, Reyes FC, Orellana A. UUA1 Is a Golgi-Localized UDP-Uronic Acid Transporter That Modulates the Polysaccharide Composition of Arabidopsis Seed Mucilage. *Plant Cell*. 2017 Jan; 29(1):129-143. doi: 10.1105/tpc.16.00465.

Restovic F, Espinoza-Corral R, Gómez I, Vicente-Carbajosa J, Jordana X. An active Mitochondrial Complex II Present in Mature Seeds Contains an Embryo-Specific Iron-Sulfur Subunit Regulated by ABA and bZIP53 and Is Involved in Germination and Seedling Establishment. *Front Plant Sci*. 2017 Feb 28;8:277. doi: 10.3389/fpls.2017.00277. eCollection 2017.

Undurraga SF, Ibarra-Henríquez C, Fredes I, Álvarez JM, Gutiérrez RA. Nitrate signaling and early responses in Arabidopsis roots. *J Exp Bot*. 2017 May 1;68(10):2541-2551. doi: 10.1093/jxb/erx041.

Roschttardt H, Bustos S, Coronas MF, Ibeas MA, Grant-Grant S, Vargas-Pérez J. Increasing Provasculature Complexity in the Arabidopsis Embryo May Increase Total Iron Content in Seeds: A Hypothesis. *Front Plant Sci*. 2017 Jun 8;8:960. doi: 10.3389/fpls.2017.00960. eCollection 2017.

Norambuena L and Tejos R. Chemical Genetic Dissection of Membrane Trafficking. *Annual Review in Plant Biology*. 2017. 68:197-224. doi:10.1146/annurev-arplant-042916-041107. Zúñiga A, Donoso RA, Ruiz D, Ruz GA, González B. Quorum-Sensing Systems in the Plant Growth-Promoting Bacterium *Paraburkholderia phytofirmans* PsJN Exhibit Cross-Regulation and Are Involved in Biofilm Formation.

Mol Plant Microbe Interact. 2017 Jul;30(7):557-565. doi: 10.1094/MPMI-01-17-0008-R.

Canales J, Contreras-López O, Álvarez JM, Gutiérrez RA. Nitrate induction of root hair density is mediated by TGA1/TGA4 and CPC transcription factors in *Arabidopsis thaliana*. *Plant J*. 2017 Oct;92(2):305-316. doi: 10.1111/tpj.13656. Epub 2017 Aug 31.

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

Seguel A, Jelenska J, Herrera-Vásquez A, Marr SK, Joyce MB, Gagesch KR, Shakoor N, Jiang SC, Fonseca A, Wildermuth M, Greenberg JT, Holuigue L. PROHIBITIN 3 forms complexes with ISOCHORISMATE SYNTHASE 1 to regulate stress-induced salicylic acid biosynthesis in Arabidopsis. *Plant Physiol*. 2018 Feb 1. pii: pp.00941.2017. doi: 10.1104/pp.17.00941.

Cifuentes-Esquivel N, Celiz-Balboa J, Henriquez-Valencia C, Mitina I, Arraño-Salinas P, Moreno AA, Meneses C, Blanco-Herrera F, Orellana A. bZIP17 regulates the expression of genes related to seed storage and germination, reducing seed susceptibility to osmotic stress. *Journal of Cellular Biochemistry* April 2018. 10.1002/jcb.26882

Major Funding Sources

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

China

Yuling Jiao yjliao@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.

Open Resources for Arabidopsis Researchers

Transcription factor library

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

Shoot cell type-specific transcriptome profiling lines

A collection of Arabidopsis transgenic lines expressing His6-FLAG tagged RPL18 under the shoot apical meristem and leaf primordium cell type-specific promoter has been developed in Dr. Yuling Jiao's group. This set of cell type marker lines allows other researchers to perform in-house

cell type-specific gene expression analysis without the need of specialized equipment. By contrast, previous analysis based on laser microdissection or fluorescence-activated cell sorting cannot be easily adopted by others. An eFP browser of the gene expression data in wild-type vegetative plants is available at <http://jiaolab.genetics.ac.cn/sa>.

New Software Tools

- AHD2.0: Arabidopsis hormone database 2.0 <http://ahd.cbi.pku.edu.cn/>
- PlantGSEA: a gene set enrichment analysis toolkit for plant community <http://structuralbiology.cau.edu.cn/PlantGSEA/>
- PlantTFDB: Plant transcription factor database <http://planttfdb.cbi.pku.edu.cn/link.php>
- PsRobot: Plant small RNA analysis toolbox <http://omicslab.genetics.ac.cn/psRobot/>
- Shoot cell type-specific expression ebrowser http://bar.utoronto.ca/efp_arabidopsis/cgi-bin/efpWeb.cgi?dataSource=Shoot_Apex

Conferences, Workshops and Outreach events

Major conferences held in 2017

- 4th International Conference on Plant Metabolism (ICPM2017), Dalian, Shenyang, July 16-20, 2017 (<http://www.cspb.org.cn/2017/icpm.asp>)
- 6th International Conference on Plant Cell Wall Biology (PCWB2017), Dalian, Shenyang, July 16-20, 2017 (<http://www.cspb.org.cn/2017/pcwb.asp>)
- 13th International Meeting on Biosynthesis, Function and Synthetic Biology (TERPNET2017), Dalian, Shenyang, July 16-20, 2017 (<http://www.cspb.org.cn/2017/terpnet.asp>)
- 19th International Botanical Congress (IBC2017), Shenzhen, Guangdong, July 23 - 29, 2017 (<http://www.ibc2017.cn/>)
- 5th International Conference on Biotic Plant Interaction (ICBPI), Xiamen, Fujian, August 17-21, 2017 (<http://english.fafu.edu.cn/5icbp/en/>)
- 2017 National Congress of Plant Biology, Chongqing, October 9-12, 2017 (<http://www.ncpb.net/2017/>)

Highlights on upcoming international events

- 2nd International Conference on Plant Meristem Biology (Meristem 2018), Hefei, Anhui, June 9-10, 2018 (www.meristem2018.com)
- 30th International Conference on Arabidopsis Research (ICAR2019) will be held in Wuhan, Hubei, 2019

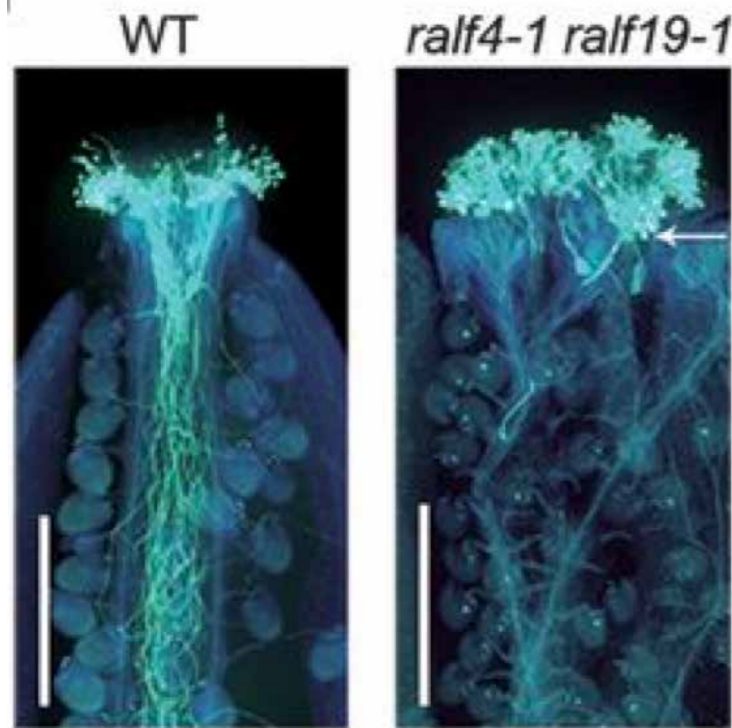


Figure 22. RALF4 and RALF19 are pollen tube-expressed and are required for pollen tube integrity. The figure shows Aniline Blue staining of wild-type (WT) and *ralf4 ralf19* pollen tubes in WT pistils at 20 hours after pollination.
<http://dx.doi.org/10.1126/science.aao3642>

Although a number of high-profile international conferences, including ICAR, have chosen China as their meeting venues, Chinese scientists are clearly under represented in some international conferences, such as the ICAR. For example, only one speaker from China talked at the recent ICAR2017. This under representation will likely negatively influence Chinese researchers' enthusiasm for attending ICAR.

Selected Publications

During 2017, Chinese researchers authored over 500 plant science papers with a portion involved work on Arabidopsis

Ge Z, Bergonci T, Zhao Y, Zou Y, Du S, Liu MC, Luo X, Ruan H, García-Valencia LE, Zhong S, Hou S, Huang Q, Lai L, Moura DS, Gu H, Dong J, Wu HM, Dresselhaus T, Xiao J, Cheung AY, Qu LJ. (2017) Arabidopsis pollen tube integrity and sperm release are regulated by RALF-mediated signaling. *Science* 358(6370):1596-1600.

Hu J, Yang H, Mu J, Lu T, Peng J, Deng X, Kong Z, Bao S, Cao X, Zuo J. (2017) Nitric oxide regulates protein methylation during stress responses in plants. *Mol. Cell* 67(4):702-710.

Li H, Ding Y, Shi Y, Zhang X, Zhang S, Gong Z, Yang S. (2017) MPK3- and MPK6-mediated ICE1 phosphorylation negatively regulates ICE1 stability and freezing tolerance in Arabidopsis. *Dev. Cell* 43(5):630-642.

Liu Z, Jia Y, Ding Y, Shi Y, Li Z, Guo Y, Gong Z, Yang S. (2017) Plasma membrane CRPK1-mediated phosphorylation of 14-3-3 proteins induces their nuclear import to fine-tune CBF signaling during cold response. *Mol. Cell* 66(1):117-128

Qi J, Wu B, Feng S, Lü S, Guan C, Zhang X, Qiu D, Hu Y, Zhou Y, Li C, Long M, Jiao Y. (2017) Mechanical regulation of organ asymmetry in leaves. *Nat. Plants* 3(9):724-733.

Su X, Ma J, Wei X, Cao P, Zhu D, Chang W, Liu Z, Zhang X, Li M. (2017) Structure and assembly mechanism of plant C2S2M2-type PSII-LHCII supercomplex. *Science* 357(6353):815-820.

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

Xu W, Xu H, Li K, Fan Y, Liu Y, Yang X, Sun Q. (2017) The R-loop is a common chromatin feature of the Arabidopsis genome. *Nat. Plants* 3(9):704-714.

Zeng J, Dong Z, Wu H, Tian Z, Zhao Z. (2017) Redox regulation of plant stem cell fate. *EMBO J.* 36(19):2844-2855.

Zhang J, Huang Q, Zhong S, Bleckmann A, Huang J, Guo X, Lin Q, Gu H, Dong J, Dresselhaus T, Qu LJ. (2017) Sperm cells are passive cargo of the pollen tube in plant fertilization. *Nat. Plants* 3(6):17079.

Zhao C, Wang P, Si T, Hsu CC, Wang L, Zayed O, Yu Z, Zhu Y, Dong J, Tao WA, Zhu JK. (2017) MAP kinase cascades regulate the cold response by modulating ICE1 protein stability. *Dev. Cell* 43(5):618-629.

Major Funding Sources

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

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

Czech Republic

Viktor Žárský
viktor@natur.cuni.cz
 Charles University, Department of Exp. Plant Biol. and Inst. of Exp. Bot. Acad. Sci. of the Czech Rep. Prague



Open Resources for Arabidopsis Researchers

BRNO - CEITEC - Central European Institute of Technology Proteomics Core Facility

<http://www.ceitec.eu/ceitec-mu/proteomics-core-facility/z8>

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

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.

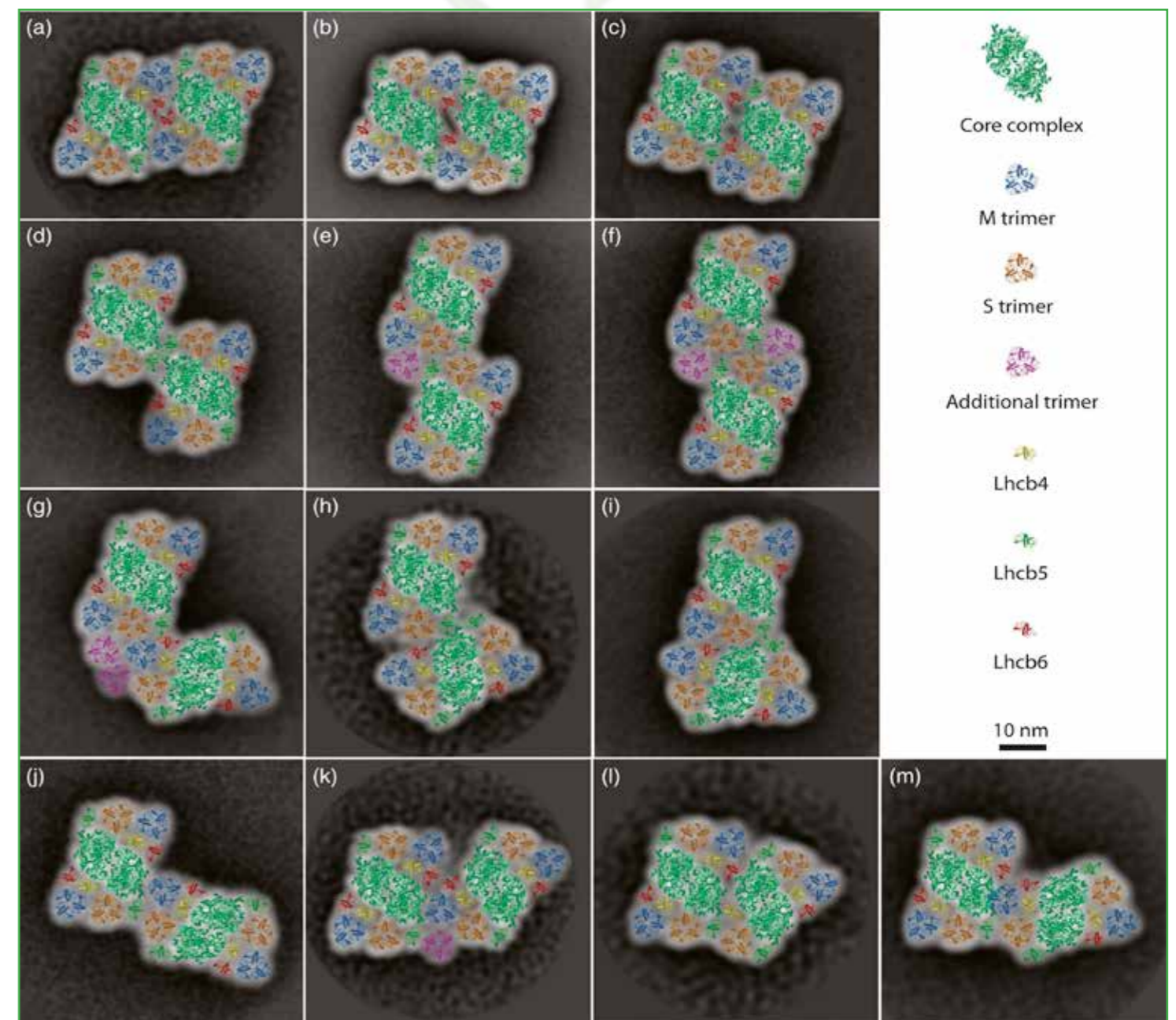


Figure 23. Structural models of the PSII megacomplexes (a–m) Photosystem II (PSII) megacomplexes fitted with the proposed PSII crystalline structure, as published by Caffarri *et al.* (2009). Individual PSII subunits are colour coded in the following manner: pale green, core complex; blue, M trimer; orange, S trimer; magenta, additional LHCII trimers; yellow, Lhcb4; green, Lhcb5; red, Lhcb6.
<https://doi.org/10.1111/tpj.13325>

Conferences, Workshops and Outreach events

Last year 2017:
- ENPER meeting 2017, Prague, “20th European Network for Plant Endomembrane Research” meeting. September 12–15, 2017, Prague

This year 2018:
- ACPD2018 - “Auxins and Cytokinins in Plant Development”, July 1–5, 2018, Prague

Selected Publications

Mandáková T, Hloušková P, German DA, Lysak MA. Monophyletic Origin and Evolution of the Largest Crucifer Genomes. *Plant Physiol.* Aug;174(4):2062-2071. doi: 10.1104/pp.17.00457, 2017.

Nosek L, Semchonok D, Boekema EJ, Ilík P, Kouřil R. Structural variability of plant photosystem II megacomplexes in thylakoid membranes. *Plant J.* Jan;89(1):104-111. doi: 10.1111/tbj.13325, 2017.

Prasad A, Sedláčková M, Kale RS, Pospíšil P. Lipoyxygenase in singlet oxygen generation as a response to wounding: *in vivo* imaging in *Arabidopsis thaliana*. *Sci Rep.* Aug 29;7(1):9831. doi: 10.1038/s41598-017-09758-1. 2017

Sabol P, Kulich I, Žárský V. RIN4 recruits the exocyst subunit EXO70B1 to the plasma membrane. *J. Exp. Bot.* 68(12):3253-3265, doi: 10.1093/jxb/erx007, 2017.

Synek L, Vukašinovic N, Kulich I, Hála M, Aldorfová K, Fendrych M, Žárský V. EXO70C2 Is a Key Regulatory Factor for Optimal Tip Growth of Pollen. *Plant Physiol.* 174:223-240, doi:10.1104/pp.16.01282, 2017.

Valuchova S, Fulneczek J, Prokop Z, Stolt-Bergner P, Janouskova E, Hofr C, Riha K. Protection of Arabidopsis Blunt-Ended Telomeres Is Mediated by a Physical Association with the Ku Heterodimer. *Plant Cell.* Jun;29(6):1533-1545. doi: 10.1105/tpc.17.00064, 2017.

Vukašinovic N, Oda Y, Pejchar P, Synek L, Pecenková T, Rawat A, Sekereš J, Potocký M, Žárský V. Microtubule-dependent targeting of the exocyst complex is necessary for xylem development in Arabidopsis. *New Phytol.* 213(3):1052-1067, 2017 - doi: 10.1111/nph.14267, 2017.

Major Funding Sources

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

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

Both institutions support also bilateral projects with selected countries. Targeted or applied research is since recently supported also by the Technology Agency of the Czech Republic (TACR) and Arabidopsis model is accepted as a driver for applications.

3. Technology Agency of the Czech Republic <http://www.tacr.cz/english/>
4. Ministry of Agriculture, National Agency for Agricultural Research (NAZV) might support projects using Arabidopsis as a driver for the applied research <https://goo.gl/JPGv1O>

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

Current Arabidopsis Projects

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

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

Selected Publications

Barghetti A, Sjögren L, Floris M, Paredes EB, Wenkel S, Brodersen P (2017) Heat-shock protein 40 is the key farnesylation target in meristem size control, abscisic acid signaling, and drought resistance. *Genes Dev.* 31:2282-2295. ’

Nielsen ME, Jürgens G, Thordal-Christensen H (2017) VPS9a Activates the Rab5 GTPase ARA7 to Confer Distinct Pre- and Postinvasive Plant Innate Immunity. *Plant Cell.* 29:1927-1937.

Hoffmann RD, Olsen LI, Husum JO, Nicolet JS, Thøfner JFB, Wätjen AP, Ezike CV, Palmgren M (2017) A cis-Regulatory Sequence Acts as a Repressor in the *Arabidopsis thaliana* Sporophyte but as an Activator in Pollen. *Mol Plant.* 10(7):775-778.

