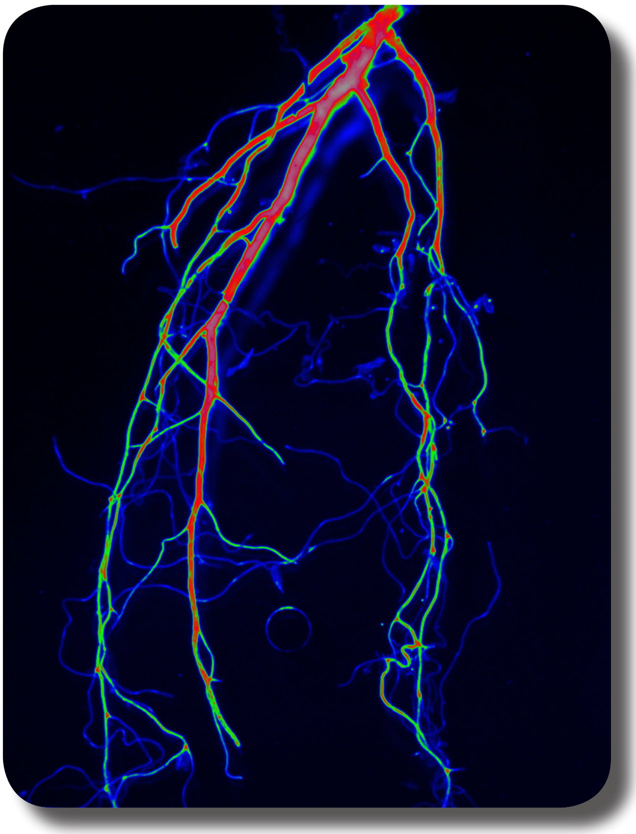
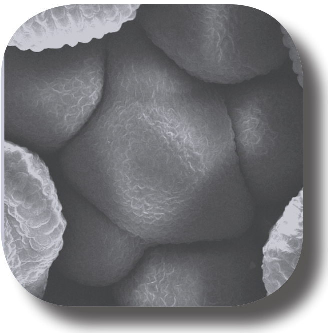
From Bench to Bountiful Harvests

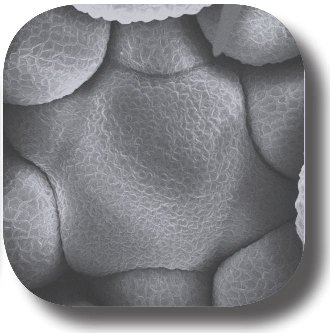
Annual Report

Multinational Arabidopsis Steering Committee (MASC)

2015/2016







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The Multinational Arabidopsis Steering Committee

Annual Report 2015/2016

Loïc Lepiniec
loic.lepiniec@versailles.inra.fr
MASC Chair

Inhwan Hwang
ihhwang@postech.ac.kr
MASC Co-chair

Marília K. F. de Campos
marilia.campos@zmbp.uni-tuebingen.de
MASC Coordinator, Executive Secretary

Parker Antin	pba@email.arizona.edu
Wagner Araújo	wlaraujo@ufv.br
Ruth Bastow	ruth@garnetcommunity.org.uk
Malcolm Bennett	malcolm.bennett@nottingham.ac.uk
Tanya Berardini	tberardi@arabidopsis.org
María Francisca Blanco	mfblanco@unab.cl
Dario Bonetta	dario.bonetta@uoit.ca
Siobhan Brady	sbrady@ucdavis.edu
Jelena Brkljacic	brkljacic.1@osu.edu
Lynette Brownfield	lynette.brownfield@otago.ac.nz
Ana I. Caño-Delgado	ana.cano@cragenomica.es
Maura Cardarelli	maura.cardarelli@uniroma1.it
Marcos Castellanos-Uribe	marcos.castellanos@nottingham.ac.uk
Sacco De Vries	sacco.devries@wur.nl
Brian Dilkes	bdilkes@purdue.edu
Joe Ecker	ecker@salk.edu
Maria E. Eriksson	maria.erikson@plantphys.umu.se
Fabio Fiorani	f.fiorani@fz-juelich.de
Joanna D. Friesner	jdfriesner@ucdavis.edu
Robert Furbank	robert.furbank@csiro.au
Erich Grotewold	grotewold.1@osu.edu
Rodrigo A. Gutiérrez	rgutierrez@bio.puc.cl
Klaus Harter	klaus.harter@zmbp.uni-tuebingen.de
Polydefkia Hatzopoulos	phat@aua.gr
Marie-Theres Hauser	marie-theres.hauser@boku.ac.at
Joshua Heazlewood	jheazlewood@unimelb.edu.au
Eva Huala	huala@phoenixbioinformatics.org
Jitendra P. Khurana	khuranaj@genomeindia.org
Masatomo Kobayashi	kobayasi@rtc.riken.jp
Marcus A. Koch	marcus.koch@cos.uni-heidelberg.de
Minami Matsui	minami@riken.jp
Sean May	sean@arabidopsis.org.uk
Blake Meyers	bmeyers@danforthcenter.org
José Luis Micol	jlmicol@umh.es
Moritz K. Nowack	moritz.nowack@vib.be
Adriano Nunes-Nesi	nunesnesi@ufv.br
Michael Palmgren	palmgren@plen.ku.dk
Geraint Parry	geraint@garnetcommunity.org.uk
Catherine Perrot-Rechenmann	catherine.rechenmann@cnrs-dir.fr
Barry Pogson	barry.pogson@anu.edu.au
Nicholas Provart	nicholas.provart@utoronto.ca
Roland Pieruschka	r.pieruschka@fz-juelich.de
J. Chris Pires	piresjc@missouri.edu
Kazuki Saito	kazuki.saito@riken.jp
Sigal Savaldi-Goldstein	sigal@technion.ac.il
Ben Scheres	ben.scheres@wur.nl
Ulrich Schurr	u.schurr@fz-juelich.de
Motoaki Seki	motoaki.seki@riken.jp
Kentaro K. Shimizu	kentaro.shimizu@ieu.uzh.ch
Ramamurthy Srinivasan	srinivasan53@gmail.com
Keiko Sugimoto	keiko.sugimoto@riken.jp
Marcela K. Tello-Ruiz	telloruiz@cshl.edu
Chris Town	cdtown@jcvi.org
Doris Wagner	wagnerdo@sas.upenn.edu
Doreen Ware	ware@cshl.edu
Wolfram Weckwerth	wolfram.weckwerth@univie.ac.at
Michael Wrzaczek	michael.wrzaczek@helsinki.fi
Misako Yamayaki	misako.yamazaki@ieu.uzh.ch
Marcelo J. Yanovsky	mjyanovsky@gmail.com
Viktor Žárský	viktor@natur.cuni.cz

The Multinational Arabidopsis Steering Committee
June 2016

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Imprint

Cover design and editing

Marília K. F. de Campos (MASC coordinator), University of Tübingen, Center for Molecular Biology (ZMBP),
Auf der Morgenstelle 32, 72076 Tübingen, Germany, marilia.campos@zmbp.uni-tuebingen.de

Cover images

Endodermal suberin plasticity (top). The root endodermis develops hydrophobic suberin switching from active absorption to protection. Suberization is highly plastic to a range of nutrient stresses in turn to modulate root function. The image shows a whole root system stained with fluorol yellow to highlight suberin. Courtesy of Marie Barberon and Niko Geldner (page 38).

Arabidopsis shoot meristems (bottom). Electron micrographs of wild-type (left) and *rock1* mutant (right), displaying an enlarged meristem. Courtesy of Tomáš Werner and Michael Niemann (page 40).

Further information

www.arabidopsisresearch.org

The MASC report 2015/16 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

Marília K. F de Campos and Loïc Lepiniec wrote articles with input from Inhwan Hwang and Luise H. Brand, if no author is stated.

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Acknowledgements

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The MASC community has been coordinated by Luise H. Brand and Marília K. F . de Campos. MASC thanks M.K.F.C. for overseeing the production of the MASC annual report 2015/2016 and the German Research Foundation (DFG) for profiding financial support during the production process.

MASC especially thanks the members of the organizing committee of the ICAR 2016, Gyeongju, Korea, for providing the funds and Ms. Chloe Choi for organizing the printing of this report.