Straub D, Wenkel S (2017) Cross-Species Genome-Wide Identification of Evolutionary Conserved MicroProteins. *Genome Biol Evol.* 9:777-789.

Castro PH, Lilay GH, Muñoz-Mérida A, Schjoerring JK, Azevedo H, Assunção AGL (2017) Phylogenetic analysis of F-bZIP transcription factors indicates conservation of the zinc deficiency response across land plants. *Sci Rep.* 7:3806

Nour-Eldin HH, Madsen SR, Engelen S, Jørgensen ME, Olsen CE, Andersen JS, Seynnaeve D, Verhoye T, Fulawka R, Denolf P, Halkier BA (2017) Reduction of antinutritional glucosinolates in Brassica oilseeds by mutation of genes encoding transporters. *Nat Biotechnol.* 35:377-382.

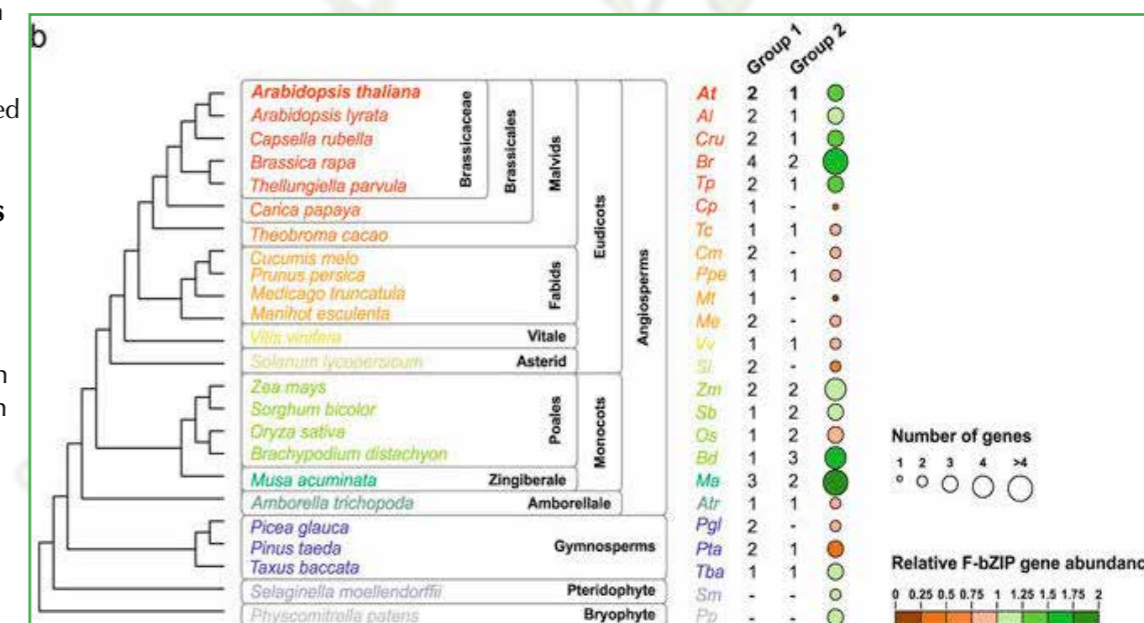


Figure 24. Phylogenetic analysis of the F-bZIP subfamily of proteins in plant species. (a) Proteins of the F-bZIP subfamily from a selection of 24 species representing all major plant taxa were used in the phylogenetic analysis. The phylogenetic tree was constructed using maximum-likelihood and bootstrap values from 1000 replicates. Numbers on each branch represent the percentages of bootstrap. Proteins of the D-bZIP subfamily from representative species of different phylogenetic groups were used as an outgroup. Asterisks indicate proteins with missing or incomplete His/Cys-rich motif (red) or bZIP domain (blue). (b) F-bZIP gene enrichment for each plant species. Bubble size represents the absolute number of genes present in each species' genome. Bubble colours indicate the relative size of the F-bZIP subfamily. The relative value was calculated as the ratio of F-bZIPs per total of genes in the genome versus the average of F-bZIPs in all species analysed. <https://doi.org/10.1038/s41598-017-03903-6>

Finland

Michael Wrzaczek
michael.wrzaczek@helsinki.fi
 Division of Plant Biology, Department of Biosciences, Viikki Plant Science Centre, University of Helsinki, Helsinki, Finland



J, Macpherson L, Mikola J, Mouhu K, Mähönen AP, Niinemets Ü, Oksanen E, Overmyer K, Palva ET, Pazouki L, Pennanen V, Puhakainen T, Poczai P, Possen BJHM, Punkkinen M, Rahikainen M, Rousi M, Ruonala R, van der Schoot C, Shapiguzov A, Sierla M, Sipilä TP, Sutela S, Teeri TH, Tervahauta AI, Vaattovaara A, Vahala J, Vetchinnikova L, Welling A, Wrzaczek M, Xu E, Paulin L, Schulman AH, Lascoux M, Albert VA, Auvinen P, Helariutta Y, Kangasjärvi K. 2017. Adaptive landscape and population genomics of silver birch. *Nature Genetics* 49(6):904-912.

Kimura S, Waszczak C, Hunter K, Wrzaczek M. 2017. Bound by fate: reactive oxygen species in receptor-like kinase signaling. *Plant Cell* 29(4): 638-654

de Dios Barajas-Lopez J, Moreno JR, Gamez-Arjona FM, Pardo JM, Punkkinen M, Zhu JK, Quintero FJ, Fujii H (2017) Upstream kinases of plant SnRKs are involved in salt stress tolerance. *PLANT J* (in press) <http://dx.doi.org/10.1111/tbj.13761>

Ruzicka K, Zhang M, Campilho A, Bodi Z, Kashif M, Saleh M, Eeckhout D, El-Showk S, Li H, Zhong S, De Jaeger G, Mongan N, Hejátko J, Helariutta Y, Fray R (2017) Identification of Factors Required for m6A mRNA Methylation in Arabidopsis Reveals a Role for the Conserved E3 Ubiquitin Ligase HAKAI. *NEW PHYTOLOGIST* 215(1), 157-172

Rahikainen M, Trotta A, Alegre S, Pascual J, Vuorinen K, Overmyer K, Moffatt B, Ravel S, Glawischnig E, Kangasjärvi S (2017) PP2A-B' modulates foliar trans-methylation capacity and formation of 4-methoxy-indol-3-yl-methyl glucosinolate in Arabidopsis leaves. *THE PLANT JOURNAL* 89(1): 112-127

Major Funding Sources

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



Use of Arabidopsis

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

Open Resources for Arabidopsis Researchers

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

New Software Tools

Groups at the University of Helsinki are developing PhenomatoR, an R package to integrate different phenotypic data from different sources (several phenotyping platforms as well as data from conventional approaches) with mathematical normalization of repeats and other features. A manuscript is currently in preparation and the software will be available as R package.

Conferences, Workshops and Outreach events

Finland is organizing the International Conference on Arabidopsis Research 2018 in Turku, Finland, from June 25 to 29. All information about the conference can be found at the website: <http://icar2018.arabidopsisresearch.org/>
 The conference is organized by groups from the Universities in Helsinki, Turku and Oulu.

Selected Publications

Salojärvi J, Smolander OP, Nieminen K, Rajaman S, Mohammadi O, Safdari P, Lamminmäki A, Immanen J, Lan T, Tanskanen J, Rastas P, Amiroussi A, Jayaprakash B, Kammonen J, Hagqvist R, Eswaran G, Ahonen VH, Serra JA, Asiegbu FO, de Dios Barajas-Lopez J, Blande D, Blokhina O, Blomster T, Broholm S, Brosché M, Cui F, Dardick C, Ehonen E, Elomaa P, Escamez S, Fagerstedt KV, Fujii H, Gauthier A, Gollan PJ, Halimaa P, Heino P, Himanen K, Hollender C, Kangasjärvi S, Kauppinen L, Kelleher CT, Kontunen-Soppela S, Koskinen JP, Kovalchuk A, Kärenlampi S, Kärkönen A, Lim KJ, Leppälä

France

Catherine Perrot-Rechenmann
catherine.rechenmann@cnrs-dir.fr



Loïc Lepiniec
Loic.Lepiniec@inra.fr
 Institut Jean-Pierre Bourgin (INRA-AgroParisTech-CNRS), Université Paris-Saclay.



Use of Arabidopsis

- About twenty research institutes

Open Resources for Arabidopsis Researchers

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

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

New Software Tools

- IPS2, FlagDB++,
<http://tools.ips2.u-psud.fr/projects/FLAGdb++/HTML/index.shtml>

Conferences, Workshops and Outreach events

- Kickoff meeting for INDEPTH Cost Actio; Clermont-Ferrand March 12-14th 2018.
<https://www.brookes.ac.uk/indepth/>

- IPBM2018, 12th Congress of the International Plant Molecular Biology, Montpellier, France, August 5-10, 2018. <https://www.ipmb2018.org>

- International SPS Conference 2018, 4-6 juillet 2018 Campus Paris-Saclay
<https://www6.inra.fr/saclay-plant-sciences/Evenements/Congres-International-SPS/International-SPS-Conference-2018>

- French Society of Plant Biology (SFBV), Young Researchers congress, 27-29th of June, Tours
<http://sfbv.iees.upmc.fr>

- 1st international Plant Systems Biology meeting, September 10-14, 2018 in Roscoff (FR),
<https://sites.google.com/site/iplantsystemsbiol/>

- Plant epigenetics and epigenomics, Summer schools, July 8-13, 2018 - Centre Port Royal, Saint-Lambert (France),
<https://www6.inra.fr/saclay-plant-sciences/Formation/Ecoles-d-ete/Ecole-d-ete-2018>

Selected Publications

Daccord, N., *et al.* (2017). High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. *Nat Genet* 49, 1099-1106.

Gronnier, J., *et al.* (2017). Structural basis for plant plasma membrane protein dynamics and organization into functional nanodomains. *Elife* 6.

Hervieux, N., *et al.* (2017). Mechanical Shielding of Rapidly Growing Cells Buffers Growth Heterogeneity and Contributes to Organ Shape Reproducibility. *Curr Biol* 27, 3468-3479 e3464.

Nicolas, W.J., *et al.* (2017). Architecture and permeability of post-cytokinesis plasmodesmata lacking cytoplasmic sleeves. *Nat Plants* 3, 17082.

Schaefer, E., *et al.* (2017). The preprophase band of microtubules controls the robustness of division orientation in plants. *Science* 356, 186-189.

Major Funding Sources

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

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

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



Germany

Klaus Harter
klaus.harter@zmbp.uni-tuebingen.de
 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.

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

Open Resources for Arabidopsis Researchers

1001 Genomes Project
<http://1001genomes.org/>

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

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

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

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

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

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

New Software Tools

qPortal: A large set of software tools and portlets are accessible via the recently established web-based science portal of the Quantitative Biology Center (QBiC) of the University of Tübingen (<https://portal.qbic.uni-tuebingen.de/portal/web/qbic/software>). qPortal provides users with an intuitive way to create, manage, and analyze quantitative biological data and comprises front-end solutions to give users access to data management and easy-to-use analysis options. qPortal provides solutions for biological projects, providing up to date analysis pipelines, quality control workflows, and visualization tools. Appropriate data models build the foundation of qPortal's biological data management system and provide possibilities to annotate data, query existing metadata for statistics and future re-analysis on high-performance computing systems via coupling of workflow management systems.

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

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

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

Conferences, Workshops and Outreach events

Conferences

6th International Meeting on Plant Genome Stability and Change, 03. – 06.06. 2018, Gatersleben, Germany

1st Cologne Conference on Food for Future, 05. – 07. September 2018, Cologne, Germany

32th Conference Molecular Biology of Plants, 18. – 21. February 2019, Dabringhausen, Germany

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

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

Workshops and Summer Schools

Dresden Summer School in Systems Biology, 11. – 18. August 2018, Dresden, Germany

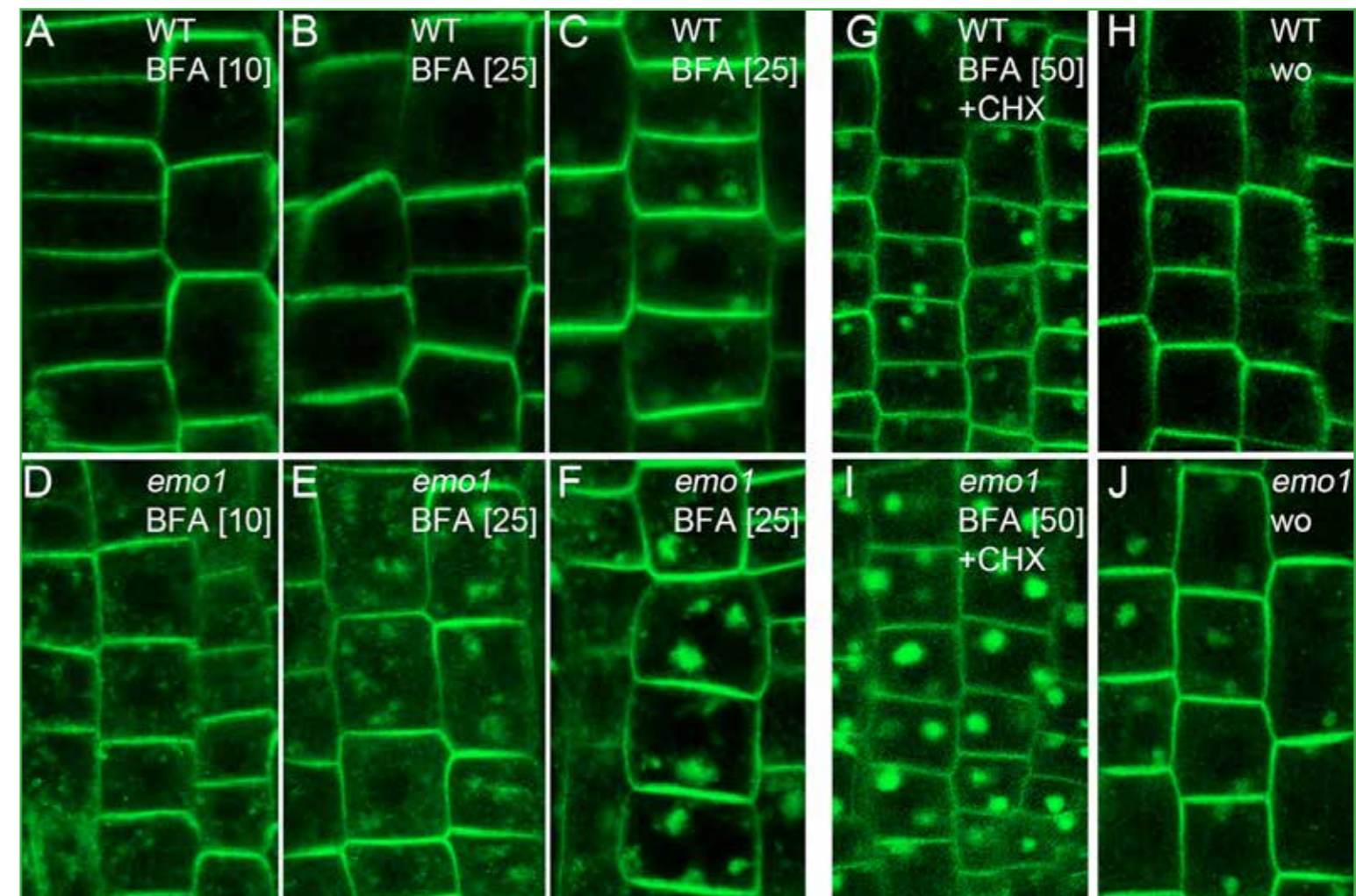


Figure 25 Ethanol-inducible emo-RNAi alters membrane trafficking processes. (A) to (F) PIN2-GFP in epidermal root cells of wild-type (A–C) and emo1-RNAi (D–F) seedlings grown for 4 days on inductive medium and treated with BFA for 10 min (A, D), 30 min (B, E) or 60 min (C, F). The BFA concentration used (μM) is given in brackets. (G) to (J) PIN2-GFP in epidermal root cells of induced (4d) wild-type (G, H) and *emo1-RNAi* (I, J) seedlings treated with cycloheximide (CHX, 50 μM) for 60 min followed by concomitant treatment with CHX and 50 μM BFA (G, I) and subsequent washout of BFA (H, J) for 60 min (wo), respectively <https://doi.org/10.7554/eLife.24336.015>

7th International Summer School on Life Cycle Approaches to Sustainable Regional Development, 25. – 28. August 2018, Leipzig, Germany

de.NBI Summer School 2018, 03. – 07. September 2018, Braunschweig, Germany

1st Black Forest Flagellated Plant Workshop, 17. – 20. September 2018, Feldberg, Germany

1st Greifswald Summer School on Mathematics of Evolution, 16. – 22. September 2018, Greifswald, Germany

Workshop on Genome-Wide Analysis of Selection Signatures and Genotype-Phenotype Associations, 22. – 26. October 2018, Berlin, Germany

Outreach Events

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

German institutions are very active in communicating plant science to the general public. Max Planck Institutes, for instance, offer guided tours, events and informative booklets for people of all ages. Some examples are below. - Wissenschaftsscheune, "The Science Barn" (<http://www.wissenschaftsscheune.de/>)

- Open House of the Tübingen MPI (<http://www.eb.tuebingen.mpg.de/institute/information-for-the-public.html>)

- Frag die Erbse, "Ask the Pea" booklet series (http://www.mpimp-golm.mpg.de/22409/Frag_die_Erbse_Booklet)

Selected Publications

Blüher D, Laha D, Thieme S, Hofer A, Eschen-Lippold L, Masch A, Balcke G, Pavlovic I, Nagel O, Schonsky A, Hinkelmann R, Wörner J, Parvin N, Greiner R, Weber S, Tissier A, Schutkowski M, Lee J, Jessen H, Schaaf G, Bonas U (2017). A 1-phytase type III effector interferes with plant hormone signaling. *Nat Commun* Dec 18;8(1):2159. doi: 10.1038/s41467-017-02195-8.

Exposito-Alonso M, Vasseur F, Ding W, Wang G, Burbano HA, Weigel D (2018). Genomic basis and evolutionary potential for extreme drought adaptation in *Arabidopsis thaliana*. *Nat Ecol Evol.* Feb;2(2):352-358. doi: 10.1038/s41559-017-0423-0.

Früholz S, Fäßler F, Kolukisaoglu Ü, Pimpl P (2018). Nanobody-triggered lockdown of VSRs reveals ligand reloading in the Golgi. *Nat Commun* 13;9(1):643. doi: 10.1038/s41467-018-02909-6.

Gaillochet C, Stiehl T, Wenzl C, Ripoll JJ, Bailey-Steinitz LJ, Li L, Pfeiffer A, Miotk A, Hakenjos J, Forner J, Yanofsky MF, Marciniak-Czochra A, Lohmann JU (2017). Control of plant cell fate transitions by transcriptional and hormonal signals. *Elife* ;6. doi: 10.7554/eLife.30135.

Hartmann M, Zeier T, Bernsdorff F, Reichel-Deland V, Kim D, Hohmann M, Scholten N, Schuck S, Bräutigam A, Hölzel T, Ganter C, Zeier J (2018). Flavin monooxygenase-generated N-hydroxypipicolinic acid is a critical element of plant systemic immunity. *Cell* 173 (2): 456-469, e16. doi: https://doi.org/10.1016/j.cell.2018.02.049.

Keicher J, Jaspert N, Weckermann K, Möller C, Throm C, Kintzi A, Oecking C (2017). *Arabidopsis* 14-3-3 epsilon members contribute to polarity of PIN auxin carrier and auxin transport-related development. *Elife*; 6. doi: 10.7554/eLife.24336.

Lenarcic T, Albert I, Böhm H, Hodnik V, Pirc K, Zavec AB, Podobnik M, Pahovnik D, Žagar E, Pruitt R, Greimel P, Yamaji-Hasegawa A, Kobayashi T, Zienkiewicz A, Gömann J, Mortimer JC, Fang L, Mamode-Cassim A, Deleu M, Lins L, Oecking C, Feussner I, Mongrand S, Anderlüh G, Nürnberger T (2017). Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. *Science* Dec 15;358(6369):1431-1434. doi: 10.1126/science.aan6874.

Mao H, Aryal B, Langenecker T, Hagmann J, Geisler M, Grebe M (2017). *Arabidopsis* BTB/POZ protein-dependent PENETRATION3 trafficking and disease susceptibility. *Nat Plants* Nov;3(11):854-858. doi: 10.1038/s41477-017-0039-z.

Wang P, Liang F-C, Wittmann D, Siegel A, Shan S-O, Grimm B (2018). Chloroplast SRP43 acts as a chaperone for glutamyl-tRNA reductase, the rate-limiting enzyme in tetrapyrrole biosynthesis. *Proc Natl Acad Sci USA* 115 (15) E3588-E3596; https://doi.org/10.1073/pnas.1719645115.

Zhou Y, Wang Y, Krause K, Yang T, Dongus JA, Zhang Y, Turck F (2018). Telobox motifs recruit CLF/SWN-PRC2 for H3K27me3 deposition via TRB factors in *Arabidopsis*. *Nature Genet*, doi: 10.1038/s41588-018-0109-9.

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



India

Jitendra P. Khurana
khuranaj@genomeindia.org
University of Delhi South Campus, New Delhi, India

Ramamurthy Srinivasan
srinivasan53@gmail.com
National Research Centre on Plant Biotechnology, IARI, New Delhi, India



Use of Arabidopsis

The numbers of institutions working on *Arabidopsis* would be around 15-20. Some of the leading institutes are:

- Centre for Cellular & Molecular Biology, Hyderabad
- Indian Institute of Science, Bangalore
- National Institute of Technology, Durgapur
- University of Delhi South Campus, New Delhi
- National Institute of Plant Genome Research, New Delhi
- National Research Center on Plant Biotechnology, New Delhi
- Jawaharlal Nehru University, New Delhi
- Institute of Himalayan Biotechnology, Palampur
- Indian Institute of Science Education and Research, Thiruvananthapuram
- Indian Institute of Science Education and Research, Mohali
- Indian Institute of Science Education and Research, Bhopal
- Indian Institute of Technology, Roorkee
- National Center for Biological Sciences, Bangalore
- National Institute of Science Education and Research, Bhubaneswar
- Regional Center for Biotechnology, New Delhi

Open Resources for Arabidopsis Researchers

The researchers working on *Arabidopsis* now meet regularly and hold an annual meeting, where they share their work and whatever resource material have been generated they are willing to share. Some teachers of undergraduate colleges have shown keen interest and procured seeds to demonstrate the use of *Arabidopsis* as a model system for research. Prof J.P. Khurana's Lab at South Campus, New Delhi, has developed a State-of-art LED sources for red, far-red and blue light for photobiology work on *Arabidopsis*.

Conferences, Workshops and Outreach events

Some of the important conferences held in India where *Arabidopsis* research work were presented and discussed are listed below:

a) International Symposium on "Insight to Plant Biology in the Modern Era" held at Bose Institute, Kolkata, on

the occasion of Bose Institute Centenary Celebrations, from February 8-10, 2017. (Many talks presented used *Arabidopsis* as a system)

b) International Conference on Plant developmental Biology and 3rd National *Arabidopsis* meeting, held at NISER, Bhubaneswar, from December 12-14, 2017. (Organized by Dr. Kishore Panigrahi, NISER)

c) Indian Society for Plant Physiology (ISPP) organized National Conference of Plant Physiology-2017 (NCPP-2017) on "Emerging Role of Plant Physiology for Food Security and Climate Resilient Agriculture" during November 23-25, 2017 at Department of Plant Physiology, Indira Gandhi Krishi Vishwavidyalaya, Raipur, India. (Many talks presented used *Arabidopsis* as a system)

Selected Publications

Giri M, Singh N, Banday ZZ, Singh V, Ram H, Singh D, Chattopadhyay S, Nandi, AK (2017) GBF1 differentially regulates CAT2 and PAD4 transcription to promote pathogen defense in *Arabidopsis thaliana*. *Plant Journal* 91: 802-815.

Sardar A, Nandi AK, Chattopadhyay D. (2017) CBL-interacting protein kinase 6 negatively regulates immune response to *Pseudomonas syringae* in *Arabidopsis*. *J. Exp. Bot.* 68: 3573-3584.

Banday ZZ, Nandi AK (2017) *Arabidopsis thaliana* Glutathione-S-Transferase Theta 2 interacts with RS11/FLD to activate systemic acquired resistance. *Mol Plant Pathol.* (doi: 10.1111/mpp.12538).

Pratibha P, Singh SK, Srinivasan R, Bhat SR, Sreenivasulu Y (2017) Gametophyte development needs mitochondrial coproporphyrinogen III oxidase function in *Arabidopsis*. *Plant Physiol.* 174: 258-275.

Singh SK, Kumar V, Srinivasan R, Ahuja PS, Bhat SR, Sreenivasulu Y (2017) The TRAF Mediated Gametogenesis Progression (TRAMGaP) gene is required for megaspore mother cell specification and gametophyte development. *Plant Physiol.* 175: 1220-1237.

Rajarammohan S, Pradhan AK, Pental D, Kaur J (2017) Genome-wide association mapping in *Arabidopsis* identifies novel genes underlying quantitative disease resistance to *Alternaria brassicae*. *Mol Plant Pathol.* (doi: 10.1111/mpp.12654).

Sanyal SK, Kanwar PK, Samtani S, Kaur K, Jha SK and Pandey GK (2017) Alternative Splicing of CIPK3 Results in Distinct Target Selection to Propagate ABA Signaling in *Arabidopsis*. *Front. Plant Sci.* 8:1924. (doi: 10.3389/fpls.2017.01924).

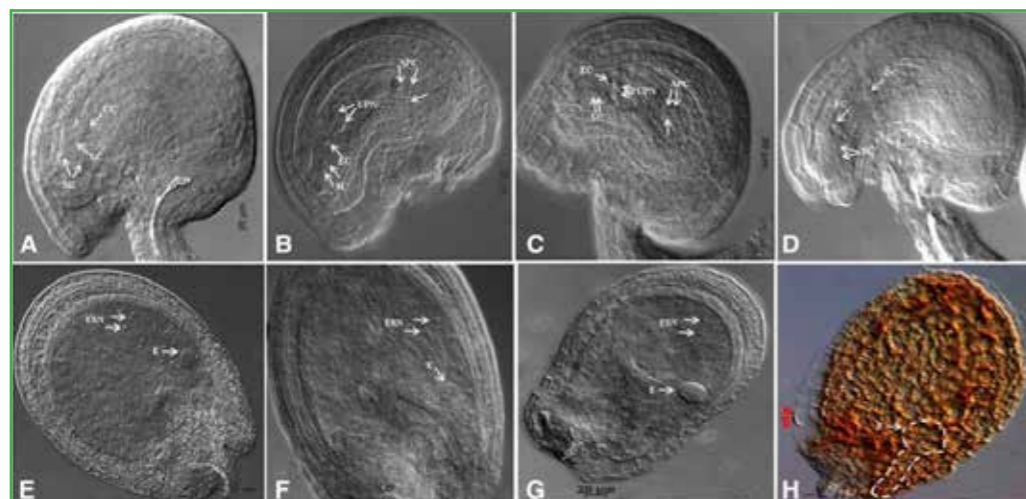


Figure 26. Showing abnormalities in pre-fertilized and post fertilized ovules of *Athemn1* mutants of *Arabidopsis*. A, Ovule in a wild-type. B, An *Athemn1-1* mutant ovule. C, An *Athemn1-2* mutant ovule. D, An ovule from *Athemn1-1* mutant complemented with the cDNA of the *AtHEMN1* gene. E, Post-fertilized ovule of a wild-type plant stage embryo. F and G, Post-fertilized ovules from the *Athemn1-1* mutant. H, Aborted seed in a mature silique from an *Athemn1-1* mutant (the degenerated globular embryo is marked with dotted lines). APC, Antipodal cell; CC, central cell; E, embryo; EC, egg cell; ESN, endosperm nucleus; SC, synergid cell; UPN, unfused polar nuclei. <https://doi.org/10.1104/pp.16.01482>

Burman N, Bhatnagar A, Khurana JP (2018) OsbZIP48, orthologous to AtHY5, exerts pleiotropic effects in light-regulated plant development. *Plant Physiol.* 176: 1262-1285.

Job N, Yadukrishnan P, Bursch K, Datta S, Johansson H (2018) Two B-box proteins regulate photomorphogenesis by oppositely modulating HY5 through their diverse C-terminal domains. *Plant Physiol.* 176: 2963-2976.

Jamsheer KM, Sharma M, Singh D, Mannully CT, Jindal S, Shukla BN, Laxmi A (2018) FCS-Like Zinc Finger 6 and 10 repress SnRK1 signaling in *Arabidopsis*. *Plant Journal* (doi: 10.1111/tj.13854)

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/>

Additional Information

The major thrust in research on *Arabidopsis* in India continues to be on unravelling molecular mechanisms involved in the development of plant organs, plant pathogen interaction, abiotic stress tolerance, light, hormone and sugar signaling.

The bZIP transcription factor, HY5, is known to be a key player in light signaling in *Arabidopsis*. Jiten Khurana's group has shown that one of the rice ortholog of AtHY5, OsbZIP48, although complements *Athy5* mutant in *Arabidopsis* but, unlike HY5, it is stable in dark and causes semi-dwarfism when over-expressed in rice, indicating that OsbZIP48 has acquired novel functions in rice during the course of evolution.

In addition, Sourav Datta's group has shown that the zinc finger transcription factors, BBX21 and BBX24, regulate HY5 activity post-transcriptionally, in opposite ways, and may be involved in executing contrasting functions in photomorphogenesis. In collaboration with Sudip Chattopadhyay, Ashish Nandi's lab has highlighted the role of GBF1 in both light and defense signaling. His group has also identified GSTT2 as a critical component of SAR signaling during pathogenesis. Using a diverse range of *Arabidopsis* accessions, Jagreet Kaur's lab showed that these accessions exhibit variable response, from complete resistance to high susceptibility to *Alternaria brassicae*; resistance to pathogen could also be attributed to multiple regions on the genome by GWAS.

Scientists from NRCPB and IHBT collaborated and characterized two novel mutants associated with the process of gametogenesis in *Arabidopsis*. Mutation in the *Arabidopsis* Coproporphyrinogen III oxidase gene (*AtHEMN1*), which adversely affected silique length, ovule number, and seed set. A block in tetrapyrrole biosynthesis in the *AtHEMN1* mutant resulted in increased ROS activity in floral tissues, thereby resulting in nonviable pollen and embryo sacs with unfused polar nuclei. Another mutation in a TRAF-like gene resulted in fewer ovules, pollen and reduced seed set. The mutation exhibited altered Megaspore Mother Cell (MMC) specification, and delayed programmed cell death in megaspores and the tapetum. This work establishes a novel link between a TRAF-like gene and reproductive development in plants

Israel

Sigal Savaldi-Goldstein
sigal@technion.ac.il
Technion - Israel Institute of Technology,
Haifa, Israel



Use of Arabidopsis

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

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

Research labs using *Arabidopsis* established by young PIs since 2016:

1. Dr. Yasmine Meroz, School of Plant Sciences and Food Security at Tel Aviv University (postdoctoral training in the lab of L. Mahadevan, Harvard University, USA).
2. Dr. Michal Lieberman Lazarovich, Ph.D. (Postdoctoral training in the lab of Prof. Jerzy Paszkowski, University of Geneva, Switzerland)
3. Dr. Tamar Avin-Wittenberg, The Hebrew University of Jerusalem, (postdoctoral training in the lab of Dr. Alisdair Fernie, Max Planck Institute of Molecular Plant Physiology, Germany).
4. Dr. Shilo Rosenwasser- Redox regulation of metabolism, stress acclimation, and cell death (Postdoctoral training in the lab of Prof. Assaf Vardi, Weizmann Inst., Israel).

Arabidopsis Projects

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

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

1. Deciphering the genetic and epigenetic factors affecting short- and long-term (trans-generational) phenotypic plasticity and adaptation to environmental changes.

2. Elucidating the mechanisms underlying the interactions of the environment with intrinsic developmental programs, and the role of phytohormones in stress responses.

3. Elucidating the key factors regulating plant metabolism and catabolism under stress with focus on the switch-points driving cell death versus cell vitality.

4. Dynamics of cell structures (cell wall, membranes, organelles, and protein complexes) and their role in stress responses.

5. Laying a foundation for a computational perspective of plant behavior under a changing environment, and predictions of selected genetic and environmental perturbations that will bring the plant to a desired metabolic or functional state.

(<http://www.icore-plants.tau.ac.il/>)
Effective funding, until 2021.

Open Resources for Arabidopsis Researchers

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

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

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

<http://www.plant-ditech.com/>

Bar Ilan University:

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

Hebrew University of Jerusalem: Establishment of Agilent 7200B Quadrupole Time-of-Flight Gas chromatography–mass spectrometer (GC-MS) for profiling of primary metabolites, organic acids and metabolic flux analysis in Arabidopsis.

Weizmann Institute: The lab of Asaph Aharoni established a set of Mass Spectrometry-based technologies to conduct cell-type level mapping of small molecules and proteins. They utilize Matrix-Assisted Laser Desorption Ionization (MALDI) and Desorption Electrospray Ionization (DESI) imaging for label-free and direct analysis of metabolites and proteins. At present, the aim is to image metabolites during biotic interactions (e.g. bacteria - root) and hormone metabolites at the cell-type resolution.

Conferences, Workshops and Outreach events

Summer course 2018: Plant Functional Phenotyping: from basic research to crop production

CropSym: Crop Abiotic Stress workshop. May 16-18, 2017, Faculty of Agriculture of the Hebrew University (Rehovot).

10th Symposium of the International Society of Root Research (ISRR10), 8-12 July, 2018, Kityat Yearim.

Publications

About 60 research articles employing Arabidopsis were published since the beginning of 2017 and until March 2018.

Major Funding Sources

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

European Research Council (ERC) (erc.europa.eu/)

Italy

Maura Cardarelli
maura.cardarelli@uniroma1.it
 IBPM-National Research Council (CNR),
 c/o Sapienza University of Rome,
 Department of Biology and Biotechnology, Rome.



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.

Open Resources for Arabidopsis Researchers

In all combined laboratories we have resources for molecular, physiological, histological and cellular techniques.

An innovative use of isolated Arabidopsis vacuoles as an heterologous system for the functional characterization of animal intracellular channels and transporters has been developed.

Different single and multiple Arabidopsis T-DNA insertion lines, as well as overexpressing lines, GUS-YFP- and GFP-tagged lines described in publications are available.

New Software Tools

Image software for light microscopy and epifluorescence.

Conferences, Workshops and Outreach events

- Giovanna Serino was the main organizer -together with the COST Proteostasis network- of the 2017 ZOMES IX Conference on “PCI complexes and Ubiquitin defining a hub for protein homeostasis” (www.zomesix.com) which took place in Rome, in February 2017 and included many talks focused on Arabidopsis by internationally renowned speakers.

- International Plant Science Conference (IPSC) Fisciano (SA), 12-15 September 2018.

Other events:

Ida Ruberti participates to the project Promotion of consumer health of the National technological cluster Agrifood.

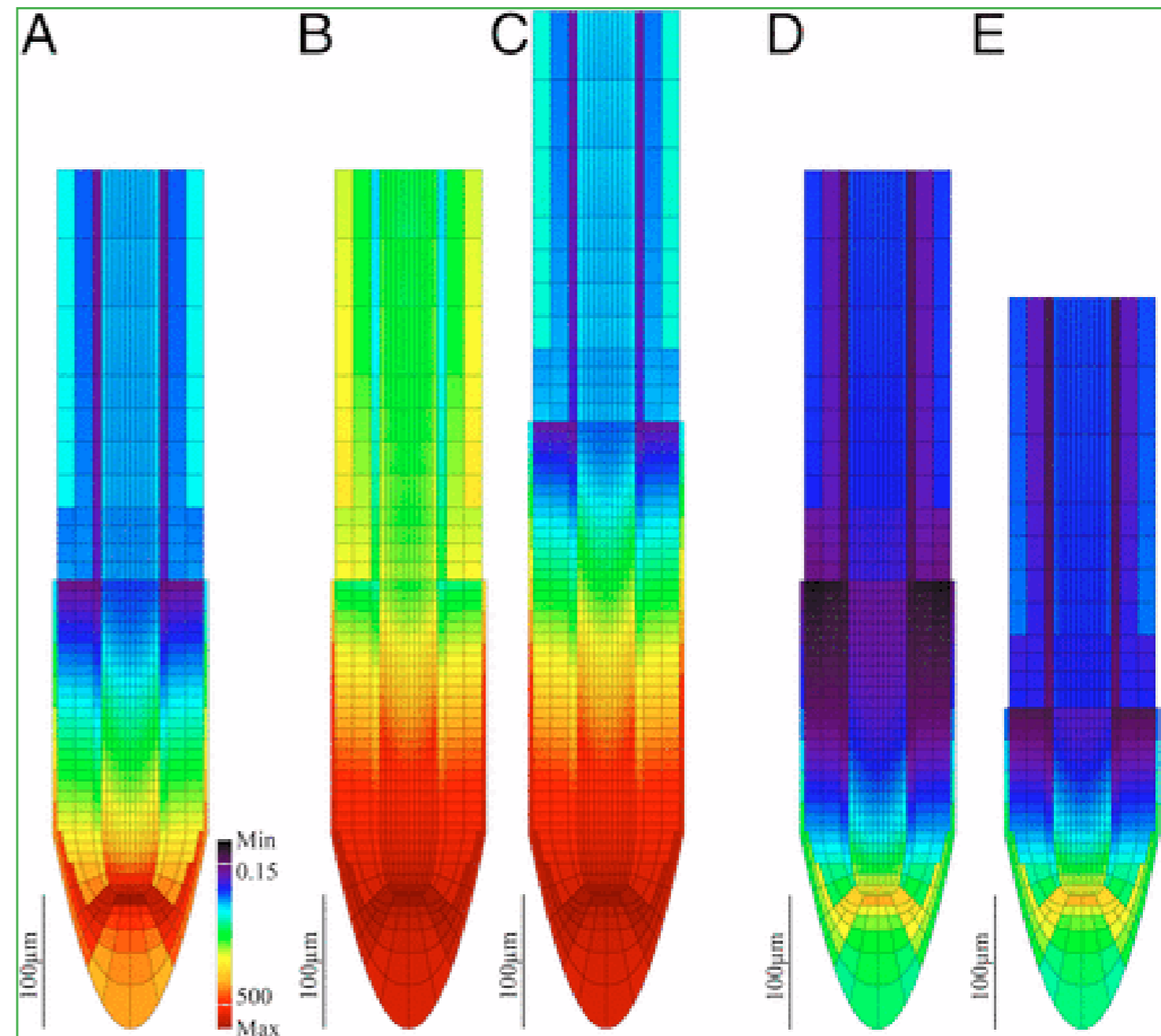


Figure 27 A Cytokinin-dependent regulation of auxin degradation and transport is essential to shape the auxin gradient. (A) Steady-state auxin heat map of wild-type root. (B) Predicted steady-state auxin pattern in simulation mimicking the effect of cytokinin depletion that results in increased PIN expression and decreased GH3.17 expression. Auxin minimum formation is affected. (C) The auxin minimum reestablishes only by increasing the number of MZ cells in the root layout. (D) Predicted steady-state auxin pattern in simulation mimicking the effect of exogenous cytokinin application that results in decreased PIN expression and increased GH3.17 expression. Such changes in PIN and GH3.17 expression prevent the formation of the auxin minimum. (E) The auxin minimum is reestablished by decreasing the number of MZ cells in the root layout. (Scale bars, 100 μm.) Color coding represents auxin concentration levels. Piecewise linear color bar indicates absolute and relative log auxin concentration for all simulations. <https://doi.org/10.1073/pnas.1705833114>

Several Arabidopsis researchers from Milan and Rome were involved in planning and organizing the Fascination of Plants day under the umbrella of EPSO (European Plant Science Organisation) on May 2017.