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Foreword to the Report

It is a great satisfaction to present the latest activities of the Multinational Arabidopsis Steering Committee in this year's MASC report. MASC started in the early 1990's, when scientists from several countries formed an *ad hoc* committee to promote large-scale research with *Arabidopsis thaliana*. 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. Foreseeing that in order to reach this long-term goal a commitment from the global Arabidopsis community was essential, actively engaged researchers developed '*The Multinational Coordinated Arabidopsis thaliana - Genome Research Project*' in 1990. The project represented the first road map guiding Arabidopsis research, and the actions therein proposed ensured the release of the Arabidopsis genome sequence by the year 2000. With this aim accomplished, the community published in 2002 a new decadal plan marking the second road map in a paper entitled '*The Multinational Coordinated Arabidopsis thaliana Functional Genomics Project*'. Although maintaining the original long-term goal, the objectives were revised and a new mission statement was proposed, which read: "To determine the function of every gene of a reference species in its cellular, organismal, and evolutionary context by the year 2010". During the 10 years spanning the Functional Genomics Project, Arabidopsis research flourished at an unprecedented pace. More than 22,700 Arabidopsis-related papers were published between 2001-2010, in contrast to 6,100 during the first road map. This success resulted from the coordinated efforts of the international Arabidopsis community, which has always encouraged open communication, guaranteeing unrestricted exchange of information and resources. MASC has been at the hub of this coordination by serving the community at different levels, e.g. by providing support for the ICAR organization, promoting and guiding discussions on future research directions, and broadcasting the community activities via annual reports and workshops.

By the end of the second road map, plant scientists profited from one of the most comprehensively annotated genomes available, and adopted a more holistic research approach by expanding the focus from single genes/gene families to studies of complex biological organization and processes. The '*Multinational Arabidopsis Steering Committee - From bench to bountiful harvests*' (Lavagi et al., 2012, Plant Cell, 24:2240-7) marks the third decadal road map, in which a plan more suitable for this new research approach was proposed. The major goal stated in the third road map is to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, in order to be able to build predictive models of an Arabidopsis plant.

Being in the middle of the road map, most of the objectives are currently ongoing and additional points have been included. For instance, in 2015 the Arabidopsis community agreed that establishing MASC as a not-for-profit organization would maximize coordination of Arabidopsis research, minimize duplication of efforts and optimize the efficient use of resources via collaboration. The implementation is ongoing and future actions will be discussed at the MASC meeting during the ICAR 2016. Road map goals that were accomplished by 2015/2016 include the successful establishment of the International Arabidopsis Informatics Consortium (IAIC), which intends to partner with the North American Arabidopsis Steering Committee (NAASC) to expand its outreach to the community via evaluation of the training needs for plant researchers of the 21st Century (see US country report, page 87). The IAIC also helped to build the Arabidopsis Information Portal (Araport, https://www.araport.org/), which has in two short years become a fully functional web portal, allowing community participants to develop and deploy their own web services and data integration applications.

The 2015/2016 annual MASC report is the 4th published under the current road map. Here you will read about the progress of MASC activities, and future action items for Arabidopsis research recommended by MASC. Members of seven from the eight MASC subcommittees, representatives of 24 from the 28 country members and directors of all resource centers and community projects engaged with MASC contributed to this year's report. We also feature a small selection of high impact Arabidopsis publications resulting from multinational collaborations, and evaluate the contributions of Arabidopsis in translational research and industry, that is, how Arabidopsis research has had an impact in crop species.

Finally, we hope to provide a comprehensive view on the success of Arabidopsis research via collaborative efforts promoted by MASC, but also to draw the attention to current concerns and challenges faced by Arabidopsis researchers worldwide. MASC thanks the local organizers of the 27th ICAR and all MASC members who contributed to this report.

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Executive Summary

50 years of Arabidopsis Research

The year 2015 marked the 50th anniversary of the most important Arabidopsis conference. Although the usage of *Arabidopsis thaliana* in pioneering plant research has been suggested about 75 years ago, it was in 1965 that researchers envisaging the potential of its application gathered at the 1st Conference on Arabidopsis Research and established one of the most active and growing scientific communities. Along with Arabidopsis' well-known biological traits and the continuous advances in technology, the collaborative efforts and readiness of the community in sharing knowledge and resources were crucial for the success of this small, yet powerful, reference plant.

The engagement of researchers and project leaders with MASC have been fundamental for this success. Arabidopsis research has evolved in an impressively fast pace, urgently requesting coordination in order to avoid duplication of efforts, which would hinder scientific productivity. This annual MASC report is one important outcome of such coordination. MASC members from several countries and research areas summarized herein their activities, many of which were only possible due to collaborative efforts. We present here not only the progress of research projects that were completed in 2015/2016 or are currently ongoing. In the sections to follow, you will also read about the recent changes in the committee organization, the outreach activities promoted by MASC members, the views and concerns shared by the community regarding the future of funding Arabidopsis research and more.

International Conference on Arabidopsis Research (ICAR)

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

26th ICAR, Paris, France: July 5th-9th 2015

27th ICAR, Gyeongju, South Korea: June 29th-July 3rd 2016

Save the dates for the upcoming ICAR!

28th ICAR, St. Louis, Missouri, USA: June 19th-23rd 2017

Progress and Activities of MASC

- MASC chair 2015/2016: Loïc Lepiniec (Jean-Pierre Bourgin Institute, France)
- MASC co-chair 2015/2016: Inhwan Hwang (Pohang University of Science and Technology, Republic of Korea)
- MASC coordinator 2016: Marília K. F. de Campos (University of Tübingen, Germany) funded by the German Science Foundation (DFG)
- 26th ICAR 2015: 974 attendees and 573 submitted poster abstracts (Figure 2, page 10)
- MASC web page: www.arabidopsisresearch.org

Analysis and Recommendations of MASC

On behalf of the Arabidopsis community, the MASC chair Loïc Lepiniec analysed the activities of the committee in the past year and concluded that Arabidopsis research remains very active, efficient and innovative. This is a result of years of collaboration and coordination among scientists from all over the globe, who did not spare efforts in promoting Arabidopsis as the model for scientific discoveries in plant biology. Still, the funding situation in several countries demonstrate a current preference for financing applied versus basic research, which lead to a few concerns regarding the future of Arabidopsis research. Via its several instruments (including this report), MASC will continue to provide a voice for the community and ensure that funding bodies and decision makers become aware of the importance of Arabidopsis not only for pioneering research, but also to serve as a pathway to translation into crops (see Analysis and Recommendations on page 11).

MASC Subcommittees

Currently 8 MASC Subcommittees monitor progress and activities as well as point out future directions of the respective field of Arabidopsis research, stay in close contact with the community and promote international cooperation (pages 13 - 26). This year all subcommittees except one contributed to the MASC report.

- Bioinformatics (page 13)
- ORFeomics (page 14)
- Epigenetics and Epigenomics (page 16)
- Metabolomics (page 17)
- Phenomics (page 18)
- Proteomics (page 23)
- Systems and Synthetic Biology (page 24).

Arabidopsis Community Projects and Resources

The Arabidopsis community and the whole plant community thrive and profit from resource and stock centers, i.e. uNASC, ABRC and RIKEN-BRC, as well as from informatics and data sharing projects and resources like the International Arabidopsis Informatics Consortium (IAIC), Arabidopsis Information Portal (Araport) and The Arabidopsis Information Resource (TAIR). Information on progress and activities of the above mentioned resources can be found in this report (pages 27 - 36). Besides the traditional community projects and resources, here you will also find information on major international collaborative research projects and resources that focus not solely on Arabidopsis but are greatly supported by Arabidopsis researchers. These include the Bio-Analytic Resource for Plant Biology (BAR), BrassiBase, CyVerse, the European Plant Phenotyping Network (EPPN), whose successful activities have led to the creation of EMPHASIS (also reported here), and Gramene, which contributed to the MASC report for the first time.

Arabidopsis Basic Research and Translational Prospects

Scientific Highlights in 2015/2016

Arabidopsis researchers published 4,197 peer-reviewed papers in 2015, a number slightly smaller than the observed in the previous two years (Figure 5, page 37). This reflects an important funding reality observed in several countries, a concern discussed throughout this report. Nevertheless, the numbers are still impressive, as is the quality and the numerous research fields covered by Arabidopsis researchers. In this report, we highlight six research papers published in 2015 and early 2016. Notably, all the selected publications resulted from collaborative efforts from researchers from at least three different countries, demonstrating the international scope of the Arabidopsis community (page 37):

- Adaptation of root function by nutrient-induced plasticity of endodermal differentiation (Cell 164: 447–59).
- DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation (eLife 4:e05255).
- MicroRNA miR396 regulates the switch between stem cells and transit-amplifying cells in Arabidopsis roots (The Plant Cell 27: 3354–66).
- VIH2 regulates the synthesis of inositol pyrophosphate Insp8 and jasmonate-dependent defenses in Arabidopsis (The Plant Cell 27: 1082-97).
- Arabidopsis ROCK1 transports UDP-GlcNAc/UDPGalNAc and regulates ER protein quality control and cytokinin activity (PNAS 1(112):291-6).
- The circadian clock rephases during lateral root organ initiation in *Arabidopsis thaliana* (Nature Communications 6(6):7641).