Selected Publications

Di Mambro R, De Ruvo M, Pacifici E, Salvi E, Sozzani R, Benfey PN, Busch W, Novak O, Ljung K, Di Paola L, Marée AFM, Costantino P, Grieneisen VA, Sabatini S. Auxin minimum triggers the developmental switch from cell division to cell differentiation in the Arabidopsis root. Proc Natl Acad Sci U S A. 2017 ;114:E7641-E7649. doi: 10.1073/pnas.1705833114.

Fasani E, Dal Corso G, Varotto C, Li M, Visioli G, Mattarozzi M and Furini A, The MTP1 promoters from *Arabidopsis halleri* reveal cis-regulating elements for the evolution of metal tolerance
New Phytologist (2017) 214: 1614–1630 doi: 10.1111/nph.14529

Lionetti V, Fabri E, De Caroli M, Hansen A R., Willats W G.T, Piro G, Bellincampi D
Plant Phys (2017) Mar;173(3):1844-1863 doi.org/10.1104/pp.16.01185

I. Pafumi, M. Festa, F. Papacci, L. Lagostena, C. Giunta, PVK Gutla, L. Cornara, A. Favia, F. Palombi, F. Gambale, A. Filippini and A. Carpaneto
Naringenin impairs two pore channel-2 activity and inhibits VEGF-induced angiogenesis
Scientific Reports (2017) 7:5121

B. Giuntoli, F Licausi, H van veen, P Perata
Functional Balancing of the Hypoxia Regulators RAP2.12 and HRA1 Takes Place in vivo in *Arabidopsis thaliana*
Plants Front. Plant Sci., 25 April 2017

Reyes-Olalde JI, Zúñiga-Mayo VM, Serwatowska J, Chavez Montes RA, Lozano-Sotomayor P, Herrera-Ubaldo H, Gonzalez-Aguilera KL, Ballester P, Ripoll JJ, Ezquer I, Paolo D, Heyl A, Colombo L, Yanofsky MF, Ferrandiz C, Marsch-Martínez N, de Folter S. The bHLH transcription factor SPATULA enables cytokinin signaling, and both activate auxin biosynthesis and transport genes at the medial domain of the gynoecium. PLoS Genet. 2017 Apr 7; 13(4):e1006726. doi: 10.1371/journal.pgen.1006726.

Fattorini L, Veloccia A, Della Rovere F, D'Angeli S, Falasca G, Altamura MM. Indole-3-butyric acid promotes adventitious rooting in *Arabidopsis thaliana* thin cell layers by conversion into indole-3-acetic acid and stimulation of anthranilate synthase activity. BMC Plant Biol. 2017;17:121.

A. Carpaneto, A. Boccaccio, L. Lagostena, E. Di Zanni, J. Scholz-Starke
The signaling lipid phosphatidylinositol-3,5-bisphosphate targets plant CLC-a anion/H⁺ exchange activity. EMBO Reports (2017) 18:1100-1107

Mravec J, Kracun SK, Rydahl MG, Westereng B, Pontiggia D, De Lorenzo G, Domozych DS, Willats WGT.
An oligogalacturonide-derived molecular probe demonstrates the dynamics of calcium-mediated pectin complexation in cell walls of tip-growing structures. Plant J. 2017 Aug;91(3):534-546. doi: 10.1111/tpj.13574.

Major Funding Sources

The Italian Ministry of Education, University and Research funded:

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

- Project FIRB (Futuro in Ricerca 2014-2017) for young researcher. Principal investigator Raffaele Dello Iorio, Sapienza University of Rome;

- Project SIR(2015-2018) for independence of young researcher, on 'MADS box transcription factor SHORT VEGETATIVE PHASE, understanding the molecular mechanism and involvement in sense and antisense transcript regulation. RBS114BTZR. Coordinator Veronica Gregis;

-Local funding from: Sapienza University of Rome and University of Milan

Other funding:

- European Commission's 7th Framework Programme ERA-CAPS ERA-NET grant "SIPIS: Decoding ligand-receptor specificities of LysM-proteins in plant immunity and symbiosis"

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

Additional Information

In the last years *Arabidopsis* research in Italy is getting little financial support.

However in 2018 National basic research programmes will be re-funded, and this will give to some groups working on *Arabidopsis* the possibility to continue research.

Japan

Motoaki Seki, motoaki.seki@riken.jp
RIKEN CSRS

David Gifford, david.gifford@riken.jp
RIKEN CSRS

Masatomo Kobayashi
masatomo.kobayashi@riken.jp
RIKEN BRC



Use of Arabidopsis

The number of labs in Japan that use *Arabidopsis*: **350**

The Leading Research Institutes and Universities:

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) (<http://www.csr.riken.jp/en/>). CSRS (Director Kazuo Shinozaki), established in 2013 to conduct basic research integrating plant scientists, chemists and chemical biologists to work for solutions to critical scientific, technical and social issues with special focus on sustainable production of natural resources and useful materials, and resilient agriculture under climate change. CSRS contributes to many goals of the United Nations Sustainable Development Goals (SDGs) and COP21 Paris Agreement goals by applied research through interdisciplinary R&D for sustainable production of energy, efficient engineering and production of useful plant biomass, renewable chemical materials and bioplastics, efficient catalysts, as well as crop production under climate change. In the next phase of CSRS, data science and chemical biology become more important for the advancement of plant science. In addition to *Arabidopsis*, CSRS uses other plants such as *Brachypodium*, cassava, rubber, sorghum and others.

RIKEN National Science Institute - BioResource Center (BRC) (<http://epd.brc.riken.jp/en/>), (plant@brc.riken.jp). The Experimental Plant Division (Masatomo Kobayashi) collects, preserves and distributes plant resources developed in Japan. The project is funded by the Japanese government through the National BioResource Project (NBRP, <http://www.nbrp.jp/index.jsp>). The *Arabidopsis* resources in RIKEN BRC include seeds (mutants, transgenic lines, and natural accessions), DNA materials (full-length cDNA clones, ORF clones of transcription factors, TAC clones, and vectors), and cultured cells (T87 and At wt cell lines). The center also distributes full-length cDNA clones and cultured cells of model plants such as rice, *Brachypodium distachyon* and tobacco to the international research community.

Kazusa DNA Research Institute (<http://www.kazusa.or.jp/>). Laboratory of Plant Genomics and Genetics, Plant DNA Analysis Group, Metabolomics Team, Bioresources team, Biomass Team. Genome Informatics Group developed the

portal site Plant Genome DataBase Japan PGDBj (<http://pgdbj.jp/?ln=en>) integrating databases related to plant omics studies. Manually curated literature information on DNA markers of 65 plants.

Creation of fundamental technologies contribute to the elucidation and application for the robustness in plants against environmental changes" Started 2015, Core Research for Evolutional Science and Technology (JST-CREST) (<http://bit.ly/1TyzoDT>) coordinated with PRESTO (Sakigake). This project will continue to 2022. CREST is led by Satoshi Tabata (Kazusa DNA Research Inst.). Two PRESTO programs are led by Kiyotaka Okada and Masashi Ninomiya, respectively.

AIST, National Institute of Advanced Industrial Science and Technology - BioProduction Research Institute (<https://unit.aist.go.jp/bpri/>). Plant research includes studies of plant gene regulation, plant molecular biology, plant biotechnology, biomaterial production, and genetic resources. Plant Gene Regulation Research Group (<http://bit.ly/1QlwEjP>) focuses on study of plant transcription factors and related molecules and techniques. Group developed CRES-T gene-silencing and other technologies for functional analysis and engineering of important traits in model and economic plants.

Nagoya University, WPI ITbM (<http://www.itbm.nagoya-u.ac.jp/>). World Premier International Research Center (WPI) Institute of Transformative Bio-Molecules (ITbM) of Nagoya University is the first MEXT WPI institute to study plant science. Ambitious full-scale collaboration between synthetic chemists, plant and animal biologists, and theoreticians led by Director Kenichiro Itami, Vice-director Tetsuya Higashiyama and others.

Determining principles in the birth of new plant species: elucidation of lock-and-key molecular systems in sexual reproduction (<http://bit.ly/2mrqD4T>). Project goal to clarify primary mechanism in the birth of new species by revealing a whole picture of molecule-leveled understanding of "lock-and-keys" in plant reproduction through active interdisciplinary collaborative research. Scientific Research on Innovative Areas MEXT Grant-in Aid Project FY2016-2020. Multi-organization representative: Tetsuya Higashiyama, ITbM/Nagoya University. Integrative system of autonomous environmental signal recognition and memorization for plant plasticity (<http://www.rs.tus.ac.jp/plantmemory/en/>). Project goal to clarify distributed response of cells and tissues of plants and determine how plants control such information through plant unique whole-organism dynamic signal transduction system in response to environmental stimuli. Scientific Research on Innovative Areas MEXT Grant-in Aid Project FY2015-2019. Multi-organization representative: Toshinori Kinoshita, ITbM/Nagoya University.

University of Tokyo. Multidimensional Exploration of Logics of Plant Development (2012-2017) (<http://logics.plantdev.biol.s.u-tokyo.ac.jp/en/>). Project to delineate systems coordinating intercellular and intracellular signals,

functions of key differentiation genes, and control of metabolism, under combined efforts of 9 core research groups, 4 supporting facilities/teams, and 19 research groups (2013-2017) using multiple model species not only Arabidopsis but also a new model of land plants, *Marchantia polymorpha*. Led by Hirokazu Tsukaya, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Nara Institute of Science and Technology. Principles of pluripotent stem cells underlying plant vitality (2017-2022)(<http://www.plant-stem-cells.jp/>). This project aims to answer the key questions: How do plants augment stem cell populations, and how do plants maintain them over long periods of time? The project members investigate the machinery of stem cell division and the regulatory system underlying maintenance of pluripotency and genome integrity. Led by Masaaki Umeda, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

National Institute for Basic Biology. (2017-2022)(<http://photosynthesis.nibb.ac.jp/>). Project goal is to elucidate the regulatory mechanisms of photosynthesis by incorporating a new perspective, the regulation of the proton motive force into basic photosynthesis research with the goal of improving photosynthetic efficiency. We expect to establish strategies to re-optimize the photosynthetic performance under any environment. Led by Jun Minagawa, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Okayama University. Innovations for Light-Energy Conversion (2017-2022)(<http://photoenergy-conv.net/>). Program goal to elucidate the molecular mechanisms of light-energy harvesting and their utilization reactions by various photosynthetic protein-complexes, especially the photosynthetic water-oxidation enzyme photosystem II, and their application to the development of artificial photosynthetic systems. Led by Jian-Ren Shen, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Tohoku University. The Plant Cell Wall as Information Processing System (2012-2017) (<https://www.plantcellwall.jp/en/>). Program goal to elucidate molecular processes for information processing and self-regulation capabilities of the cell wall by understanding molecular mechanisms by which land plants sense and interact with environment via information processing systems in cell walls. Led by Kazuhiko Nishitani, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Open Resources for Arabidopsis Researchers

RIKEN CSRS
PRIME Platform for RIKEN Metabolomics (<http://prime.psc.riken.jp/>). Arabidopsis metabolomics platform publicly available platform resources:

- Widely-targeted metabolomics (in Drop Met <http://bit.ly/2HU2AC1>)

- AtMetExpress Arabidopsis metabolome expression database (<http://bit.ly/1P2YByw>)
- LC-MCS Branch (<http://bit.ly/1P2Zhtnt>)
- PRIME Web Applications
- MeKO Metabolite Profiling Database for Knock-Out Mutants in Arabidopsis (MeKO) (<http://bit.ly/1QQBWYI>)
- PRIMELink integrates 3 above databases (AtMetExpress, MS2T and ReSpect) for bi-directional search from gene or metabolite (<http://bit.ly/1RCX4Bc>)
- ReSpect RIKEN MSn Spectral database for phytochemicals (<http://bit.ly/1P2Zalv>)
- Distribution and Redistribution
- Drop Met mass-spec based metabolome analyses (<http://bit.ly/1LVEfwq>)
- Other RIKEN CSRS developed tools and resources:
- AtGenExpress Arabidopsis Gene Expression profile database (<http://bit.ly/1P2YT8v>)
- KNAPsack Comprehensive species-metabolite relationship database (<http://bit.ly/1LFFkyZ>) (NAIST)
- Plant-PrAS (Plant-Protein Annotation Suite) database of physicochemical and structural properties, and novel functional region in plant proteomes (<http://plant-pras.riken.jp/>)

RIKEN BRC

- Resources including seed catalogs (<http://epd.brc.riken.jp/en/>)
- Experimental Plant Division Arabidopsis Seed, DNA, Cell line (<http://bit.ly/2mri7Tq>)
- Phenotype database of natural accessions (<http://bit.ly/2mrkm9m>)
- The ABRANA (Arabidopsis-Brassica Network Access) DB. Resources related with TAIR cDNAs and annotations through sequences (<http://www.abrana.jp/>)
- Kazusa DNA Research Institute
- - KOMICS Kazusa Metabolomics Database portal (<http://bit.ly/1QWjzok>)
- - MassBase: a plant metabolome database (<http://bit.ly/1Rlf9Dd>)
- - MS-MS Fragment Viewer database (<http://bit.ly/1QWjPUm>)
- - PGDBj Plant Genome DataBase Japan (<http://pgdbj.jp/?ln=en>)
- - KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (<http://kpv.kazusa.or.jp/>)
- Gifu University
- - Plant Promoter Database, ppdb (<http://ppdb.agr.gifu-u.ac.jp/ppdb/cgi-bin/index.cgi>) updated ver. 3.0. Large TSS data of NGS incorporated into database.

New Software Tools

Kazusa DNA Research Institute

- MFSearcher molecular formula searcher (<http://bit.ly/1RN2BFp>)

 RIKEN CSRS
 PRIME Platform for RIKEN Metabolomics (<http://prime.psc.riken.jp/>). Arabidopsis metabolomics platform publicly

available platform resources:
 PRIME Web Applications
 - HiFi Heteroatom-containing Ion Finder (<http://bit.ly/1nBxjJ6>)
 - PASMmet - Prediction, Analysis and Simulation of Metabolic Reaction Networks (<http://pasmnet.riken.jp/>)

Conferences, Workshops and Outreach events

- Mar. 28-30, 2018: 59th Annual Meeting of Japanese Society of Plant Physiologists. Sapporo Convention Center (<http://www.knt.co.jp/ec/2018/jssp2018/en.html>)

Selected Publications

- Ariga H, Katori T, Tsuchimatsu T, Hirase T, Tajima Y, Parker JE, Alcázar R, Koornneef M, Hoekenga O, Lipka AE, Gore MA, Sakakibara H, Kojima M, Kobayashi Y, Iuchi S, Kobayashi M, Shinozaki K, Sakata Y, Hayashi T, Saijo Y and Taji T (2017) NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. *Nature Plants* 3:17072. doi:10.1038/nplants.2017.72.
- Chen P, Takatsuka H, Takahashi N, Kurata R, Fukao Y, Kobayashi K, Ito M and Umeda M (2017) Arabidopsis R1R2R3-Myb proteins are essential for inhibiting cell division in response to DNA damage. *Nat Commun*. 8(1):635. doi: 10.1038/s41467-017-00676-4.
- Inagaki S, Takahashi M, Hosaka A, Ito T, Toyoda A, Fujiyama A, Tarutani Y, and Kakutani T (2017) Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis. *EMBO J*. 36: 970-980. doi:10.15252/embj.201694983
- Kim JM, To KT, Matsui A, Tanoi K, Kobayashi NI, Matsuda F, Habu Y, Ogawa D, Sakamoto T, Matsunaga S, Bashir K, Rasheed S, Ando M, Takeda H, Kawaura K, Kusano M, Fukushima A, Endo AT, Kuromori T, Ishida J, Morosawa T, Tanaka M, Torii C, Takebayashi Y, Sakakibara H, Ogihara Y, Saito K, Shinozaki K, Devoto A and Seki M (2017) Acetate-mediated novel survival strategy against drought in plants. *Nature Plants* 3: 17097. doi:10.1038/nplants.2017.97.
- Kosetsu K, Murata T, Yamada M, Nishina M, Boruc J, Hasebe M, Damme DV and Goshima G (2017) Cytoplasmic MTOCs control spindle orientation for asymmetric cell division in plants. *Proc Natl Acad Sci USA* 114(42):E8847-E8854. doi: 10.1073/pnas.1713925114.
- Li W, Nguyen KH, Chu HD, Ha CV, Watanabe Y, Osakabe Y, Leyva-González MA, Sato M, Toyooka K, Voges L, Tanaka M, Mostofa MG, Seki M, Seo M, Yamaguchi S, Nelson DC, Tian C, Herrera-Estrella L and Tran LSP (2017) The karrikin receptor KAI2 promotes drought resistance in *Arabidopsis thaliana*. *PLoS Genet*. 13(11):e1007076. doi: 10.1371/journal.pgen.1007076.

- Ohkubo Y, Tanaka M, Tabata R, Ohnishi MO and Matsubayashi Y (2017) Shoot-to-root mobile polypeptides involved in systemic regulation of nitrogen acquisition. *Nature Plants* 3: 17029. doi:10.1038/nplants.2017.29.

- Selvaraj MG, Ishizaki T, Valencia M, Ogawa S, Dedicova B, Ogata T, Yoshiwara K, Maruyama K, Kusano M, Saito K, Takahashi F, Shinozaki K, Nakashima K, Ishitani M (2017) Overexpression of an *Arabidopsis thaliana* galactinol synthase gene improves drought tolerance in transgenic rice and increased grain yield in the field. *Plant Biotechnol J* 15(11):1465-1477. doi: 10.1111/pbi.12731.

- Suga M, Akita F, Sugahara M, Kubo M, Nakajima Y, Nakane T, Yamashita K, Nakabayashi M, Umena Y, Yamane T, Nakano T, Suzuki M, Masuda T, Inoue S, Kimura T, Nomura T, Yonekura S, Yu L.-J, Sakamoto T, Motomura T, Chen J.-H, Kato Y, Noguchi T, Tono K, Joti Y, Kameshima T, Hatsui T, Nango E, Tanaka R, Naitow H, Matsuura Y, Yamashita A, Yamamoto M, Nureki O, Yabashi M, Ishikawa T, Iwata S, Shen JR (2017) Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. *Nature* 543:131-135. doi: 10.1038/nature21400.