Contributions of Arabidopsis Research to Applied Research and Industry in 2015/2016

A way of demonstrating the increasing applicability of Arabidopsis research is to look at the number of filed patents (Figure 6, page 41). In 2015, 2,567 international patent applications were published referring to Arabidopsis, 217 less than in the previous year but still following the trend from the last 10 years. The interdependency of basic and applied research is highlighted in this report by four examples of recent applied studies that vitally depend on Arabidopsis data and resources (page 41):

- Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity (Nature Biotechnology, DOI:10.1038/nbt.3535).
- Transgenic citrus expressing an Arabidopsis *NPR1* gene exhibit enhanced resistance against Huanglongbing (HLB; Citrus Greening) (PLoS ONE, DOI:10.1371/journal.pone.0137134).
- PvNAC1 and PvNAC2 are associated with leaf senescence and nitrogen use efficiency in Switchgrass (Bioenerg. Res. 8:868–880).
- Targeted mutagenesis, precise gene editing, and site-specific gene insertion in Maize using Cas9 and guide RNA (Plant Physiology 169: 931-45).

Country Highlights

The wider Arabidopsis and plant community supports MASC by appointing individual country representatives, who are nationally and internationally well connected Arabidopsis researchers. To date 28 countries support MASC and the international Arabidopsis community. Out of these, 24 countries contributed to this MASC annual report (page 45). Researchers from all over the world who are working with Arabidopsis are highly encouraged to get involved in MASC in order to further strengthen the network, international collaboration and data sharing.

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Progress and Activities of MASC

In 2015, Loïc Lepiniec succeeded Nicholas Provart to become **MASC chair** and Inhwan Hwang became **co-chair** (Figure 1). Inhwan Hwang will become new MASC chair when Loïc Lepiniec steps down following the 27th International Conference on Arabidopsis Research (ICAR) 29th June- 3rd July, 2016 in Gyeong Ju, Korea. The **MASC activities were coordinated** by Marília K. F. de Campos from January to June 2016. A three year grant was awarded to Klaus Harter and Detlef Weigel by the German Science Foundation (DFG) for coordination of MASC and the German Arabidopsis Functional Genomics Network (AFGN, www.dbg-afgn.de), performed by Luise Brand until July 2015. The coordinator position was established in 2002 and has been previously supported by the NSF (US) for six years, by the DFG (Germany) for one year and the BBSRC (UK) for three years. The MASC coordinator provides help and coordination to MASC, and the larger Arabidopsis research community. The coordinator's duties include:

1. Serving as executive secretary of MASC
2. Providing assistance to local representatives in the organization of the annual ICAR
3. Writing and editing of the annual MASC progress report with input from MASC members
4. Serving as liaison between members of MASC, the international research community, funding agencies, databases and stock centers
5. Maintaining and updating the MASC web pages to inform the global research community about various opportunities, collaborations, large-scale activities and research progress
6. Organizing the annual MASC meeting during the ICAR.

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

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from seven of the eight current subcommittee chairs/co-chairs: Bioinformatics, ORFeomics, Epigenetics and Epigenomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics and Systems and Synthetic Biology (page 13). The requirements for a subcommittee to be considered active were formulated in 2009:

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

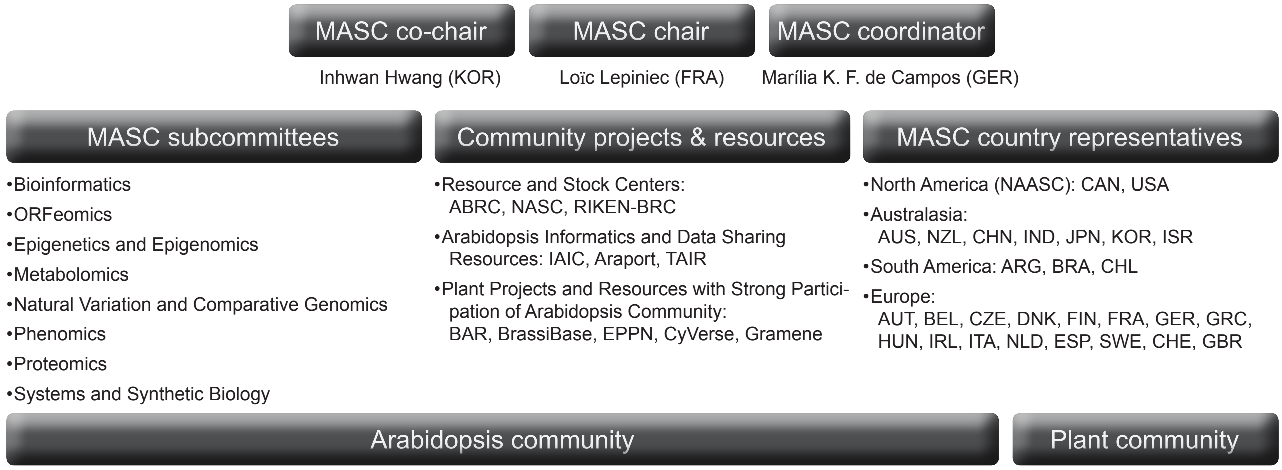

Figure 1. Multinational Arabidopsis Steering Committee (MASC). For explanation of abbreviations see MASC subcommittee (page 13), Arabidopsis community projects and resources (page 27) and MASC country reports (page 45)

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Representatives of **Arabidopsis community projects and resources** attend the annual MASC meeting and contribute to the annual MASC report to broadcast their progress, activities and goals to the community (page 27). The three resource and stock centers, i.e. the Arabidopsis Biological Resource Center (ABRC, US), the Nottingham Arabidopsis Stock Centre (uNASC, UK) and the RIKEN BioResource Center (RIKEN BRC, Japan), continue to encourage donations to keep their stocks up-to-date following the newest technologies. In order to ensure a broader and more efficient distribution of resources within the community, the stock centers operate coordinately with each other, as well as with Arabidopsis online portals. Progress of Arabidopsis informatics and data sharing resources is also highlighted in this year's report, including updates from The International Arabidopsis Informatics Consortium (IAIC), the Arabidopsis Information Portal (Araport) and The Arabidopsis Information Resource (TAIR). Efforts of five community projects and resources with strong participation of the Arabidopsis community are also herein presented (page 33).

Country representatives attend the annual MASC meeting held during ICARs and contribute to the annual MASC report by submitting country reports. In 2015/2016, 28 countries have been involved in MASC and 24 contributed to this year's report. Brazil and Chile joined MASC in 2016, being represented by Wagner Araújo and Rodrigo A. Gutiérrez, respectively. Jorge J. Casal stepped down as the Argentinian representative and Marcelo J. Yanovsky and Javier Palatnik stepped in as co-chairs. Maura Cardarelli now represents Italy following Giovanna Serino. MASC thanks the former country representatives for their valuable contributions and highly encourages researchers working on Arabidopsis to get involved in MASC activities, e.g. subcommittees, projects and resources or as country representatives.

Since December 2013 the **MASC websites** are hosted at www.arabidopsisresearch.org. The coordinator began to transfer the data from the MASC pages hosted at TAIR to the new server and the process is to be finished soon. TAIR will continue to kindly provide access to the old MASC pages at http://www.arabidopsis.org/portals/masc/index.jsp. The independent hosting of the MASC sites will contribute to a better visibility of MASC and the connection between the International Conference on Arabidopsis Research (ICAR) and MASC can be represented from now on by hosting of the ICAR websites at www.arabidopsisresearch.org.

The **26th International Conference on Arabidopsis Research** (ICAR) was held in Paris, France from July 5th - 9th 2015 and was organized by Catherine Perrot-Rechenmann and Loïc Lepiniec. The meeting was very successful and there was a great atmosphere celebrating the 25th anniversary of the ICAR. 974 people attended the 26th ICAR in Paris and almost 60% of the attendees (573) submitted a poster abstract (Figure 2). On average 63% of the attendees presented a poster during the ICARs over the last 10 years. The MASC report 2014/15 was distributed to every attendee at the 26th ICAR. Around 54% of ICAR attendees either read most of the report, or looked at it and found it useful. The success of the 26th ICAR was also due to efforts of many MASC members who were involved in the program. For instance:

- ABRC and NASC booth, RIKEN booth, TAIR booth;
- 5 community workshops: "Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology", "From Systems Biology to Synthetic Biology in plants", "Epigenomics", "Novel Tools and Techniques: MASC workshop", "The Arabidopsis Information Portal for Users and Developers";
- and many sessions related to road map goals, e.g. "Translational Biology and Biotechnologies: from Arabidopsis to Crops", "Natural Variation and Evolution", "Systems Biology and New Approaches", just to name a few.

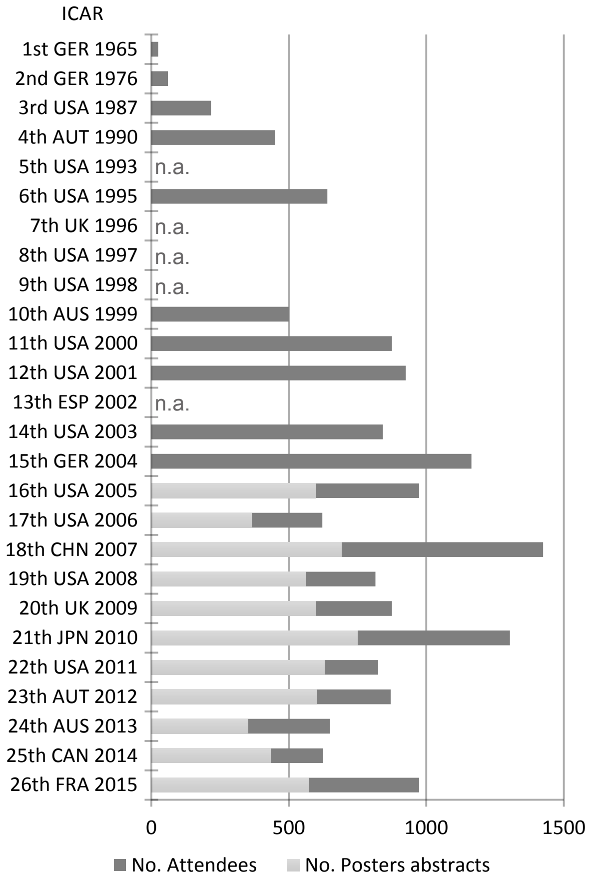

Figure 2. Number of attendees (dark grey) and number of posters presented (light grey) at the International Conference on Arabidopsis Research since 1965 (n.a. - no data available,1965-2004 no number of posters available).

Analysis and Recommendations by MASC

Compiled by Loïc Lepiniec with input from Nicholas Provart and Marília K. F. de Campos, along with comments from the wider Arabidopsis community.

Coordinating Arabidopsis Research

The main objective of MASC is to promote and facilitate research on Arabidopsis, a powerful reference system for molecular and genetic approaches. Thus, the main activities of MASC comprise fostering international collaborations, supporting scientific meetings and outreach activities, providing a cohesive voice for the community, and developing biological resources and bioinformatics tools. As emphasized by the recent review "50 years of Arabidopsis research" (Provart et al., 2015), significant progress has been made in all these areas during the last decade. As described in this report and briefly exemplified below, the year 2015 followed along the same lines, generating new scientific knowledge, fruitful meetings and useful resources and tools. Nevertheless, a few concerns arise about the future, which include the funding of basic research in some countries, and lead to questions about the future of Arabidopsis research and the model and role of MASC.

As described in more detail in this annual report, all the stock centers continue to encourage donations to keep their stocks up-to-date (sharing your CRISPR/Cas9 mutants with the stock centers will reduce your workload!). An efficient and wide distribution of resources is ensured by the strong collaboration between ABRC and NASC, who also joined efforts to work on a common Stock Centre Module. Concerning informatics resources, Araport has completed the most up-to-date re-annotation of the Col-0 genome. The International Arabidopsis Informatics Consortium (IAIC) is exploring the possibility for continuing its activity in conjunction with the new US NSF Research Collaboration Network "ART-21" (Arabidopsis Research and Training for the 21st Century) award to S. Brady (PI) and J. Friesner (co-PI), which envisages outreach to community members to enable analysis of future training needs and emerging bioinformatics and computational skills. A new BAR homepage has been implemented, where more than 54,000 Arabidopsis papers and their citations from the Provart et al. review can be interactively explored (http://bar.utoronto.ca/50YearsOfArabidopsis/). The iPlant Collaborative has been rebranded as CyVerse and has expanded to provide support to all life sciences. The existing database Gramene contributed to this year's report for the first time; it provides integrated data resource for comparative functional genomics in crops and model plant species. Nevertheless, the use of (and contribution to) new informatics tools such as Araport is growing more slowly than expected.

The country and subcommittees reports show that Arabidopsis research is very active worldwide and well interconnected. The last ICAR conference in Paris (ICAR 2015) was a great success with almost one thousand attendees, and the preliminary number of registrations for the 2016 conference (Gyeongju, Korea) is more than encouraging! We are also happy to welcome two new country memberships (Chile and Brazil), both with a growing Arabidopsis community. Globally, Arabidopsis remains the choice for pioneering molecular and genetic approaches, to address fundamental questions and modeling biological systems, to unravel molecular mechanisms, to identify and test gene function and to act as a model for discovery, serving as pathway to translation (see Figure 5, page 37). Nevertheless, the total number of Arabidopsis publications has stopped increasing. Some countries (4) mentioned good support of Arabidopsis research funding with positive prospects, but an increasing number of countries (7) have reported concerns about decreasing funding for basic research mainly due to a trend towards funding applied research. In addition, other countries (5) either have traditionally a strong focus in crop research or are encouraged by governments, industrial partners and funding agencies to demonstrate applicability of the findings using Arabidopsis, as well as to enhance collaboration between universities and breeding companies.

In conclusion, the results obtained over the past year demonstrate that Arabidopsis research remains very active, efficient and innovative. The fact that the number of publications remains fairly constant even with declining funding must be considered encouragingly. However, several concerns have arisen. Different ways to strengthen and sustain Arabidopsis research at the international level have been proposed by the MASC Future Subcommittee (R. Bastow, S. Brady, L. Brand, A. Caño-Delgado, J. Friesner, K. Harter, B. Pogson, N. Provart, and K. Sugimoto). Analyzing the different options, it was decided during the last ICAR meeting in Paris to transform the MASC into a not-for-profit corporation. Thanks to N. Provart, the implementation is in progress and will be achieved in the coming months. The impacts on the future of the MASC, its objectives, activities, organization and funding model will be discussed during ICAR 2016 in Korea.

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Reports of the MASC Subcommittees

Bioinformatics

http://arabidopsisresearch.org/index.php/subcommittees/bioinformatics

By Nicholas Provart (chair) with contributions from subcommittee members and the wider Arabidopsis community.

Tools and Resources

Compiled by Nicholas Provart with input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community. 11 Apr 2016.

Araport.org: Work towards creating a new Arabidopsis Information Portal by the International Arabidopsis Informatics Consortium continued (International Arabidopsis Informatics Consortium, 2012), with community meetings held at the ICAR in Paris in 2015, and at the PAG Conference in San Diego in January 2016. The new portal has been online since April 2014 at http://araport.org. The Araport team has also mapped 113 RNA-seq data sets from the Sequence Read Archive at NCBI in order to identify novel splice variants for the newest Arabidopsis genome release (Araport11). This release of the Araport11 protein coding gene set contains 27,655 loci with 48,359 transcripts. Of TAIR10 protein-coding gene models, 68.9% (24,385/35,385) have been updated among which 4.7% (1,191) and 95.3% (24,367) have altered CDS and UTR sequences respectively. The number of genes in Araport11 with splice variants (10,696; 38.7%) of the genes is much higher than reported in TAIR10 (20.8%). The functional annotation of over 5000 of the TAIR10 loci has been updated. In addition, a total of 747 new loci and 12,973 new splice isoforms were added in this current release.

Eva Huala and colleagues at TAIR have successfully moved to a subscription-based model, and their non-profit organization, Phoenix Bioinformatics, continues TAIR's annotation work (Reiser et al., 2016). They released the 5th Public Release of new annotations in January 2016, containing annotations and other data added through the end of December 2014. Data added in 2014 and publicly released in 2015 included updates to gene summaries, new allele and phenotype data, a total of 677 new gene symbols, and new GO and PO annotations for 17,876 genes (including experiment-based annotations from published research articles for 2,936 genes). In addition to freely releasing all new data after one year, TAIR also continues to provide free access for students using TAIR in their coursework upon request from the course organizer.

Shisong Ma from the Dinesh-Kumar Lab at UC Davis published their "AtGGM2014", a gene co-expression network, derived from ~10,000 ATH1 microarrays (Ma et al., 2015). It uses partial correlation coefficient (Pcor) to calculate co-expression patterns between genes. 651 gene modules functioning in various developmental, stress response, hormone response, or housekeeping pathways were identified. These modules can be used by plant biologists for hypothesis generation. It is accessible at http://dinesh-kumarlab.genomecenter.ucdavis.edu/atggm2014.html. In related work, but based on large numbers of CATMA array data sets, Véronique Brunaud and colleagues at INRA in France published their GEM2Net tool (Zaag et al., 2015) to identify 681 coexpression clusters under biotic and abiotic stress conditions, see http://urgv.evry.inra.fr/GEM2NET/.