- Ushijima T, Hanada K, Gotoh E, Yamori W, Kodama Y, Tanaka H, Kusano M, Fukushima A, Tokizawa M, Yamamoto YY, Tada Y, Suzuki Y and Matsushita T (2017) Light controls protein localization through phytochrome-mediated alternative promoter selection. *Cell* 171: 1316-1325. doi:10.1016/j.cell.2017.10.018.

Major Funding Sources

- RIKEN is supported by MEXT.
- Kazusa projects are supported by Chiba-Prefecture.
- Grants-in-Aid for Science from MEXT (<http://www.jsps.go.jp/english/e-grants/>)
- CREST of Japan Science and Technology Corporation (<http://bit.ly/2218avZ>)
- ALCA (Advanced Low Carbon Technology Research and Development Program) (<http://www.jst.go.jp/alca/en/index.html>)
- Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project. (<http://www.jst.go.jp/inter/english/sicorp/index.html>)
- "Impulsing Paradigm Change through Disruptive Technologies" (ImPACT) (<http://www.jst.go.jp/impact/en/outline.html>)
- MEXT "Cross-ministerial Strategic Innovation Promotion Program" (SIP) in 2014. (<http://www.mext.go.jp/english/topics/1345957.htm>)

Additional Information

Current Arabidopsis Projects
 Kazusa DNA Research Institute
 Kazusa Metabolomics Database (KOMICS) web portal to databases, tools and other information was developed

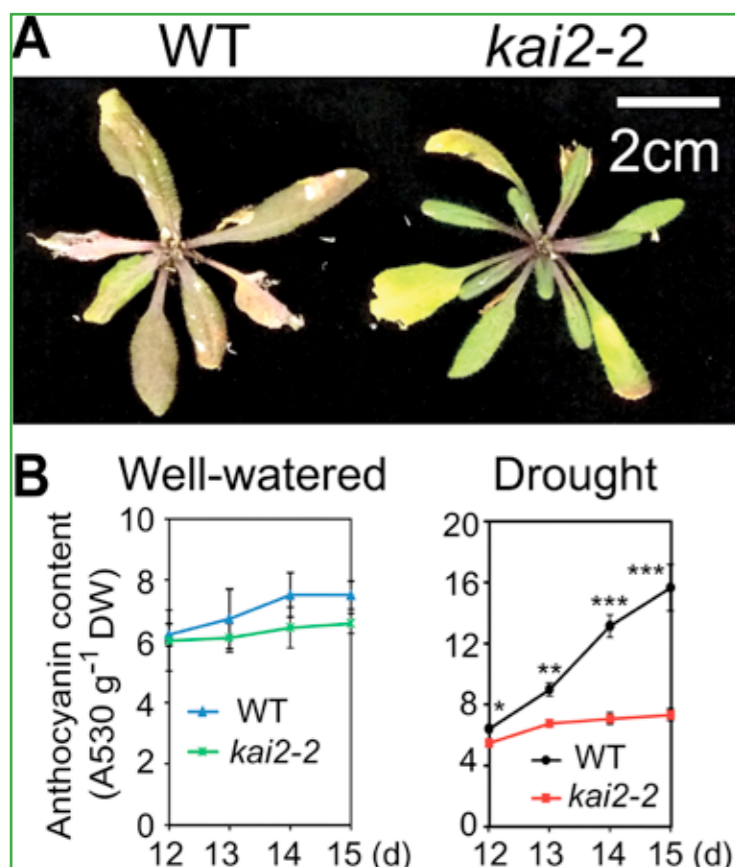


Figure 28. Anthocyanin production in *kai2-2* and WT plants. (A) *kai2-2* and WT plants were grown for 5 weeks, and watering was withheld for 10 days. Inflorescences were cut from representative plants before photographing. (B) Anthocyanin content in *kai2-2* and WT plants under well-watered and drought conditions. Data represent the means and standard errors (n = 4 plants). Asterisks indicate significant differences between the genotypes under drought conditions as determined by a Student's t-test, *P < 0.05; **P < 0.01; ***P < 0.001. <https://doi.org/10.1371/journal.pgen.1007076>

related TAIR gene models and annotations, by specifying a Resource ID, a TAIR AGI code or a keyword. All SABRE resources are available from the core facilities of NBRP (National BioResource Project) (<http://sabre.epd.brc.riken.jp/>)

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) Metabolome platform using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi, Tetsuya Sakurai). CSRS established the Arabidopsis metabolomics platform (<http://prime.psc.riken.jp/>), consisting of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics.

MassBank (Masanori Arita, Takaaki Nishioka, K. Saito) Public repository of mass spectral data for sharing spectra among research communities. The data is useful for chemical identification and structure elucidation of metabolites detected by mass spectrometers. (<http://www.massbank.jp/en/about.html>)

Plant-PrAS (Plant-Protein Annotation Suite) (A. Kurotani, Y. Yamada, AA. Tokmakov, Y. Kuroda, Y. Fukami, K. Shinozaki, T. Sakurai) Analyzed predicted multiple physicochemical and secondary structural parameters using over 20 analysis tools with whole amino acid sequences from genomes of representative plant species (*Arabidopsis thaliana*, *Glycine max*, *Populus trichocarpa*, *Oryza sativa*, *Physcomitrella patens*, and *Cyanidioschyzon merolae*) for which genome sequencing was achieved, and organized those results as Plant-PrAS. (<http://plant-pras.riken.jp/>)

RIPPS (RIKEN Plant Phenotyping System) (K. Shinozaki, Miki Fujita, Kaoru Urano, and Takaya Tanabata) Automated system for evaluating plant growth under environmental stress conditions developed by the Gene Discovery Research Group of CSRS. RIPPS provides high-throughput and accurate measurements of plant traits, facilitating understanding of gene function in a wide range of environmental conditions (<http://bit.ly/1sObBEE>)

PASMet - Prediction, Analysis and Simulation of Metabolic Reaction Networks (Kansuporn Sriyudthsak, Masami Hirai) PASMet is a web-based platform for predicting, modelling and analyzing metabolic systems. Non-commercial and user-friendly tool to assist non-experts in mathematical modelling, in silico computing or programming to work on computational biology (<http://pasmnet.riken.jp/>)

High-throughput genome-wide biochemical analysis using wheat germ cell-free-based protein array technology. The method developed by Proteo-Science Center of Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) (<http://bit.ly/21ssVcQ>) and RIKEN CSRS (M. Seki and K. Shinozaki) is useful for in vitro screening of substrate protein, interacting protein or chemical compound.

through plant metabolomics studies of Daisuke Shibata, including integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, co-expressed gene search tools and regulatory network research. (<http://www.kazusa.or.jp/komics/en/>)

AIST Bioproduction Research Institute, Gene Regulation Research Group CRES-T was applied to more than 1,600 Arabidopsis transcription factors and most T2 seeds were harvested individually. For transcriptional repressors, the group produced more than 300 VP16-fused constructs and harvested individual T2 seeds. The group also prepared Gateway entry clones of ca. 2,000 transcription factors (without stop codon) in collaboration with M. Matsui group in RIKEN. The group developed yeast one-/two-hybrid library using the entry clones and established high-throughput screening system. (<http://bit.ly/1QIwEjP>)

RIKEN National Science Institute - BioResource Center (BRC) SABRE2: database connecting plant EST/Full-Length cDNA Clones with Arabidopsis information. Plant resources with homologous genes are searched, together with

Hormonome platform and RIKEN Plant Hormone Research Network: (Hitoshi Sakakibara, Mitsunori Seo) CSRS established highly sensitive high-throughput phytohormone quantification platform consisting of mass spectrometry-based technology. Platform is conducting a wide range of collaborative research in plant hormone biology (<http://hormones.psc.riken.jp/>)

JST-NSF "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society" (<http://bit.ly/2HU5Car>), research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and K. Saito (RIKEN), Oliver Fiehn (Univ. of California at Davis) and M. Arita (NIG).

U. Tokyo, RIKEN, JIRCAS, with others of IRRI, CIAT, CIMMYT, Embrapa DREB project: Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat supported by MAFF and JIRCAS; (<http://bit.ly/227H1Tp>) (Kazuko Yamaguchi-Shinozaki U. Tokyo, Kazuo Shinozaki RIKEN, Kazuo Nakashima JIRCAS and others of IRRI, CIAT, CIMMYT, Embrapa) After identifying and applying DREB genes in Arabidopsis, DREB gene function in stress tolerance were recognized as well conserved in any important crops. Project develops stress-tolerant soybean, rice and wheat. Recently, transgenic rice lines with Arabidopsis *GolS2* gene were shown to produce higher amount of seeds than non-transgenic rice in the dry field conditions

New Zealand

Lynette Brownfield lynette.brownfield@otago.ac.nz 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, Dunedin, New Zealand.

Plant Science Central, 4-6 July, 2017, Palmerston North, New Zealand.

Queenstown Molecular Biology Meeting (including a Plant Satellite) August 28-31, Queenstown, New Zealand.

Selected Publications

Brendolise C, Espley RV, Lin-Wang K, Laing W, Peng Y, McGhie T, Dejnopratt S, Tomes S, Hellens RP and Allan AC (2017) Multiple copies of a simple MYB-binding site confers trans-regulation by specific flavonoid-related R2R3 MYBs in diverse species. *Frontiers in Plant Science* 8: 1864.

About, S, Leask, MP, Varghese S, Yi J, Peters B, Conze LL, Köhler C and Brownfield L (2017). The meiotic regulator JASON utilizes alternative translation initiation sites to produce differentially localized forms. *Journal of Experimental Botany*, 68: 4205-4217.

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

Jibrán R, Hunter DA, Cooney J, Tahir J and Dijkwel P (2017). Arabidopsis AGAMOUS regulates sepal senescence by driving jasmonate production. *Frontiers in Plant Science* 8: 2101.

Pathirana R, West P, Hedderley D and Eason J. (2017). Cell death patterns in Arabidopsis cells subjected to four physiological stressors indicate multiple signalling pathways and cell cycle phase specificity. *Protoplasma*, 254: 635-647.

Ridge S, Deokar A, Lee R, Daba K, Macknight RC, Weller J L and Tar'an, B (2017). The chickpea Early Flowering 1 (Efl1) locus is an ortholog of Arabidopsis ELF3. *Plant Physiology*, 175: 802-815.

Major Funding Sources

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

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

- Core funding to Crown Research Institutes

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

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

- The Agricultural and Marketing Research and

Norway

Thorsten Hamann
thorsten.hamann@ntnu.no
 Norwegian University of Science and Technology



wheat and Norway spruce. The scientific activities of the well-organized conference were complemented by the social program involving a conference dinner aboard the historic side-wheel paddle steam boat "Skibladner" while exploring Lake Mjøsa.

Selected Publications

With respect to publication activities, 2017 was a very good year with more than 30 articles having been published that contain contributions from members of the Norwegian Arabidopsis community. Here attention is being drawn to just a few representative publications in journals like PNAS, J. Ex. Bot. and Plant, Cell and Environment, which illustrate nicely the breadth of Arabidopsis research in Norway. The articles cover topics like endosperm-based hybridization barriers explaining gene flow (Lafon-Placette *et al.*, 2017); peptide-based signaling processes during stress response and abscission (Vie *et al.*, 2017) and the impact of protein phosphatase 2A methylation on environmental stress responses (Creighton *et al.*, 2017).

Creighton, M. T., Kolton, A., Kataya, A. R. A., Maple-Grodem, J., Averkina, I. O., Heidari, B. and Lillo, C. (2017). Methylation of protein phosphatase 2A-Influence of regulators and environmental stress factors. *Plant. Cell Environ.* 40, 2347–2358.

Lafon-Placette, C., Johannessen, I. M., Hornslien, K. S., Ali, M. F., Bjerkan, K. N., Bramsiepe, J., Glöckle, B. M., Rebernig, C. A., Brysting, A. K., Grini, P. E., *et al.* (2017). Endosperm-based hybridization barriers explain the pattern of gene flow between *Arabidopsis lyrata* and *Arabidopsis arenosa* in Central Europe. *Proc. Natl. Acad. Sci.* 114, E1027–E1035.

Vie, A. K., Najafi, J., Winge, P., Cattan, E., Wrzaczek, M., Kangasjärvi, J., Miller, G., Brembu, T. and Bones, A. M. (2017). The IDA-LIKE peptides IDL6 and IDL7 are negative modulators of stress responses in *Arabidopsis thaliana*. *J. Exp. Bot.* 68, 3557–3571.

Major Funding Sources

Research Council of Norway
www.rcn.no

The annual plant biology conference was also financially supported through grants by the Norwegian research council and the Scandinavian Plant Physiology Society
www.spps.se

Use of Arabidopsis

In 2017 the Norwegian plant biology community held their national conference in Hamar in central Norway with around 60 attendees from all Norwegian universities and research institutes as well as invited speakers from eight different countries. The scientific program during the two-day event covered a diverse range of topics in lectures as well as workshops and public panels where questions like "how to inspire the next generation of plant scientists?" or "Public and political acceptance for genome editing in plant based food production" were discussed. In parallel Karin Metzloff from the European Plant Science Organization (EPSO) gave a presentation introducing the organization, its aims and activities.

The scientific program was quite diverse illustrated by the examples like: heritable phenotypic changes induced by epigenetic reprogramming; gene and genome dosage on hybridization barriers in *Arabidopsis lyrata* and *A.arenosa*; PP2A as a regulator of methionine metabolism in plant immunity and linking CALPAIN-controlled development to gene expression networks through transcriptomics. It was also interesting to see how often Arabidopsis had originally acted as foundation for targeted follow up research projects in crop species like strawberry,

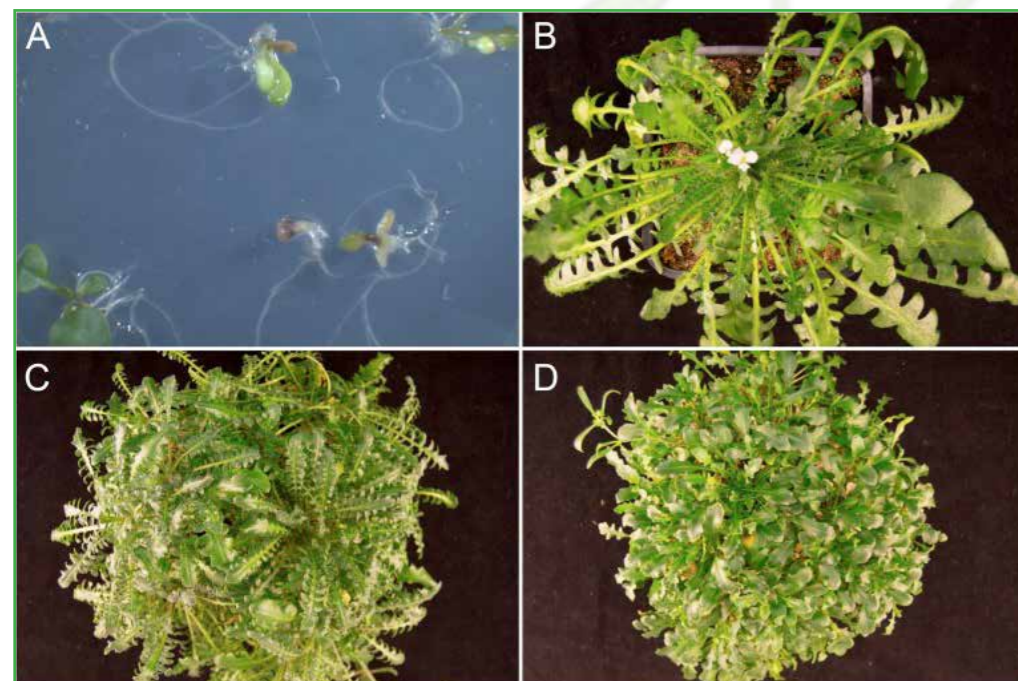
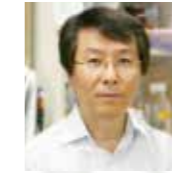


Figure 29. Viable *A. lyrata* × *A. arenosa* hybrid plants obtained from in vitro embryo rescue. (A) Three-week-old *A. lyrata* × *A. arenosa* seedlings grown on MS plate. (B) Fully grown *A. lyrata* × *A. arenosa* plant transferred to soil. (C) Fully grown *A. arenosa* plant. (D) Fully grown *A. lyrata* plant.
<https://doi.org/10.1073/pnas.1615123114>

South Korea

Inhwan Hwang
ihhwang@postech.ac.kr
 Pohang University of Science and Technology



Use of Arabidopsis

100 Institutions and 500 labs

Conferences, Workshops and Outreach events

- Plant Winter Conference of Korean Society of Plant Biologists
- Annual meeting of Korean Society of Plant Biologists
- Annual meeting of Korean Society of Molecular and Cell Biologists
- The first Asian conference on Plant-based Pharmaceuticals.

Selected Publications

Kim JH, Cho SK, Oh TR, Ryu MY, Yang SW, Kim WT. (2017) MPSR1 is a cytoplasmic PQC E3 ligase for eliminating emergent misfolded proteins in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 114:E10009-E10017.

Lee DH, Park SJ, Ahn CS, Pai HS. (2017) MRF Family Genes Are Involved in Translation Control, Especially under Energy-Deficient Conditions, and Their Expression and Functions Are Modulated by the TOR Signaling Pathway. *Plant Cell.* 29:2895-2920.

Lee JH, Jung JH, Park CM. (2017) Light Inhibits COP1-Mediated Degradation of ICE Transcription Factors to Induce Stomatal Development in Arabidopsis. *Plant Cell.* 29:2817-2830.

Khare D, Choi H, Huh SU, Bassin B, Kim J, Martinoia E, Sohn KH, Paek KH, Lee Y. (2017) Arabidopsis ABCG34 contributes to defense against necrotrophic pathogens by mediating the secretion of camalexin. *Proc Natl Acad Sci U S A.* 114:E5712-E5720.

Ahn G, Kim H, Kim DH, Hanh H, Yoon Y, Singaram I, Wijesinghe KJ, Johnson KA, Zhuang X, Liang Z, Stahelin RV, Jiang L, Cho W, Kang BH, Hwang I. (2017) SH3 Domain-Containing Protein 2 Plays a Crucial Role at the Step of Membrane Tubulation during Cell Plate Formation. *Plant Cell.* 29:1388-1405.

Ha JH, Lee HJ, Jung JH, Park CM. (2017) Thermo-Induced Maintenance of Photo-oxidoreductases Underlies Plant Autotrophic Development. *Dev Cell.* 41:170-179.e4.

Arnaud D, Lee S, Takebayashi Y, Choi D, Choi J, Sakakibara H, Hwang I. (2017) Cytokinin-Mediated Regulation of Reactive Oxygen Species Homeostasis Modulates Stomatal Immunity in Arabidopsis. *Plant Cell.* 29:543-559.