Large-scale biology (selected): Steven Clouse's group at the NC State University published an autophosphorylation site database for leucine-rich repeat receptor-like kinases covering 592 phosphorylation events in Arabidopsis at http://www4.ncsu.edu/~sclouse/Clouse2010.htm (Mitra et al., 2015). Murray Grant's group in Exeter published a high-resolution timecourse of RNA dynamics in Arabidopsis leaves following challenge with *Pseudomonas syringae* pv tomato DC3000 and the same strain lacking HrpA to tease apart events associated with microbial-associated molecular pattern-triggered immunity versus effector-triggered susceptibility (Lewis et al., 2015). John McKay's group at Colorado State University used gene expression and epistasis to identify candidate genes for drought-associated QTLs in Arabidopsis (Lovell et al., 2015). The Gregory Lab at the University of Pennsylvania published a comprehensive data set of RNA-binding protein/RNA interactions and nuclear RNA secondary structure as determined using their nuclear PIP-seq method (Gosai et al., 2015). The data are available at http://gregorylab.bio.upenn.edu/PIPseq_AtTotalNuc/.

In terms of large-scale image analysis, George Bassel's group in Birmingham developed 3DCellAtlas to extract biologically relevant information from quantitative 3D image data (Montenegro-Johnson et al., 2015).

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Zaag R, Tamby JP, Guichard C, Tariq Z, Rigaill G, Delannoy E, Renou JP, Balzergue S, Mary-Huard T, Aubourg S, Martin-Magniette ML, Brunaud (2015) GEM2Net: from gene expression modeling to -omics networks, a new CATdb module to investigate Arabidopsis thaliana genes involved in stress response. Nucleic Acids Res. 43: D1010-7; doi: 10.1093/nar/gku1155.

Clone-Based Functional Genomics Resources (ORFeomics)

http://arabidopsisresearch.org/index.php/subcommittees/orfeomics

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

Progress Towards Road Map Goals

The subcommittee goal is to keep tracking progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes.

Future Goals

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

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

Our recent search showed that now about 23,000 Arabidopsis protein-coding genes have been isolated as Full-length cDNA (ORF) clones. One of the last unexplored continents of Arabidopsis are the remaining 6,000 protein-coding genes. After that, only the non-coding genes remain to be isolated.

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

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

Tools and Resources

We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Table 1).

The revised ones are shown in italics. New clones include Gateway clones for 73 kinase genes.

Selected Publications

- Breton G, Kay SA, Pruneda-Paz JL. (2016) Identification of Arabidopsis Transcriptional Regulators by Yeast One-Hybrid Screens Using a Transcription Factor ORFeome. Methods Mol Biol. 2016;1398:107-18.

Table 1. Arabidopsis ORF and cDNA clone repositories. Stock centres distributing Arabidopsis clone repertoires:

- Arabidopsis Biological Resource Center (ABRC, USA), http://www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm
- RIKEN BioResource Center (BRC, Japan), http://www.brc.riken.jp/lab/epd/Eng/catalog/pDNA.shtml
- GABI Primary Database (GABI/RZPD, Germany), http://gabi.rzpd.de/
- National Resources Centre for Plant Genomics (CNRGV, France), http://cnrgv.toulouse.inra.fr/ENG/index.html
- European Arabidopsis Stock Centre (NASC, United Kingdom), http://arabidopsis.info/
- BCCM/LMBP Plasmid and DNA library collection (BCCM/LMBP, Belgium), http://bccm.belspo.be/db/lmbp_gst_clones/
- Open Biosystems Inc., www.openbiosystems.com/

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14.398	signal.salk.edu	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12.114	signal.salk.edu	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 sub-cellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/ sheenweb/category_genes.html	ABRC
Steve Clouse	***Gateway expression***	***N-terminal Flag/His tagged kinases***		***855 (73 new in 2015)***	***http://www4.ncsu.edu/~sclouse/Clouse2010.htm***	***ABRC***
Frommer et al.	Gateway entry, no stop	Membrane and signaling proteins	5' and 3' end seq.	2.712	http://associomics.org	ABRC
Frommer et al.	Gateway Expression (mbSUS clones)	Membrane and signaling proteins	5' and 3' end seq.	5.414	http://associomics.org	ABRC
AIST/RIKEN	***Gateway entry, no stop***	***Transcription factor***	***Full sequence***	***1.996***		***BRC***
RIKEN	***Gateway entry, no stop***	***Transcription factor***	***Full sequence***	***400***		***BRC***
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	pIX-HALO vector			12.069		ABRC
Guillaume Pilot	pDONRZEO vector	Membrane protein	5' and 3' end seq	192		ABRC
Pruneda-Paz et al.	Gateway Entry, stop	Transcription factor	Full sequence	1.956		ABRC
Pruneda-Paz et al.	Gateway Destination, stop, pDEST22	Transcription factor	Full sequence	1.956		ABRC
Lao et al.	Gateway DONR, no stop, pDONR223	glycosyltransferases	Full sequence	429	http://gt.jbei.org/	ABRC
Amita Kaundal et al.	Gateway DONR, no stop, pDONR201			26		ABRC
cDNA clones						
RIKEN/SSP/ Salk Insitute	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	25.000	www.brc.riken.go.jp/lab/ epd/Eng/order/order.shtml	BRC
MPI-MG	Gateway expression		5' end seq.	4.500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28.866	www.genoscope.cns.fr/ Arabidopsis	CNRGV

- Nemoto K, Takemori N, Seki M, Shinozaki K, Sawasaki T. (2015) Members of the Plant CRK Superfamily Are Capable of Trans- and Autophosphorylation of Tyrosine Residues. J. Biol. Chem. 290(27):16665-77.
- Ramadan A, Nemoto K, Seki M, Shinozaki K, Takeda H, Takahashi H, Sawasaki T. (2015) Wheat germ-based protein libraries for the functional characterisation of the Arabidopsis E2 ubiquitin conjugating enzymes and the RING-type E3 ubiquitin ligase enzymes. BMC Plant Biol. 15:275.

Epigenenetics and Epigenomics

http://arabidopsisresearch.org/index.php/subcommittees/epigenomics

By Doris Wagner

Progress Towards Road Map Goals

The four AIMS of the EPIC/MASC initiative were:

1) Identify intellectual questions, transformative methodologies and infrastructure required to advance plant epigenomics.

2) Establish an international epigenomics research network to communicate and coordinate research activities in countries/regions including the US, South America, Australia, Asia, UK, and continental Europe.

3) Coordinate access to plant epigenomics information via a central website, (to serve primarily as a resource for researchers, as well as an educational resource for teachers and students).

4) Establish a user-friendly epigenome browser platform that allows easy upload and display of user-generated epigenomic datasets and published datasets. Develop standards for plant epigenomics data collection, deposition and display.

The EPIC RCN ended April 2016.

Major Activities:

The EPIC initiative organized 5 scientific symposia with associated EPIC organizational meetings. These were held at the Chinese Academy of Sciences in 2012, at the John Innes Centre in Norwich UK in 2013, at the University of Pennsylvania in 2014, in Suzhou with Cold Spring Harbor Asia in 2015 and in Taos NM with Keystone Symposia in 2016. Additional organizational meetings include one held in conjunction with PAG in 2010 and a Banbury meeting in 2011. Yearly workshops were held at PAG (2010-2016) and at ICAR (2010-2016).

In addition EPIC, together with the Gordon and Betty Moore Foundation, iPLant and PGRP has developed a unified plant epigenome browser platform (https://genomevolution.org/wiki/index.php/EPIC-CoGe).

Specific Objectives:

Enhance the understanding of the role and regulation of plant epigenomes.

Significant Results:

The combined activities of EPIC have much enhanced the appreciation and understanding of plant epigenetic/epigenomics and have enabled international collaborations aimed at understanding the roles and regulation of plant epigenetics/epigenomics.

The jbrowse EPIC CoGE browsers (Arabidopsis, maize, soybean, rice) being developed will greatly facilitate comparative plant epigenomic analyses.

A white paper, detailing the challenges and approaches to be used to tackle understanding of the plant epigenome, was published in the Plant Cell in 2012.

Key outcomes or Other achievements:

General awareness and interest in epigenetics and epigenomics has increased. In the last year alone Plant Physiology, the Plant Journal and Molecular Plant all had special focus issues on Plant Epigenetics. The ICAR and related conferences also now have a session on Plant Epigenetics.

Future Goals

EPIC will continue with a newly formed steering committee consisting of Doris Wagner (transition only), Nathan Springer (USA), Toshiro Ito (Japan) and 1-2 european members (TBA) to organize symposia and EPIC organizational meetings every 2 years. In addition this group will continue to promote development and improvement of the EPIC CoGe browser. Finally, it will strive to enhance training in plant epigenetics and help forge bridges to other plant biology disciplines as well as to breeders and to industry.

Tools and Resources

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

Conferences and Workshops

- The EPIC initiative organized scientific symposia with associated EPIC organizational meetings.
- Symposium on Epigneetics and Development Suzhou China with Cold Spring Harbor Asia in 2015 (organized by Xiao Feng Cao , Justin Goodrich and Doris Wagner).
- Symposium on Epigenetics and adaptation to the environment in Taos NM with Keystone Symposia in February 2016 (organized by Scott Michaels, Nathan Springer and Doris Wagner).
- A workshops was held at PAG in San Diego, CA (January 2016) organized by Rob Martienssen.
- A workshop was held at the ICAR in Paris, France (July 2015) organized by Francois Roudier and Doris Wagner.

Selected Publications

- Nick Provart et al. (2016). 50 years of Arabidopsis research: highlights and future directions. New Phytologist. 3 921-944. Chapter on Epigenetics by Craig Pikaard, Vincent Colot and Doris Wagner.
- Special issue on Plant Epigenetics in Plant Physiology, edited by Anna Amtmann, Hong Ma and Doris Wagner.

Metabolomics

http://arabidopsisresearch.org/index.php/subcommittees/metabolomics

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

Progress Towards Road Map Goals

Since metabolomics is an important component of Arabidopsis omics, a continuous goal of this subcommittee will be to promote metabolomics research of Arabidopsis leading to functional genomics and systems biology. For this purpose we plan to establish a website for the initial process of consolidating Arabidopsis metabolomics activities making them more visible for the community. Full integration of Arabidopsis-based metabolomics research with the activity of the Metabolomics Society (http://www.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 Goals

To realize the goals, we aimed to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. This subcommittee website has been launched at (www.masc-metabolomics.org). 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. A MASCM gator portal is under development comparable with the MASCP gator portal (http://gator.masc-proteomics.org/). The webinterface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases.

Tools and Resources

- www.masc-metabolomics.org

  Metabolomics subcommittee website
- http://prime.psc.riken.jp/

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

- www.plantmetabolomics.org

  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 is a database for Metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments and is a collaborative multi-laboratory effort including groups specialising in plant metabolism.

Conferences and Workshops

- 2015/6/29-7/2, Metabolomics 2015, San Francisco, US
- 2015/7/19-24, Gordon Research Conference, Plant Metabolic Engineering, Waterville Valley, US
- 2015/12/15-20, Pacifichem 2015, Genomics and Metabolomics for Phytochemical Research, Honolulu, US
- 2016/6/27-30, Metabolomics 2016 in partnership with Plant Metabolomics Forum, Dublin, Ireland
- 2016/7/24-27, 9th Joint Natural Products Conference 2016, Copenhagen, Denmark
- 2016/8/6-10, 55th Annual Meeting of th Phytochemical Society of North America, Davis, US
- 2016/11/21-24, International PSE Symposium, Plant Omics and Biotechnology for Human Health, Gent, Belgium

Selected Publications

- Higashi Y, Okazaki Y, Myouga F, Shinozaki K, Saito K (2015) Landscape of the lipidome and transcriptome under heat stress in *Arabidopsis thaliana*. Scientific Reports 5: 10533 doi:10.1038/srep10533
- Sumner LW, Lei Z, Nikolau BJ, Saito K (2015) Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. Natural Products Reports 32: 212-229
- Schulz E, Tohge T, Zuther E, Fernie AR, Hincha DK (2015) Natural variation in flavonol and anthocyanin metabolism during cold acclimation in *Arabidopsis thaliana* accessions. Plant Cell & Environment 38: 1658–1672

Phenomics

http://arabidopsisresearch.org/index.php/subcommittees/phenomics

By Fabio Fiorani (co-chair), Robert Furbank (former co-chair), Justin Borevitz, John Doonan, Joe Ecker and Christine Granier

Progress Towards Road Map Goals

- In 2015 there has been a continued development of automated platforms and methods including new software for non-invasive phenotyping of Arabidopsis and crop phenotyping, increasing the capacity and the number of research centers that are engaged in large-scale phenomics research.
- There were significant examples of comprehensive pipeline approaches to link genome to phenome and enable multi-trait analysis towards this goal.
- Comprehensive efforts continued in 2015 within The International Plant Phenotyping Network, the European Plant Phenotyping Network (providing access to external users), the EU COST Action Phenotyping, and the implementation of national phenotyping networks in Germany (DPPN), France (Phenome), UK (UKPPN), and Australia (APPF), in particular.
- There were multiple training activities in phenotyping organized in Europe.

Future Goals

- Promote best practices in phenotyping experimentation. This includes consideration to best practices for validating the identity of genetic stocks and the effects of genetic variants as recently suggested in a letter to Plant Cell (http://www.plantcell.org/content/early/2016/03/08/tpc.15.00502.full.pdf+html?utm_content=buffer67a68&utm_medium=social&utm_source=twitter.com&utm_campaign=buffer).
- Coordinated efforts will be required across phenotyping centers regarding germplasm used for sequencing (e.g.1001 genome project) and mutant collections would be desirable. Notable examples include to phenotype all re-sequenced Arabidopsis accessions under a series of defined challenging environments and phenotype the "no phenotype" T-DNA knock-out mutants by subjecting the collection of homozygous T-DNA k.o. mutants, or double mutants hitherto without a discernable mutant phenotype to deep phenotyping under a series of well-defined challenging environments.
- Continue the development of methods for phenotyping across well-defined environmental conditions.

Tools and Resources

Updates by Stijn Dhondt, Dirk Inzé (VIB, Gent, Belgium), Minami Matsui, David Gifford (RIKEN, Japan), Lukás Spíchal (Olomouc, Czech Republic), Christine Granier (INRA Montpellier), Astrid Junker and Thomas Altmann (IPK Gatersleben)

RIKEN and University of Tokyo

- RIPPS (RIKEN Plant Phenotyping System) (K. Shinozaki, Miki Fujita, Kaoru Urano, Takanari Tanabata) is an automated system for evaluating plant growth under environmental stress conditions developed by the Gene Discovery Research Group of CSRS. RIPPS provides high-throughput and accurate measurements of plant traits, facilitating understanding of gene function in a wide range of environmental conditions (http://bit.ly/1sObBEE). Recent research results from RIPPS include studies of Arabidopsis transgenics that perform well under drought conditions without growth reduction. Recent research includes results from the RIPPS which helped by its ability to focus on water use efficiency, not just growth or leaf shape (Kuromori et al., 2016).
- A phenotype analysis program was developed at the University of Tokyo to characterize the pattern of epidermal cells and guard cells of Arabidopsis leaves and seedlings. Research is funded by JST Project (http://bit.ly/22oyHC6) for evaluation of morphological measurement. CARTA (clustering-aided rapid training agent) software was developed for auto learning system (Dr. Kutsuna, N. and Hasezawa, S., University of Tokyo; Higachi et al., 2015).
- RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) is an integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary, with both RIKEN RAPID and CSHL Trapper DB for Ac/Ds transposon tagged lines in Arabidopsis. (Akiyama et al., 2014; Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki)(http://rarge-v2.psc.riken.jp/).
- The Chloroplast Function Database II is a comprehensive database analyzed by combining genotypic and phenotypic multiparametic analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins. The phenotype and segregation data of Arabidopsis Ds/Spm and T-DNA-tagged mutants of nuclear genes encoding chloroplast proteins includes more than 300 morphological mutants and 48 transmission electron microscopic images of mutant plastid (Fumiyoshi Myouga and Kazuo Shinozaki) (http://rarge-v2.psc.riken.jp/chloroplast/).
- PosMed Positional Medline (Y. Makita, et al. RIKEN Synthetic Genome Research Group) Semantic web association study (SWAS) search engine ranks resources including Arabidopsis genes and metabolites, using associations between user-specified phenotypic keywords and resources connected directly or inferentially via a semantic web of biological databases such as MEDLINE, OMIM, pathways, co-expressions, molecular interactions and ontology terms (http://omicspace.riken.jp/).
- For Genome to Phenome, location information of T-DNA in the genome is available for RIKEN Arabidopsis Activation Tagging lines (Minami Matsui collaboration with NEC Soft co ltd.) (http://metadb.riken.jp/metadb/db/SciNetS_ria37i) and around 10,000 Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA Over-eXpressing) lines is available (http://ricefox.psc.riken.jp/).
- The RIKEN MetaDatabase portal site is used to provide information on RIKEN's various life science databases. In this database phenotype information of Activation tagging lines, Ac/ Ds transposon lines and FOX lines are available (http://metadb.riken.jp/).
- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) selected about 4,000 transposon insertion lines which have the Ds transposon in gene coding region, and observed visible phenotypes systematically depending on growth stage. Phenotypic descriptions were classified into eight primary and fifty secondary categories, then all recorded images can be searched by the line number or the phenotype categories (http://rarge-v2.psc.riken.jp/phenome/).