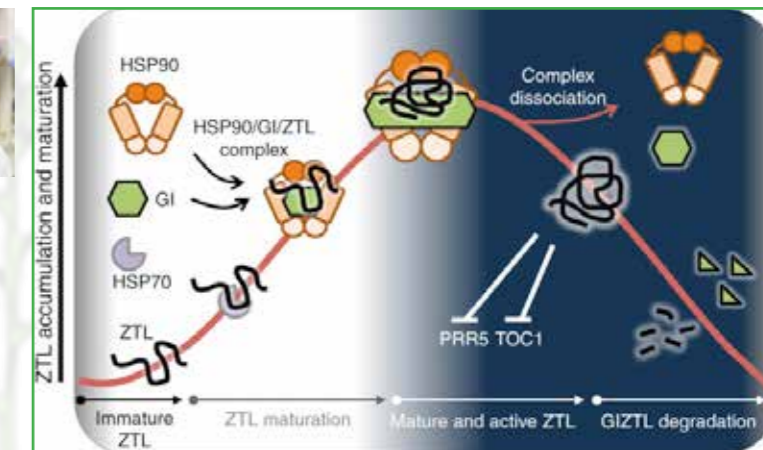


Figure 30. Post-transcriptional oscillation of ZTL is regulated by GI and HSP90. Nascent ZTL may be first captured by HSP70 in an early complex, and then transferred to a second complex comprising HSP90 and the co-chaperone GI. Order of ZTL interaction with GI and HSP90 is unknown. GI oligomerization and ZTL interaction is enhanced in the light, which may increase the binding capacity with ZTL and HSP90. Matured/active ZTL dissociates from the complex, to form SCFZTL which ubiquitylates PRR5 and TOC1. During the dark period ZTL is degraded together with GI <http://dx.doi.org/10.1038/s41467-016-0014-9>.

Cha JY, Kim J, Kim TS, Zeng Q, Wang L, Lee SY, Kim WY, Somers DE. (2017) GIGANTEA is a co-chaperone which facilitates maturation of ZEITLUPE in the Arabidopsis circadian clock. *Nat Commun.* 8:3.

Nawkar GM, Kang CH, Maibam P, Park JH, Jung YJ, Chae HB, Chi YH, Jung IJ, Kim WY, Yun DJ, Lee SY. (2017) HY5, a positive regulator of light signaling, negatively controls the unfolded protein response in Arabidopsis. *Proc Natl Acad Sci U S A.* 114:2084-2089.

Hwang Y, Choi HS, Cho HM, Cho HT. (2017) Tracheophytes Contain Conserved Orthologs of a Basic Helix-Loop-Helix Transcription Factor That Modulate ROOT HAIR SPECIFIC Genes. *Plant Cell.* 29:39-53

Park JS, Frost JM, Park K, Ohr H, Park GT, Kim S, Eom H, Lee I, Brooks JS, Fischer RL, Choi Y. (2017) Control of DEMETER DNA demethylase gene transcription in male and female gamete companion cells in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 114:2078-2083.

Major Funding Sources

- Systems & Synthetic Agrobiotech Center (~ 10 M USD/yr by Rural Development Administration, Korea).
- Agricultural Life Science Center (~ 10 M USD/yr by Rural Development Administration, Korea).
- Systems understanding of plant senescence and life history (~9 M USD/yr for 10 years by Institute of Basic Research)
- Woojangchoon Project focusing on carbon metabolism reengineering (0.9 M USD/yr for 5 years) supported by Rural Developmental Agency, Korea

Spain

José Luis Micol
jlmicol@umh.es
 Universidad Miguel Hernández, Elche,
 Spain;



NRP1 is blocked by cytochrome c. *Nucleic Acids Research* 45: 2150-2165.

Martín G, Rovira A, Veciana N, Soy J, Toledo-Ortiz G, Gommers CMM, Boix M, Henriques R, Minguet EG, Alabadí D, Halliday KJ, Leivar P and Monte E (2018) Circadian waves of transcriptional repression shape PIF-regulated photoperiod-responsive growth in *Arabidopsis*. *Current Biology* 28: 311-318.

Martínez-Pérez M, Aparicio F, López-Gresa MP, Bellés JM, Sánchez-Navarro JA and Pallás V (2017) *Arabidopsis* m(6)A demethylase activity modulates viral infection of a plant virus and the m(6)A abundance in its genomic RNAs. *Proceedings of the National Academy of Sciences of the United States of America* 114: 10755-10760.

Pérez-Ruiz JM, Naranjo B, Ojeda V, Guinea M and Cejudo FJ (2017) NTRC-dependent redox balance of 2-Cys peroxiredoxins is needed for optimal function of the photosynthetic apparatus. *Proceedings of the National Academy of Sciences of the United States of America* 114: 12069-12074.

Vergara Z, Sequeira-Mendes J, Morata J, Peiró R, Hénaff E, Costas C, Casacuberta JM and Gutierrez C (2017) Retrotransposons are specified as DNA replication origins in the gene-poor regions of *Arabidopsis* heterochromatin. *Nucleic Acids Research* 45: 8358-8368.

Zhou Y, Romero-Campero FJ, Gómez-Zambrano A, Turck F and Calonje M (2017) H2A monoubiquitination in *Arabidopsis thaliana* is generally independent of LHP1 and PRC2 activity. *Genome Biology* 18: 69.

Major Funding Sources

About 80 grants from the Ministry of Economy, Industry and Competitiveness of Spain fund *Arabidopsis* research projects at individual laboratories.

Additional Information

Prof. Carmen Fenoll was elected President of the Spanish Society of Plant Physiology.

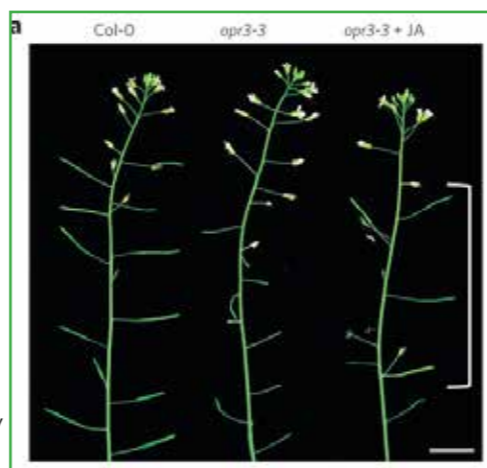


Figure 31. (a) Inflorescences of 7-week-old plants are shown. *opr3-3* mutants are sterile, and JA treatment (bracket) rescues male fertility. Scale bar, 1 cm. <http://dx.doi.org/10.1038/nchembio.2540>

Use of Arabidopsis

About 100 laboratories.

Conferences, Workshops and Outreach events

The “XV Spanish - Portuguese Congress on Plant Physiology” was organized by plant biologists lead by Prof. Teresa Altabella in Barcelona (June 26-30, 2017).

Selected Publications

Authors from laboratories studying *Arabidopsis* in Spain published about 400 papers in the last year.

Balanzà V, Martínez-Fernández I, Sato S, Yanofsky MF, Kaufmann K, Angenent GC, Bemer M and Ferrandiz C (2018) Genetic control of meristem arrest and life span in *Arabidopsis* by a FRUITFULL-APETALA2 pathway. *Nature Communications* 9: 565.

Barbado C, Córdoba-Canero D, Arizaa RR and Roldán-Arjona T (2018) Nonenzymatic release of N7-methylguanine channels repair of abasic sites into an AP endonuclease-independent pathway in *Arabidopsis*. *Proceedings of the National Academy of Sciences of the United States of America* 115: E916-E924.

Carrasco-López C, Hernández-Verdeja T, Perea-Resca C, Abia D, Catalá R and Salinas J (2017) Environment-dependent regulation of spliceosome activity by the LSM2-8 complex in *Arabidopsis*. *Nucleic Acids Research* 45: 7416-7431.

Castaño-Miquel L, Mas A, Teixeira I, Seguí J, Perearnau A, Thampi BN, Schapire AL, Rodrigo N, La Verde G, Manrique S, Coca M and Lois LM (2017) SUMOylation inhibition mediated by disruption of SUMO E1-E2 interactions confers plant susceptibility to necrotrophic fungal pathogens. *Molecular Plant* 10: 709-720.

Chini A, Monte I, Zamarreno AM, Hamberg M, Lassueur S, Reymond P, Weiss S, Stintzi A, Schaller A, Porzel A, García-Mina JM and Solano R (2018) An OPR3-independent pathway uses 4,5-didehydrojasmonate for jasmonate synthesis. *Nature Chemical Biology* 14: 171-178.

González-Arzola K, Díaz-Quintana A, Rivero-Rodríguez F, Velázquez-Campoy A, De la Rosa MA and Díaz-Moreno I (2017) Histone chaperone activity of *Arabidopsis thaliana*

Sweden

Maria E. Eriksson
maria.eriksson@umu.se
 Umeå University, Umeå Plant Science
 Centre, Umeå



Use of Arabidopsis

At least ten institutions use *Arabidopsis* as one of their major plant model species.

Open Resources for Arabidopsis Researchers

National resources available to the *Arabidopsis* community

- Max Lab hosted by Lund University; <https://www.maxiv.lu.se/>

Dedicated to high-throughput, nanovolume characterization and crystallization of biological macromolecules

- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government, <http://www.scilifelab.se>

- Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis <http://www.upsc.se>, found under “resources”

- The Swedish Metabolomics Centre in Umeå is a national resource, <http://www.swedishmetabolomicscentre.se/>

New Software Tools

The PlantGenIE platform; web portals for enabling in-depth exploration of poplar, Norway spruce, and *Arabidopsis* <http://plantgenie.org>

Computational Genetics Division Uppsala University, Carlborg Lab
<http://www.computationalgenetics.se/>

Conferences, Workshops and Outreach events

Meetings in 2018:
 The European Congress on Photosynthesis Research, organized by the International Society for Photosynthesis Research, June 25 – 28, Uppsala, Sweden

The 13th European Nitrogen Fixation Conference 2018, August 18 – 21, Stockholm, Sweden

‘Fascination of Plants Day’ is celebrated at most major plant science centres across Sweden, which also regularly host outreach activities to highlight research on plants.

Selected Publications

Hafrén A, *et al.* (2017) Selective autophagy limits cauliflower mosaic virus infection by NBR1-mediated targeting of viral capsid protein and particles. *Proceedings of the National Academy of Sciences of the U. S. A.* 114(10): E2026-E2035

Lafon-Placette C, *et al.* (2017) Endosperm-based hybridization barriers explain the pattern of gene flow between *Arabidopsis lyrata* and *Arabidopsis arenosa* in Central Europe. *Proceedings of the National Academy of Sciences of the U. S. A.* 114(6): E1027-E1035

Ganeteg U, *et al.* (2017) Amino acid transporter mutants of *Arabidopsis* provides evidence that a non-mycorrhizal plant acquires organic nitrogen from agricultural soil. *Plant, Cell & Environment* 40(3):413-423

Matías-Hernández L, *et al.* (2017) AaMYB1 and its orthologue AtMYB61 affect terpene metabolism and trichome development in *Artemisia annua* and *Arabidopsis thaliana*. *The Plant Journal* 90(3):520-534

Meyer HM, *et al.* (2017) Fluctuations of the transcription factor ATML1 generate the pattern of giant cells in the *Arabidopsis* sepal. *eLife* 6:e19131

Jonsson K, Boutté Y, Singh RK, Gendre D, & Bhalerao RP (2017) Ethylene Regulates Differential Growth via BIG ARF-GEF-Dependent Post-Golgi Secretory Trafficking in *Arabidopsis*. *The Plant Cell* 29(5):1039

Teixeira PF, *et al.* (2017) A multi-step peptidolytic cascade for amino acid recovery in chloroplasts. *Nature Chemical Biology* 13:15

Majda M, *et al.* (2017) Mechanochemical Polarization of Contiguous Cell Walls Shapes Plant Pavement Cells. *Developmental Cell* 43(3):290-304.e294

Zhang B, *et al.* (2017) BLADE-ON-PETIOLE proteins act in an E3 ubiquitin ligase complex to regulate PHYTOCHROME INTERACTING FACTOR 4 abundance. *eLife* 6:e26759

Applied research (spruce)
 Jokipii-Lukkari S, *et al.* (2017) NorWood: a gene expression resource for evo-devo studies of conifer wood development. *New Phytologist*: 216:482-494

Additional Information

Examples (not complete list) of grants awarded for Arabidopsis related research 2017:

Prof Catherine Bellini, UPSC, Umeå University; On control of adventitious root initiation in *Arabidopsis thaliana*: deciphering the increasing complexity of molecular cross-talks, a project grant awarded by the Swedish research council (VR), 3,420 kSEK (SEK= Swedish krona)

Prof Örjan Carlborg, Uppsala University; On the connection between genotype and phenotype, the genetics of complex traits, a project grant awarded by VR, 3,375 kSEK

Dr Olivier Van Aken, Lund University; On investigating the signalling from organelle to nucleus in plants under strain, a project grant awarded by VR, 3,518 kSEK

Prof Åsa Strand, UPSC, Umeå University; Systems Biology Research grant for characterization of plant stress responses awarded by the Swedish Foundation for Strategic Research (SSF), 35,000 kSEK

Major Funding Sources

- The Swedish Research Council (VR; <http://www.vr.se>) a core funder of researcher-initiated basic research.
- The Swedish Foundation for Strategic Research (<http://www.stratresearch.se>) supports strategic research in natural science, engineering and medicine.
- The Swedish Agency for Innovation Systems (VINNOVA; <http://www.vinnova.se>) promotes sustainable growth by funding needs-driven research and the development of effective innovation systems.
- The Royal Academy of Science/ (<http://www.kva.se>) Agriculture and Forestry (<http://www.ksla.se>)

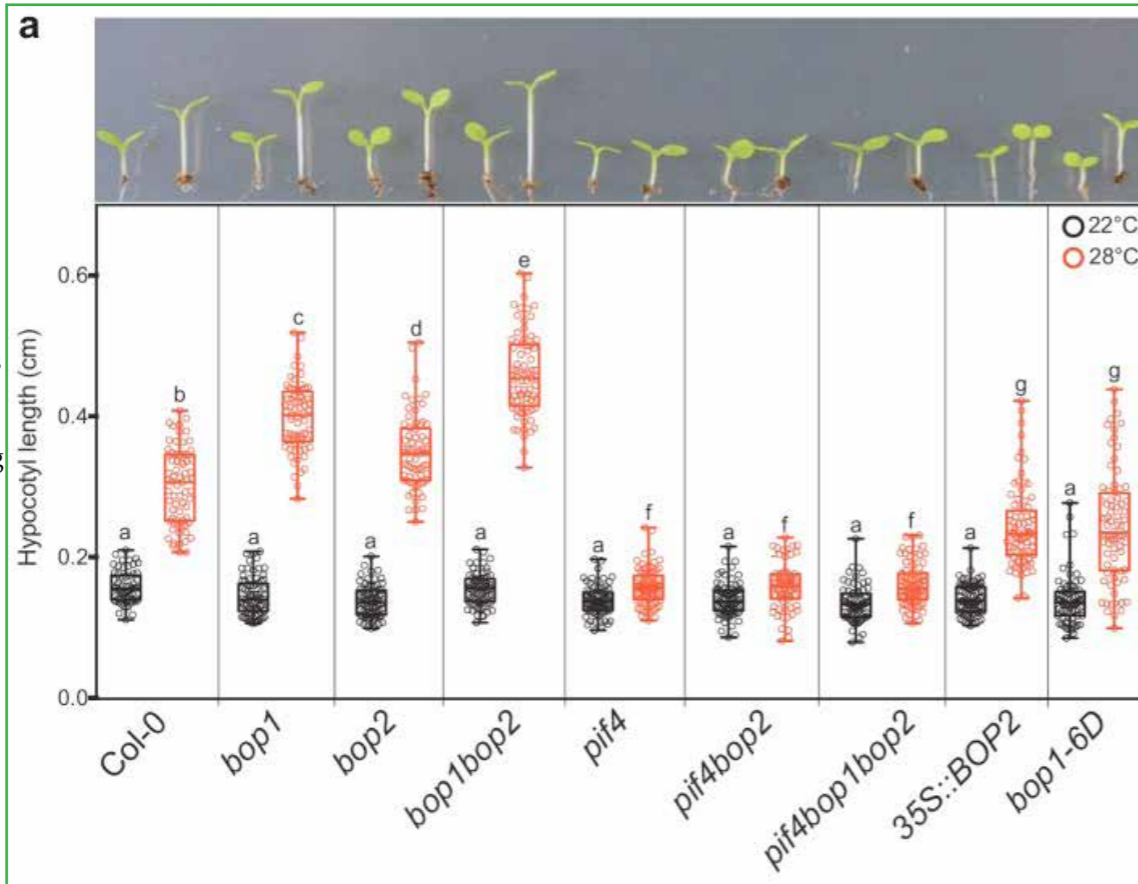


Figure 32. BOP2 modulates the PIF4 abundance in temperature response. (a) Hypocotyl lengths of indicated seedlings in response to the temperature of 28°C. Seedlings were grown firstly at 22°C in constant white light for 4 days then transferred to 28°C or kept in 22°C for another 4 days. The upper panel shows the hypocotyl length phenotypes of indicated lines. The lower panel shows a box-and-whiskers plot of the data. Multiple comparison was performed in a post ANOVA Fisher's test and lines that do not share any letters are significantly different from each other. Circles represent each measured individual, n > 60, p<0.01. <https://doi.org/10.7554/eLife.26759>

- The Swedish Research Council Formas (<http://www.formas.se>) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.
- The Wallenberg Foundations (<http://www.wallenberg.org/en>) private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.
- Carl Tryggers Foundation for Scientific Research (<http://www.carltryggersstiftelse.se/>) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.
- The Kempe Foundations (<http://www.kempe.com>) private foundations devoted to support scientific research in Northern Sweden
- Stiftelsen Olle Engkvist Byggmästare (<http://engkviststiftelserna.se/>)
- Sven and Lily Lawski's foundation for research in Natural Sciences (Biochemistry and Genetics); <http://www.lawskistiftelsen.se/> A private foundation supporting basic science

Switzerland

Kentaro K. Shimizu
kentaro.shimizu@ieu.uzh.ch
 Misako Yamazaki
misako.yamazaki@ieu.uzh.ch
 University of Zurich
 Zurich-Basel Plant Science Center
info-plantscience@ethz.ch
 Swiss Plant Science Web
coordination-spsw@unibas.ch



- PSC Summer School 2018, Responsible Research and Innovation in Plant Sciences 10-14 September 2018, Einsiedeln, Switzerland
<https://www.plantsciences.uzh.ch/en/teaching/summerschool.html>

- PSC Symposium 2018, Working Title: 20th Anniversary Symposium Zurich-Basel Plant Science Center – Breakthroughs in Plant Sciences – From the laboratory to the world, 5 December 2018, Zurich

Workshops
 Molecular studies in natura - How plants sense and react in the nature, 19 February 2018, Zurich

Plant Development and Evolution from molecules to ecosystems, 20-22 February 2018, Zurich

Use of Arabidopsis

c.a. 12 institutions and c.a 100 labs.

Open Resources for Arabidopsis Researchers

- Swiss-Prot database contributes to TAIR database
- Genevestigator (<https://genevestigator.com/gv/>)

As a facility or database, we have these resources below.