VIB, Plant Systems Biology, Gent, Belgium

- An integrated network of Arabidopsis growth regulators was built. Next, this network was used for gene prioritization (Sabaghian et al., 2015). Several review papers were published looking into plant growth via gene regulatory networks and how phenotypic measurements and tools can support this integrative analysis (Vanhaeren et al, 2016; Vanhaeren et al, 2015; Wuyts et al, 2015; González et al, 2015).
- Clauw et al. (2015) analyzed leaf and rosette growth response of six *Arabidopsis thaliana* accessions to mild drought stress. They employed the automated phenotyping platform WIWAM, which strictly controls the applied watering regime via allowing an automated weighing, watering and imaging of the plants. Analysis of growth related phenotypes and results from genome-wide transcriptome analysis (using RNA sequencing) indicate the existence of a robust response over different genetic backgrounds to mild drought stress in developing leaves. The analysis of a larger set of natural accessions is currently ongoing.
- Van Landeghem et al. (2016) presents a generic, ontology-driven framework to infer, visualise and analyse an arbitrary set of condition-specific responses against one reference network. To this end, they have implemented novel ontology-based algorithms that can process highly heterogeneous networks, accounting for both physical interactions and regulatory associations, symmetric and directed edges, edge weights and negation. As an illustrative application, they demonstrate its usefulness on a plant abiotic stress study and experimentally confirmed a predicted regulator.

- Stützel et al. (2016) propose the establishment of a European Consortium for Open Field Experimentation (ECOFE) that will allow easy access of European plant and soil scientists to experimental field stations that cover all major climatological regions. Coordination and quality control of data extraction and management systems will greatly impact on our ability to cope with grand challenges such as climate change and food security.

The Centre of the Region Haná for Biotechnological and Agricultural Research, Palacky University Olomouc, Czech Republic

Our department is equipped with two phenotyping systems PlantScreenTM (PSI, Brno, Czech Republic) dedicated to integrative phenotyping of shoots of various plant species (Humplík et al. 2015a). Phenotyping platform allows measurement of plant growth, chlorophyll fluorescence, leaf temperature and leaf reflectance in fully controlled environment. Experiments performed in the systems are mainly focused on the evaluation of effectivity of synthetic growth regulators or potential bio-stimulants (Bahaji et al. 2015), but the selection of mutants or cultivars can be also provided upon request. As a response on global demand we are developing protocols for assessing impact of various abiotic stresses in different plant developmental stages. One of our aims is selection of cold-tolerant cultivars of field pea (*Pisum sativum* L.), for which the optimized measuring protocol was developed (Humplík et al. 2015b). Another applied analysis deals with the problem of salinity in the early development of crop species. Recently, we have developed crop seedling emergence software that reveals ability of seeds to germinate and of the seedlings to reach the light before the reserves are exhausted. This high-throughput bioassay (60 variants, 6600 seeds; in one run) automatically provides information about emergence rate as well as the total number of emerged seedlings. Further standardized protocols include in vitro screening of Arabidopsis growth by RGB camera in 24-well or 6-well plates (up to 11 000 seedlings) or complex phenotyping of Micro-Tom tomatoes and baby-lettuce grown in pots.

INRA LEPSE Montpellier, France

Over the past 10 years, the Phenopsis platform has proven its efficiency to disentangle the integrated phenotype of *Arabidopsis thaliana* under controlled environmental conditions. Phenopsis is part of the Montpellier Plant Phenotyping Platforms (M3P), including three installations PhenoArch, Phenodyn and Phenopsis, hosted and developed by the same research group, INRA-LEPSE (https://www6.montpellier.inra.fr/m3p/). The huge genetic diversity of *A. thaliana* already investigated in Phenopsis has still been increased with genetically modified lines (Massonnet et al., 2015), collection of accessions (Bac-Molenaar et al., 2015, 2016), populations of recombinant inbred lines (Vasseur et al., 2014) and epigenetic hybrids (Dapp et al., 2015). High-throughput phenotyping effort was combined with genetic analyses (Bac-Molenaar et al., 2015, 2016), statistical modelling (Lièvre et al., 2016) or molecular profiling know-hows (Baerenfaller et al., 2015), giving insights into the regulation of phenotypic changes under various environmental conditions. In the last years, there has been considerable effort in extending the limits for precision phenotyping and exploring the capacities for developing efficient translational biology from models to cultivated species. Beyond the consequence of a significant decrease in research funding dedicated to model species at the benefit of applied research programs it appears important to develop comparative approaches (Blonder et al. 2015). To meet this challenge, recent developments of the Phenopsis platform include the possibility to grow plants in greater soil volume without impairing automated watering and image acquisition that take into account aerial architecture. Greater effort is also put into the exploration of more diverse climatic scenarios including continuous vs. intermittent moderate and severe water deficit combined with other abiotic and biotic factors (Bresson et al. 2015). Promising results have been obtained on the plasticity of plant development in response to drought stress in canola, tomato and *Brachypodium distachion*.

IPK Gaterlseben, Germany

- The whole plant phenotyping infrastructure at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben, Germany) comprises three conveyor belt-based, automated, high throughput plant-to-sensor phenotyping facilities (Junker et al. 2015). The system for small plants such as Arabidopsis is situated inside a phytochamber and allows for growth and automated imaging as well as weighing/watering of up to 4608 plants in parallel under fully controlled environmental conditions. Imaging in the RGB and near-infrared wavelength ranges, imaging of static and functional fluorescence in combination with 3D surface scanning enables the quantification of a hundreds of plant features ranging from plant architectural traits (plant height and width, projected leaf area (top, side view), estimated volume, Klukas et al. 2014), through physiological traits (color-related traits, Klukas et al. 2014, CHL fluorescence-related such as Fv/Fm, Fv'/Fm', PhiPSII, relations to moisture content by NIR), to 3D related traits (leaf angles, 3D corrected projected areas).
- Experience cumulated since 2011 was used to establish appropriate experimental procedures and designs that support the detection of genotypic and environmental effects on plant growth, development, and performance (Junker et al. 2015). This includes procedures for estimation of variance components and appropriate correction of potential inhomogeneities of conditions in the plant growth area. To enable the logging of the environmental regime the plants are exposed to during the course of experiments, a wireless sensor network has been installed for the continuous monitoring of light intensity (PAR), air temperature,

rel. air humidity, light spectrum, radiation balance, and CO_2 concentration at any place inside the growth chamber. Further upgrades are intended in order to enable simultaneous root and shoot phenotyping.

- Standard experimental procedures are implemented that enable phenotypic analyses of plants under various treatments such as drought and salt stress (Muscolo et al. 2015, Harshavardhan et al. 2014) and the assessment of specific plant traits such as flowering timepoint, water use efficiency and plant organ movements. Recent and future activities involve the phenotypic characterization of an Arabidopsis accession panel under controlled environmental variation as well as hybrids and segregating populations with respect to the detailed analysis of the genetic basis of growth and metabolism control and heterosis.
- The existing image analysis platform (IAP, Klukas et al. 2014) is currently being extended for the integrated/combinatorial analysis of the data (projected 2D images, 3D point clouds) derived from the various camera and scanning installations of the multi-sensor setup in order to retrieve novel information and to increase the precision (spatial resolution) of phenotypic trait extraction and data interpretation.
- Resources: IAP - Integrated Analysis Platform (http://iapg2p.sourceforge.net/), has been designed and developed to support the analysis of large-scale image data sets of different camera systems. It aims at bridging various -omics domains and offers integrated approaches for image analysis up to data post-processing. (Klukas et al. 2014); PGP - Plant Genomics and Phenomics Research Data Repository (http://edal.ipk-gatersleben.de/repos/pgp/) provides infrastructure to publish plant research data, in particular cross-domain datasets and phenomics datasets and respective metadata information, which are assigned with citable DOIs for access and reuse by the scientific community (Arend et al. 2016).

IBG2, Forschungszentrum Jülich, Germany

- Bühler et al. (2015) developed a new software for leaf vein segmentation and analysis named phenoVein. This is a user-friendly tool designed for automated, fast and accurate leaf vein traits including model-based vein width determination. Validation included the quantitative measurement of vein length, width and density in *Arabidopsis thaliana* using a set of previously described vein structure mutants (*hve-2*, *ond3*, *as2-101*) compared to the wild type accessions Col-0 and Ler-0. phenoVein is freely available as open source software (http://www.fz-juelich.de/ibg/ibg-2/EN/methods/phenovein/phenovein_node.html).
- Minervini et al. (2015) presented a collection benchmark datasets for the development and evaluation of computer vision and machine learning algorithms in the context of plant phenotyping. In this paper they provide annotated imaging data and suggest suitable evaluation criteria for leaf segmentation procedures. Data sets are publicly available at http://www.plant-phenotyping.org/datasets. This effort is designed to trigger additional efforts by the general computer vision community to experiment upon.
- Barboza-Barquero et al. (2015) investigated whether semi-dwarfism has a pleiotropic effect at the level of the root system and also whether semi-dwarfs might be more tolerant of water-limiting conditions. The root systems of different Arabidopsis semi-dwarfs and GA biosynthesis mutants were phenotyped in vitro using the GROWSCREEN-ROOT image-based software. In addition, root phenotypes were investigated in soil-filled rhizotrons. Rosette growth trajectories were analysed with the GROWSCREEN-FLUORO setup based on non-invasive imaging.
- High throughput phenotyping experiments were also performed using RGB and fluorescence camera systems in automated climate chambers, using 80 Arabidopsis ecotypes from the 1001 genome project investigating heat stress conditions (Körber et al, unpublished).