- Functional Genomics Center Zurich
- The Neuchâtel Platform of Analytical Chemistry (the Mass Spectrometry and Metabolomics Unit and the Nuclear Magnetic Resonance Unit, <http://www.unine.ch/npac>)
- Bio-molecular Analysis Platform (collaborative basis, <http://biveg.unige.ch/en/services/bma/>)
- Genetic Diversity Center (e.g. genome-wide polymorphisms of *Arabidopsis halleri*)

Conferences, Workshops and Outreach events

- Conferences**
- PSC Summer school 2017, Understanding Risks and Resilience in Plant Systems, 29 May – 2 June 2017, Einsiedeln
https://www.plantsciences.uzh.ch/dam/jcr:a5bb24c5-840b-419c-9232-32ceddea37bf/Flyer_PSC_Summer_School_2017.pdf
 - PSC Symposium 2017, Dynamics of Plant Development & Evolution
 30 November - 1 December 2017, Zurich
<http://www.plantsciences.uzh.ch/en/outreach/conferences/Dynamics-of-Plant-Development-and-Evolution.html>
 - SwissPLANT 2018 Symposium, 31 January - 2 February 2018, Meiringen
<https://swissplantscienceweb.ch/de/swissplant-2018-symposium/>
 - Lausanne Genomics Days 2018, 5 – 6 February 2018, Lausanne
<http://www.genomyx.ch/mon-feb-5-tues-feb-6-2018-lausanne-genomics-days-2018/>

Outreach Activities

- Plant Science at School
 Continuing Education Program in Plant Sciences for Secondary School Teachers
 Over the past seven years, this program has become a national example of successful collaboration between researchers, teachers and regional learning centers.
<http://www.plantsciences.uzh.ch/outreach/atschool.html>
- PSC Discovery Program for Youth – new Agora project
 In collaboration with educators of the ETH MINT Lernzentrum, the Zurich-Basel Plant Science Center (PSC) offers workshops for school classes at the secondary school level.
<http://www.plantsciences.uzh.ch/de/outreach/discovery.html>
<http://www.snf.ch/en/funding/science-communication/agora/Pages/default.aspx>

Selected Publications

- Diffusible repression of cytokinin signalling produces endodermal symmetry and passage cells.
 Andersen TG, Naseer S, Ursache R, Wybouw B, Smet W, De Rybel B, Vermeer JEM, Geldner N.
 Nature. 2018 Mar 14 doi: 10.1038/nature25976.
- Local auxin production underlies a spatially restricted neighbor-detection response in Arabidopsis.
 Michaud O, Fiorucci AS, Xenarios I, Fankhauser C.
 Proc Natl Acad Sci U S A. 2017 Jul 11;114(28):7444-7449 doi: 10.1073/pnas.1702276114.
- Local adaptation (mostly) remains local: reassessing environmental associations of climate-related candidate SNPs in Arabidopsis halleri.
 Rellstab C, Fischer MC, Zoller S, Graf R, Tedder A, Shimizu KK, Widmer A, Holderegger R, Gugerli F.
 Heredity (Edinb). 2017 Feb;118(2):193-201.
 doi: 10.1038/hdy.2016.82.

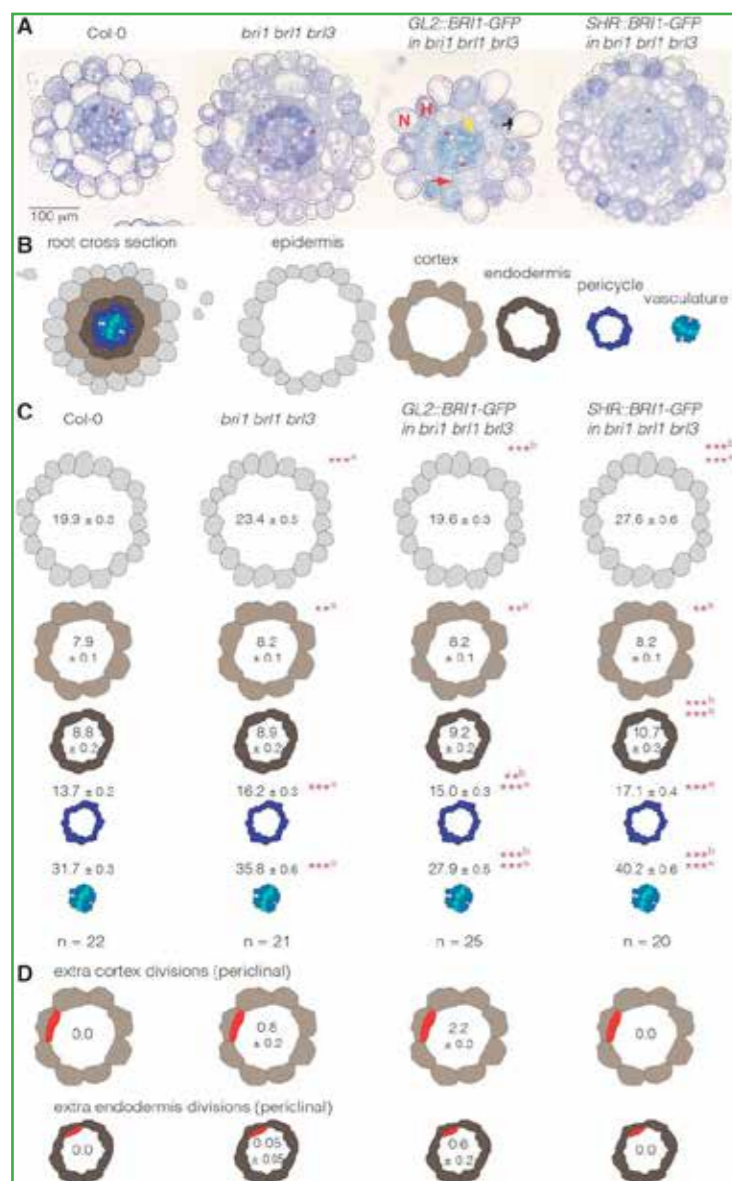


Figure 33. Quantification of radial meristem phenotypes in 5-day-old brassinosteroid receptor mutants. (A) Toluidine Blue-stained root sections, taken at the position where protophloem poles (asterisks) have already differentiated, but protoxylem has not. Epidermal H and N cells are indicated for GL2::BRI1-GFP triple. Red arrow points out an extra cortex division, yellow arrow an extra endodermis division. (B) Schematics of the different root tissue layers in a cross-section of a Col-0 wild-type plant. (C) Quantification (mean±s.e.m.) of cell number in the different tissues. (D) Quantification (mean±s.e.m.) of extra cortex or endodermis divisions. **P<0.01; ***P<0.001; ^aversus Col-0; ^bversus *bri1 bri1 bri3* (Student's t-test). <https://doi.org/10.1242/dev.145623>

- Brassinosteroid signaling directs formative cell divisions and protophloem differentiation in Arabidopsis root meristems. Kang YH, Breda A, Hardtke CS. *Development*. 2017 Jan 15;144(2):272-280. doi: 10.1242/dev.145623.

- Mechanistic basis for the activation of plant membrane receptor kinases by SERK-family coreceptors. Hohmann U, Santiago J, Nicolet J, Olsson V, Spiga FM, Hothorn LA, Butenko MA, Hothorn M. *Proc Natl Acad Sci U S A*. 2018 Mar 12. pii: 201714972. doi: 10.1073/pnas.1714972115.

Additional Information

Highlight 2018 - Switzerland has had regularly a high-quality publications (e.g. Andersen *et al.*, *Nature* 2018, Mecchia *et al.*, *Science* 2017).

- A 5.5-year joint project for Japan and Switzerland on polyploid Arabidopsis and crop species was funded by Japan Science and Technology Agency (JST) (PI, Kentaro Shimizu).

Major Funding Sources

1. Swiss National Science Foundation (SNSF) <http://www.snf.ch/en/Pages/default.aspx>
2. European Research Council (ERC), <https://erc.europa.eu/>
3. SystemsX.ch, <http://www.systemsx.ch/>
4. Syngenta (Plant Science Center - Syngenta Fellowship), <https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html>
5. Research and Innovation Staff Exchange (RISE) of European Commission http://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange_en
6. State Secretariat for Education, Research, and Innovation (SERI), <https://www.sbf.admin.ch/sbf/en/home.html>
7. University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Beat Keller, Ueli Grossniklaus, University of Zurich) <http://www.evolution.uzh.ch/en.html>
8. Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), <https://www.jst.go.jp/kisoken/crest/en/>

- Agrobacterium-mediated floral dip transformation of the model polyploid species Arabidopsis kamchatica. Yew CL, Kakui H, Shimizu KK. *J Plant Res*. 2018 Mar;131(2):349-358. doi: 10.1007/s10265-017-0982-9.

- RALF4/19 peptides interact with LRX proteins to control pollen tube growth in Arabidopsis. Mecchia MA *et al* *Science*. 2017 Dec 22;358(6370):1600-1603. doi: 10.1126/science.aao5467.

United Kingdom

Geraint Parry geraint@garnetcommunity.org.uk
GARNet, Cardiff University, UK



Use of Arabidopsis

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

The BBSRC is the major funder of Arabidopsis research, which includes institutional support for the John Innes Centre, IBERS in Aberystwyth and Rothamsted Research.

Open Resources for Arabidopsis Researchers

- The Eurasian Arabidopsis Stock Centre (uNASc) is based at the University of Nottingham. <http://arabidopsis.info/>

New Software Tools

- The Centre for Integrative Biology based at the University of Nottingham has developed a range of open source software, hardware and other resources. <https://www.cpiib.ac.uk/tools-resources/>

- The Bassal Lab at the University of Birmingham have developed tools for analysis of gene expression and interaction networks in Arabidopsis seeds. <http://www.georgebassellab.com/online-tools/>
In addition they have developed 3DCellAtlas that describes a computational approach to perform digital single cell analyses in 3D plant organs. <http://www.georgebassellab.com/3d-cell-atlas/>

- The Millar lab at the University of Edinburgh has developed BioDare2 as a repository for circadian, biological data, providing a platform for data sharing and period analysis. <https://biodare2.ed.ac.uk/welcome>

- Research at the John Innes Centre have developed Leaf-GP (Growth Phenotypes) an open and automated software application for measuring growth phenotypes for arabidopsis and wheat <https://github.com/Crop-Phenomics-Group/Leaf-GP/releases>

- The Tsiftaris lab at the University of Edinburgh have developed Phenotiki is an affordable, easy-to-use, maintain and deploy image-based plant phenotyping platform. <http://phenotiki.com/>

- Plant Methods published in the UK have collated a set of resources entitled 'Plants in Computer Vision': <https://www.biomedcentral.com/collections/PCV>

- The Cell Architect program has been developed by researchers at the John Innes Centre and is designed to recognise microtubule (MT) and measure MT pattern changes induced by different chemicals <https://github.com/TeamMacLean/CellArchitect>

Conferences, Workshops and Outreach events

In 2017 and 2018 GARNet have and will organise conferences and workshops attended by Arabidopsis researchers:

- SEB-GARNet meeting on From Proteome to Phenotype: role of post-translational modifications: University of Edinburgh December 11th-13th 2017 <http://www.sebiology.org/events/event/from-proteome-to-phenotype>

- GARNet Gene Editing Workshop: University of Bristol March 26-27th 2018 <http://garnet-ge-workshop.weebly.com/>

- GARNet2018: a Plant Science Showcase: September 18-19th 2018 <http://www.garnet2018.weebly.com/>

- New Phytologist Next Generation Scientists: Norwich 24th-26th July 2017 <https://www.newphytologist.org/news/view/124>

- Sainsbury Lab Symposium: The Coordination of Development. Sept 19th-21st 2018 <https://www.slcu.cam.ac.uk/SLS18>

- Plastid Preview 2018. University of Lancaster September 3rd-4th 2018 <http://wp.lancs.ac.uk/plastidpreview2018/>

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/>

Di Mambro R, De Ruvo M, Pacifici E, Salvi E, Sozzani R, Benfey PN, Busch W, Novak O, Ljung K, Di Paola L, Marée AFM, Costantino P, Grieneisen VA, Sabatini S (2017) Auxin minimum triggers the developmental switch from cell division to cell differentiation in the Arabidopsis root. *Proc Natl Acad Sci U S A* 10.1073/pnas.1705833114

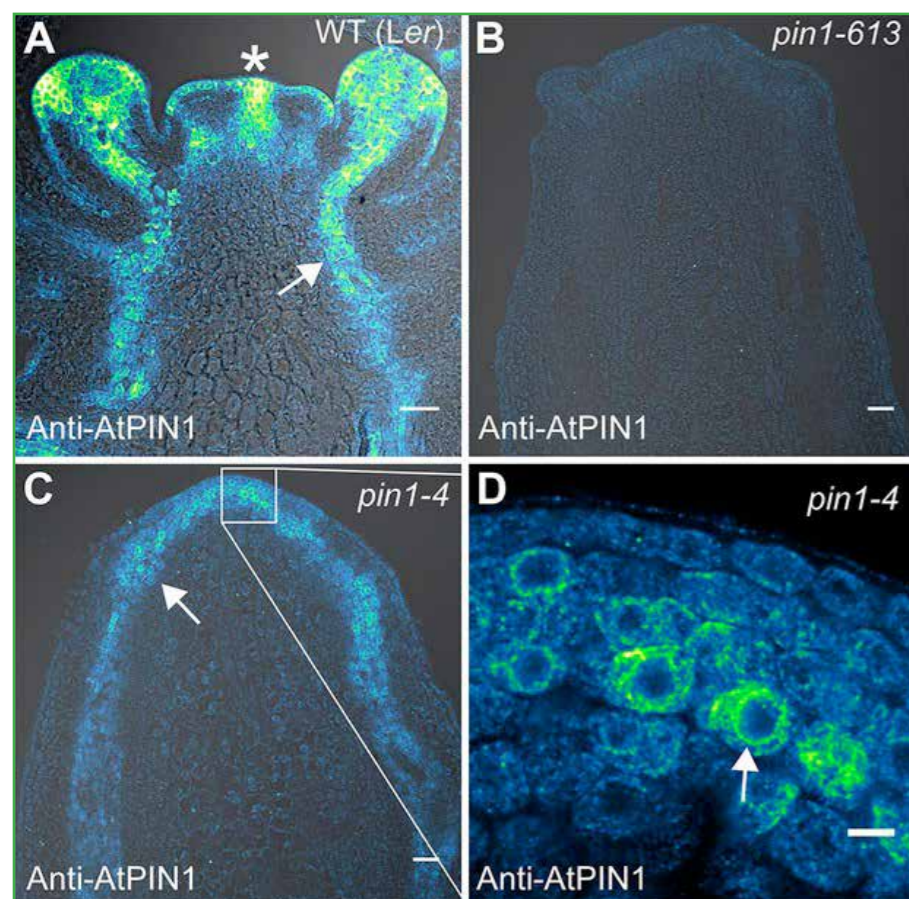


Figure 34. AtPIN1 protein immunolocalization in wild-type, *pin1-613*, and *pin1-4* meristems. (A) AtPIN1 protein accumulation in wild-type Ler inflorescence apex shows polar PIN protein at the sites of initiating organs (asterisk), and during vein patterning below the apex (arrow). (B) No AtPIN1 protein is detected in *pin1-613* null mutant pin-formed apices. (C) Abundant AtPIN1 protein is detected in *pin1-4* pin-formed apices, primarily in provascular tissues below the meristem apex (arrow). Box shows region of detail in (D). (D) Detail of boxed area shown in (C). AtPIN1 protein in *pin1-4* accumulates in a perinuclear domain (arrow). All samples are 9 μ m longitudinal sections. Scale bars: 25 μ m in A-C, and 5 μ m in D. <https://doi.org/10.7554/eLife.31804.025>

Elena López-Calcagno P, Omar Abuzaid A, Lawson T, Anne Raines C (2017) Arabidopsis CP12 mutants have reduced levels of phosphoribulokinase and impaired function of the Calvin-Benson cycle. *J Exp Bot* <http://dx.doi.org/10.1093/jxb/erx084>

Harumain ZA, Parker HL, Muñoz García A, Austin MJ, McElroy CR, Hunt AJ, Clark JH, Meech JA, Anderson CW, Ciacci L, Graedel TE, Bruce NC, Rylott EL (2017) Towards financially viable phytoextraction and production of plant-based palladium catalysts. *Environ Sci Technol*. <http://dx.doi.org/10.1021/acs.est.6b04821>

Jackson MD, Xu H, Duran-Nebreda S, Stamm P, Bassel GW (2017) Topological analysis of multicellular complexity in the plant hypocotyl. *Elife* <http://dx.doi.org/10.7554/eLife.26023>

O'Connor DL, Elton S, Ticchiarelli F, Hsia MM, Vogel JP, Leyser O (2017) Cross-species functional diversity within the PIN auxin efflux protein family. *Elife*. doi: 10.7554/eLife.31804

Pass DA, Sornay E, Marchbank A, Crawford MR, Paszkiewicz K, Kent NA, Murray JAH (2017) Genome-wide chromatin mapping with size resolution reveals a dynamic sub-nucleosomal landscape in Arabidopsis. *PLoS Genet*. doi: 10.1371/journal.pgen.1006988

Rizza A, Walia A, Lanquar V, Frommer WB, Jones AM (2017) In vivo gibberellin gradients visualized in rapidly elongating tissues. *Nat Plants*. doi: 10.1038/s41477-017-0021-9

Zhang H, Gannon L, Hassall KL, Deery MJ, Gibbs DJ, Holdsworth MJ, van der Hoorn RAL, Lilley KS, Theodoulou FL (2017) N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. *New Phytol*. doi: 10.1111/nph.14909

Major Funding Sources

Biotechnology and Biological Sciences Research Council (BBSRC) <http://www.bbsrc.ac.uk/>
The Gatsby Charitable Foundation <http://www.gatsby.org.uk/>
European Research Council http://ec.europa.eu/research/era/index_en.htm

Natural Environment Research Council <http://www.nerc.ac.uk>
The Gates Foundation <http://www.gatesfoundation.org/>

Additional Information

The GARNet YouTube channel includes interviews with academics about recent papers.

<https://www.youtube.com/channel/UC89b0H0Mvu5SRbgFNhf2rfQ>

United States of America



<https://www.araport.org/community/group/naasc>

Joanna Friesner
jdfriesner@ucdavis.edu

University of California, Davis, NAASC Coordinator, with input from the North American Arabidopsis Steering Committee (NAASC): Doris Wagner, NAASC President (University of Pennsylvania); Rick Vierstra (Washington University in St. Louis); Sarah Assmann (Penn State University); Erich Grotewold (Michigan State University); Elizabeth Haswell (Washington University in St. Louis); Jose Dinnyen, NAASC Treasurer (Stanford University), Roger Innes (Indiana University), Peter McCourt (University of Toronto- Canada); Sean Cutler (University of California, Riverside); and Jennifer Nemhauser (University of Washington, Seattle);

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.

Open Resources for Arabidopsis Researchers

There are a large number of US institutions, companies, and facilities that conduct Arabidopsis research and it would be impossible to list them all. Therefore, we list the primary resource entity, ABRC (<https://abrc.osu.edu/seed-handling>), the US stock center which, in partnership with the European Stock Centre (NASC, UK) and RIKEN BioResourceCenter (Japan), provide valuable Arabidopsis seed and other resources to the global community.

The Arabidopsis Biological Resource Center collects, preserves, reproduces and distributes diverse seed and other stocks of *Arabidopsis thaliana* and related species. Resources are donated by researchers from around the world. ABRC has been providing Arabidopsis and related species seed and other resources for research and education since 1991. At present ABRC has about 4,000 characterized mutant and 2,000 transgenic lines.

Overall the seed collection is approaching half a million (~490,000) counting all the characterized and uncharacterized T-DNA lines, as well as the natural accessions. More than 100,000 samples are shipped annually to researchers and educators from 60 countries.

ABRC holdings include: Arabidopsis seed stocks and clones, Arabidopsis cell lines and protein chips, seed and clone resources from related species, Cloning vectors and host strain, Education kits.

New Software Tools

(1) A new discrete dynamic model of ABA-induced stomatal closure predicts key feedback loops. Albert R, Acharya BR, Jeon BW, Zañudo JGT, Zhu M, Osman K, Assmann SM. *PLoS Biol*. 2017 Sep 22;15(9):e2003451. <http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.2003451>

(2) GRACE (Gene Regulatory network inference ACCuracy Enhancement); Enhancing gene regulatory network inference through data integration with markov random fields. Michael Banfa,1 and Seung Y. Rhee. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5286517/>

(3) GENIST is an algorithm to infer gene regulatory networks from spatial and temporal datasets. <https://github.com/madeluis/GENIST>

(4) eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. <https://academic.oup.com/database/article/doi/10.1093/database/bax081/4627699>

(5) Bowtie 2 is an ultrafast and memory-efficient tool for aligning sequencing reads to long reference sequences. <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>

(6) UpSetR: an R package for the visualization of intersecting sets and their properties. <https://academic.oup.com/bioinformatics/article/33/18/2938/3884387>

(7) Workflow and web application for annotating NCBI BioProject transcriptome data. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5467576/>

(8) <http://araport.org/> The Arabidopsis Information Portal, started through work by the International Arabidopsis Informatics Consortium in 2012. The new portal has been online since April 2014. While not a new tool, this is a key contribution by the US Arabidopsis community.

(9) <https://www.arabidopsis.org/> TAIR have successfully moved to a subscription-based model, and their non-profit organization, Phoenix Bioinformatics, continues TAIR's annotation work. Open access is available after one year, and TAIR continues to provide free access for students using TAIR in their coursework upon request from the course organizer. While not a new tool, this is a key contribution by the US Arabidopsis community.

Conferences, Workshops and Outreach events

The North American Arabidopsis Steering Committee (NAASC) hosted the 28th International Conference on Arabidopsis Research (ICAR): “Arabidopsis Research in 2017 and Beyond”, June 2017 in St. Louis, Missouri, USA. 470 attendees from 20 countries participated in 29 sessions including 4 Keynote lectures, 18 plenary and concurrent sessions, and 7 workshops. The program focused especially on female and early career speakers; of 46 invited speakers, 46% were female (including 3 of 4 Keynotes), and 41% were ‘early-career’ speakers at the level of assistant professor or earlier. Of 10 concurrent session chairs, 5 were female and 6 were early-career invited speakers, providing exposure and a diverse program since chairs selected the 50 talks from submitted abstracts.

Platform sessions featured nearly 100 oral presentations and there were nearly 350 poster presentations. NAASC encouraged session chairs to prioritize early-career researchers and diversity in submitter gender and location. NAASC developed for ICAR 2017 new career-building and enhancing activities that proved to be successful.

Three pre-ICAR skills-based workshops were developed in collaboration with the Danforth Plant Sciences Center and funded by an award from the US National Science Foundation (NSF). Two additional early career-focused workshops were held during ICAR 2017. The skills-based workshops included (1) “Data Carpentry”: an example-driven workshop on basic concepts, skills and tools for working more effectively with data via short tutorials alternate with hands-on practical exercises. (2) “ATAC-seq Hands-on Workshop on mapping chromatin accessibility and TF footprints”: a wet-lab and computational introduction to the ATAC-seq process. (3) “Hackathon for High-throughput Phenotyping”: an activity that expanded on the introduction to genomics data and data management and analysis for genomics research.

The career-exploration panel workshops were, firstly, “Careers Beyond the Academy” including Working in Science Communication; Career Development for Success in Industry and Elsewhere; Working at USDA and Other Government Jobs; Working at a PUI (Primarily Undergraduate Institution); Advocating for Plant Science and Careers in Science Policy; Careers for Scientists in Intellectual Property (IP) Law; and Industry Job Search in US and France; and secondly, “Careers in Industry” featuring panelists from NewLeaf Symbiotics, BioGenerator, CONVIRON, and Monsanto. In the workshops, four of seven, and three of four panelists, respectively, were female.

Several community-organized workshops at ICAR 2017 addressed impacts on scientists including “Communicating Your Science to Peers and Beyond”, and “Overcoming the Imposter Phenomenon in Academic Science – an

Interactive Workshop to Combat Imposter Thoughts.” As a bit of extra fun, science and networking, the ICAR 2017 party was hosted by the Danforth Center which generously opened its doors with an open house, including site tours, for conference attendees. NAASC and Danforth staff collaborated to develop a scientific and social program that enabled science exchange in an informal setting. The activities concluded with a party featuring VO5, a live 9-piece disco band, and lots of great local food and dancing.

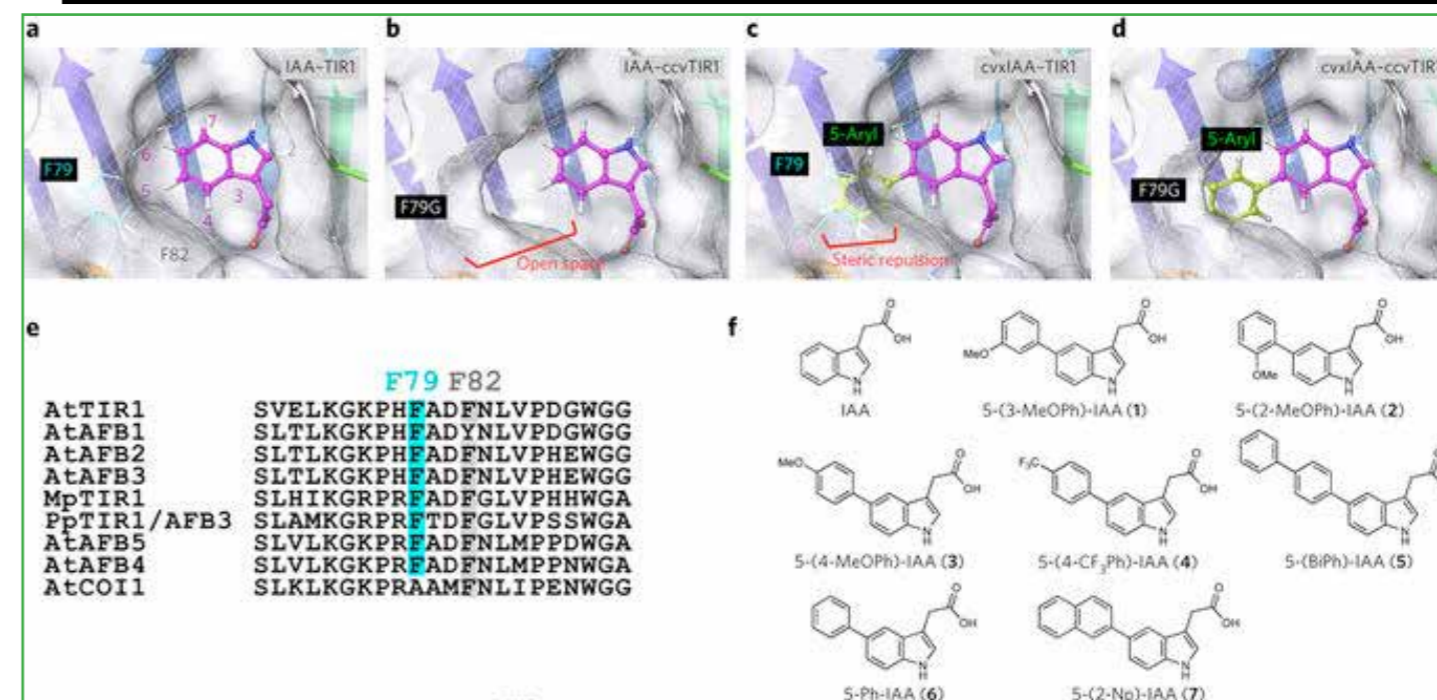
Planning for ICAR 2020- US- is underway. NAASC members assembled an international External Advisory Board (EAB) for ICAR 2020 which is scheduled to return to the US after rotations in Europe and Asia. The EAB began discussions and meetings in winter 2017 to envision new approaches, sessions, and activities for the US-located ICAR to ensure the meeting stays relevant and valuable to the international Arabidopsis community. The discussion by the EAB has primarily involved considering new and exciting scientific plant biology topics, an invigorated focus on bringing in new voices from the community, and novel activities and approaches to enhance collaboration, participation, and information sharing. NAASC members are expected to announce the selected date and location for ICAR 2020 during ICAR 2018 in Finland.

Selected Publications

The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. Friesner J, Assmann SM, Bastow R, Bailey-Serres J, Beynon J, Brendel V, Buell CR, Bucksch A, Busch W, Demura T, Dinneny JR, Doherty CJ, Eveland AL, Falter-Braun P, Gehan MA, Gonzales M, Grotewold E, Gutierrez R, Kramer U, Krouk G, Ma S, Markelz RJC, Megraw M, Meyers BC, Murray JAH, Provart NJ, Rhee S, Smith R, Spalding EP, Taylor C, Teal TK, Torii KU, Town C, Vaughn M, Vierstra R, Ware D, Wilkins O, Williams C, Brady SM. *Plant Physiol.* 2017 Dec;175(4):1499-1509. doi: 10.1104/pp.17.01490.

Chemical hijacking of auxin signaling with an engineered auxin-TIR1 pair.
Uchida N, Takahashi K, Iwasaki R, Yamada R, Yoshimura M, Endo TA, Kimura S, Zhang H, Nomoto M, Tada Y, Kinoshita T, Itami K, Hagiwara S, Torii KU. *Nat Chem Biol.* 2018 Mar;14(3):299-305. doi: 10.1038/nchembio.2555.

The MBD7 complex promotes expression of methylated transgenes without significantly altering their methylation status.
Li D, Palanca AMS, Won SY, Gao L, Feng Y, Vashisht AA, Liu L, Zhao Y, Liu X, Wu X, Li S, Le B, Kim YJ, Yang G, Li S, Liu J, Wohlschlegel JA, Guo H, Mo B, Chen X, Law JA. *Elife.* 2017 Apr 28;6. pii: e19893. doi: 10.7554/eLife.19893.



Mechanism of Dual Targeting of the Phytochrome Signaling Component HEMERA/pTAC12 to Plastids and the Nucleus.
Nevarez PA, Qiu Y, Inoue H, Yoo CY, Benfey PN, Schnell DJ, Chen M. *Plant Physiol.* 2017 Apr;173(4):1953-1966. doi: 10.1104/pp.16.00116.

A Multipurpose Toolkit to Enable Advanced Genome Engineering in Plants.
Cermák T, Curtin SJ, Gil-Humanes J, Cegan R, Kono TJY, Konečná E, Belanto JJ, Starker CG, Mathre JW, Greenstein RL, Voytas DF. *Plant Cell.* 2017 Jun;29(6):1196-1217. doi: 10.1105/tpc.16.00922.

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 may come from these sources:
US Department of Agriculture (USDA): <http://www.usda.gov/>
US Department of Energy (DOE): <http://energy.gov/>
National Institutes of Health (NIH): <http://www.nih.gov/>

Private Sources:
Howard Hughes Medical Institute (HHMI)- alone and partnered with several other organizations, support a number of US Arabidopsis researchers and educators:

HHMI Faculty Scholars (1); e.g. Siobhan Brady, Jose Dinneny, Elizabeth Haswell, Jennifer Nemhauser, Elizabeth Sattely

HHMI Investigators (2); e.g. Phil Benfey, Dominique Bergmann, Xuemei Chen, Joanne Chory, Jeff Dangl, Xinnian Dong, Joe Ecker, Mark Estelle, Sheng Yang He, Steve Jacobsen, Rob Martienssen, Elliot Meyerowitz, Keiko Torii and Ning Zheng

HHMI Professors (3); e.g. Rick Amasino, Bonnie Bartel, and Bob Goldberg

(1) <http://www.hhmi.org/programs/biomedical-research/faculty-scholars>
(2) <http://www.hhmi.org/programs/biomedical-research/investigator-program>
(3) <https://www.hhmi.org/developing-scientists/hhmi-professors>

Members of the MASC subcommittees

Bioinformatics

Nicholas Provart
University of Toronto, Canada
nicholas.provart@utoronto.ca
(Chair)

Sébastien Aubourg
INRA, Evry, France
aubourg@evry.inra.fr

Sean May
University of Nottingham, UK
sean@Arabidopsis.info

Klaus Mayer
Helmholtz Zentrum München, Germany
Kmayer@gsf.de

Yasukazu Nakamura
Kazusa DNA Research Institute, Japan
yn@kazusa.or.jp

Yves Van Den Peer
VIB / Ghent University, Belgium
yvdp@psb.UGent.be

Christopher Town
J. Craig Venter Institute, US
cdtown@jcv.org

Tetsuro Toyoda
RIKEN BASE, Japan
toyoda@base.riken.jp

Clone-Based Functional Genomics Resources (ORFeomics)

Motoaki Seki
RIKEN Center for Sustainable Resource Science (CSRS), Japan
motoaki.seki@riken.jp
(chair)

Joe Ecker
The Salk Institute for Biological Studies, US
ecker@salk.edu
(co-chair)

Pascal Braun
Technische Universität München, Germany
pascal.falter-braun@helmholtz-muenchen.de

Satoshi Iuchi
RIKEN Bioresource Center, Japan
satoshi.iuchi@riken.jp

Debbie Crist
ABRC, Ohio State University
crist.30@osu.edu

Epigenetics and Epigenomics

Robert Schmitz
University of Georgia, US
(co-chair)
schmitz@uga.edu

Xuehua Zhong
University of Wisconsin, US
(co-chair)
xuehua.zhong@wisc.edu

Metabolomics

Kazuki Saitov
RIKEN / Chiba University, Japan
kazuki.saito@riken.jp
(Chair)

Wolfram Weckwerth
University of Vienna; Austria
wolfram.weckwerth@univie.ac.at
(Co-chair)

Mike Beale
Rothamsted Research, UK
mike.beale@rothamsted.ac.uk

Alisdair Fernie
Max Planck Institute for Molecular Plant Physiology, Germany
Fernie@mpimp-golm.mpg.de

Oliver Fiehn
University of California, US
ofiehn@ucdavis.edu

Tony Larson
University of York, UK
trl1@york.ac.uk

Rob Last
Michigan State University, US
lastr@msu.edu

Basil Nikolau
Iowa State University, US
dimmas@iastate.edu

Natural Variation and Comparative Genomics

J. Chris Pires
University of Missouri, US
piresjc@missouri.edu
(Chair)

Brian P. Dilkes
Purdue University, US
bdilkes@purdue.edu
(Co-chair)

Justin Borevitz
Australian National University, Australia
justin.borevitz@anu.edu.au

Graham King
Southern Cross University, Australia
graham.king@scu.edu.au

Dan Kliebenstein
University of California-Davis, US
kliebenstein@ucdavis.edu

Marcus A. Koch
University of Heidelberg, Germany
marcus.koch@cos.uni-heidelberg.de

Nicholas Provart
University of Toronto, Canada
nicholas.provart@utoronto.ca

M. Eric Schranz
Wageningen University, Netherlands
eric.schranz@wur.nl

Detlef Weigel
Max Planck Institute for Developmental Biology, Germany
weigel@tue.mpg.de

Phenomics

Fabio Fiorani
Forschungszentrum Jülich, Germany
f.fiorani@fz-juelich.de
(Chair)

Christine Granier
INRA-SUPAGRO, France
granier@supagro.inra.fr (Co-Chair)

Justin Borevitz
Australian National University, Australia
justin.borevitz@anu.edu.au

Stijn Dhondt
VIB, Gent, Belgium
stijn.dhondt@ugent.vib.be

John Doonan
Aberystwyth University, UK
john.doonan@aber.ac.uk

Joe Ecker
Salk Institute, US
ecker@salk.edu

Proteomics

Joshua Heazlewood
Lawrence Berkeley National Laboratory, US
lheazlewood@lbl.gov
(Chair)

Katja Bärenfaller
Federal Institute of Technology, Switzerland
bkatja@ethz.ch

Sacha Baginsky
Martin-Luther-Universität Halle-Wittenberg, Germany
sacha.baginsky@biochemtech.uni-halle.de

Hans-Peter Braun
Leibniz Universität Hannover, Germany
braun@genetik.uni-hannover.de

Steve Briggs
University of California, US
sbriggs@ad.ucsd.edu

Geert De Jaeger
VIB Ghent University, Belgium
gejae@psb.vib-ugent.be

Alexandra Jones
University of Warwick, Coventry, UK
alex.jones@warwick.ac.uk

Harvey Millar
The University of Western Australia, Australia
harvey.millar@uwa.edu.au

Hans-Peter Mock
Institute for Plant Genetics and Crop Plant Research, Germany
mock@ipk-gatersleben.de

Hirofumi Nakagami
RIKEN Center for Sustainable Resource Science, Japan
hirofumi.nakagami@riken.jp

Scott Peck
University of Missouri, US
pecks@missouri.edu

Loïc Rajjou
AgroParisTech, France
loic.rajjou@versailles.inra.fr

Sigrun Reumann
University of Stavanger, Norway
sigrun.reumann@uis.no

Norbert Rolland
CEA, Grenoble, France
norbert.rolland@cea.fr

Véronique Santoni
INRA, France
santoniv@supagro.inra.fr

Waltraud Schulze
University of Hohenheim, Stuttgart, Germany
wschulze@uni-hohenheim.de

Nicolas Taylor
The University of Western Australia, Australia
ntaylor@cyllene.uwa.edu.au

Jay Thelen
University of Missouri, US
thelenj@missouri.edu

Klaas van Wijk
Cornell University, USA
kv35@cornell.edu

Wolfram Weckwerth
University of Vienna, Austria
wolfram.weckwerth@univie.ac.at

Julian Whitelegge
University of California, US
jpw@chem.ucla.edu

Stefanie Wienkoop
University of Vienna, Austria
stefanie.wienkoop@univie.ac.at

Systems and Synthetic Biology

Siobhan Brady
(Co-chair)
University of California, US
sbrady@ucdavis.edu

Malcolm Bennett
(Co-chair)
University of Nottingham, UK
malcolm.bennett@nottingham.ac.uk

Leah Band
University of Nottingham, UK
leah.band@nottingham.ac.uk

Pascal Falter-Braun
Technische Universität München, Germany
pbraun@wzw.tum.de

Rodrigo A. Gutiérrez
P. Universidad Católica de Chile, Chile
rgutierrez@bio.puc.cl

Gabriel Krouk
CNRS, France
krouk@supagro.inra.fr

Nicola Patron
Earlham Institute, UK
nicola.patron@earlham.ac.uk



French Graduate School of Research:
research, teaching, training and innovation
in plant sciences

Understanding the genetic, molecular and cellular mechanisms controlling the physiology and development of plants, as well as their interactions with fluctuating biotic and abiotic environments

- Over 50 plant sciences research teams from 5 laboratories in the Paris area
- About 700 staff members (400 permanent positions, 150 postdocs and PhD students)
- Over 200 publications per year

Developing high-tech resources and cutting-edge technologies

- 14 scientific platforms: imaging, cytology, biochemistry, chemistry, metabolism, genomics, epigenomics, transcriptomics, proteomics, protein-protein interactions, plant culture, biological stock centers
- 5500 m² of greenhouses / About 100 growth chambers / Different biosafety levels

Training plant sciences researchers, engineers and leaders of tomorrow

- About 12,000 hours of innovative theoretical and experimental teaching and training
- More than 100 training opportunities in SPS laboratories per year
- State of the art equipment for the practical training of students

Going from basic research to a socio-economic and environmental impact

- Applications in: Plant breeding and biotechnologies / Plant adaptation to the environment / Seeds and yield / Feed, food and nutrition / Cosmetics and health / Bioenergy and bio-based materials
- More than 70 ongoing contracts, including 20 with private partners

www.saclayplantsciences.fr