Conferences and Workshops

- EPPN Plant Phenotyping Symposium: Next generation plant phenotyping for trait discovery, breeding, and beyond: transnational access to European platforms, 11-12 November 2015, Barcelona, Spain
- The European Plant Phenotyping Network organized a Spring School on Plant Phenotyping, Aberystwyth, 9 -13 March, 2015
- VIB – Ghent University organized an EMBO practical course entitled “Insights into plant biological processes through phenotyping” together with University of Louvain and University of Liège from 13-19 September 2015
- The German Plant Phenotyping Network (DPPN) and the EURoot project co-organized a Winter School in Root Phenotyping at Forschungszentrum Jülich, IBG2 Plant Sciences, 2-6 November, 2015
- 1st General Meeting of the COST action FA1306 “The quest for tolerant varieties - Phenotyping at plant and cellular level”, 22-24 June 2015, IPK Gatersleben, Germany
- Recent progress in drought tolerance: from genetics to modelling, 8-9 June, 2015, Le Corum – Montpellier, France, organized by DROPS and EUCARPIA.
- Measuring the Photosynthetic Phenome, 7-9 July, Wageningen, the Netherlands
- International Plant and Algal Phenomics Meeting (IPAP), 27-30 June 2015, Prague, Czech Republic

Selected Publications

- Bac-Molenaar JA, Granier C, Vreugdenhil D, Keurentjes JJB (2016) Genome wide association mapping of time-dependent growth responses to moderate drought stress in Arabidopsis. Plant, Cell & Environment. 39: 88-102

- Baerenfaller K, Massonnet C, Hennig L, Russenberger D, Sulpice R, Walsh S, Stitt M, Granier C, Gruissem W (2015) A long photoperiod relaxes energy management in Arabidopsis leaf six. Current Plant Biology. 2: 34-45
- Bühler J, Rishmawi L, Pflugfelder D, Huber G, Scharr H, Hülskamp M, Koornneef M, Schurr U, Jahnke S (2015) phenoVein - A tool for leaf vein segmentation and analysis. Plant Physiology. 169: 2359-2370
- Clauw P, Coppens F, De Beuf K, Dhondt S, Van Daele T, Maleux K, Storme V, Clement L, Gonzalez N, Inzé D (2015) Leaf responses to mild drought stress in natural variants of Arabidopsis. Plant Physiology. 167(3):800-16
- Higaki T, Kutsuna N, Akita K, Sato M, Sawaki F, Kobayashi M, Nagata N, Toyooka K, Hasezawa S (2015) Semi-automatic organelle detection on transmission electron microscopic images. Scientific Reports. 5:7794

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Proteomics

http://www.masc-proteomics.org/ and http://arabidopsisresearch.org/index.php/subcommittees/proteomics

By Joshua Heazlewood (chair)

Progress Towards Road Map Goals

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

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

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

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

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

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

Future Goals

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

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

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

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

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

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

Tools and Resources

- Pep2Pro - proteo-genomic resource (http://fgcz-pep2pro.uzh.ch/) by Baerenfaller
- ProMEX - mass spectral resource (http://promex.pph.univie.ac.at/promex/) by Wienkoop and Weckwerth
- GelMap - 2-DE proteomic repository (https://gelmap.de/projects-arabidopsis/) by Braun

- APP - targeted proteomics (SRM) tool (http://www.plant-energy.uwa.edu.au/APP/) by Taylor and Millar
- SUBA - subcellular database (http://www.suba.bcs.uwa.edu.au/) by Millar
- PPDB - plant protein database (http://ppdb.tc.cornell.edu/) by van Wijk
- AT_CHLORO - plastid proteomic resource (http://www.grenoble.prabi.fr/at_chloro/) by Rolland and Ferro
- AraPerox - peroxisome proteomic databse (http://www3.uis.no/AraPeroxV1/) by Reumann
- PhosPhAt - phosphoproteome database (http://phosphat.uni-hohenheim.de/) by Schulze
- P3DB - plant phosphoproteome databse (http://p3db.org/) by Thelen
- RIPP-DB - phosphoproteome database (http://bit.ly/22I73wm or http://metadb.riken.jp/metadb/db/SciNetS_ria102i/) by Nakagami
- MASCP Gator - proteomics aggregation portal (http://gator.masc-proteomics.org/) by MASCP
- 1001 Proteomes - non-synonomous SNPs from natural variants (http://1001proteomes.masc-proteomics.org/) by Heazlewood
- MRMaid - MRM design tool (http://elvis.misc.cranfield.ac.uk/mrmaid/) by Jones

Selected Publications

- Choudhary MK, Nomura Y, Wang L, Nakagami H, Somers DE (2015) Quantitative Circadian Phosphoproteomic Analysis of Arabidopsis Reveals Extensive Clock Control of Key Components in Physiological, Metabolic, and Signaling Pathways. Mol Cell Proteomics 14: 2243-2260
- Szymanski WG, Zauber H, Erban A, Gorka M, Wu XN, Schulze WX (2015) Cytoskeletal Components Define Protein Location to Membrane Microdomains. Mol Cell Proteomics 14: 2493-2509
- Heard W, Sklenar J, Tome DF, Robatzek S, Jones AM (2015) Identification of Regulatory and Cargo Proteins of Endosomal and Secretory Pathways in *Arabidopsis thaliana* by Proteomic Dissection. Mol Cell Proteomics 14: 1796-1813
- Minkoff BB, Stecker KE, Sussman MR (2015) Rapid Phosphoproteomic Effects of Abscisic Acid (ABA) on Wild-Type and ABA Receptor-Deficient *A. thaliana* Mutants. Mol Cell Proteomics 14: 1169-1182
- Kohorn BD, Hoon D, Minkoff BB, Sussman MR, Kohorn SL (2016) Rapid Oligo-Galacturonide Induced Changes in Protein Phosphorylation in Arabidopsis. Mol Cell Proteomics

Systems and Synthetic Biology

http://arabidopsisresearch.org/index.php/subcommittees/systems-biology

By Siobhan Brady (chair) and Malcolm Bennett (co-chair) with contributions from subcommittee members Pascal Braun, Gloria Coruzzi, Rodrigo A. Gutiérrez, Gabriel Krouk, Susannah Lydon, Geraint Parry (GARNET) and the wider Arabidopsis community.

Progress Towards Road Map Goals

(A) Build a predictive model of an Arabidopsis plant from its molecular parts: Millennium Nucleus for Plant Systems and Synthetic Biology; The Millennium Nucleus Center for Plant Systems and Synthetic Biology (PSSB) represents a new initiative in Chile to establish a research center of excellence using cutting-edge technologies for advancing Plant Sciences and Biotechnology addressing its scientific goals by taking advantage of cutting-edge Systems and Synthetic Biology strategies. We propose to take our systems-level efforts to the next level by integrating, interpreting and modeling new high-quality data we generate with available public datasets to explore gene function in cells and in whole organisms over developmental time and after specific environmental perturbations.

Systematic mapping of the Arabidopsis protein interaction network is continuing (Braun lab) and an expanded map covering a 12k x 12k search space (expected 12k interactions) as well as map of the phytohormone signaling network is progressing - the data will be disseminated through existing channels, including the IntAct and BioGrid databases and TAIR.

(C) Establish an effective knowledge exchange pipeline from the laboratory to the field: EVO Net DOE, Chile & USA

This collaborative project exploits the genomes of “extreme survivor” plants adapted to thrive in marginal, extremely Nitrogen (N) poor soils in the arid Chilean Andes. It uses a previously validated systems biology and phylogenomics approach, and a “paired species” sampling strategy, to identify the genes that distinguish these “extreme survivors” in Chile from their related species adapted to similarly dry regions in California (CA) that are not constrained by N. The Chile and California species pairings were chosen as these two regions are in same “floristic province”, comprising 2/6 of the Mediterranean provinces world-wide. These “extreme survivor” species broadly cover the main branches in flowering plants, and include 7 species in the grasses, which are of particular interest for biofuels, and a focus of our validation studies

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

Araport and the Arabidopsis Interactions Viewer have tools generated by Nicholas Provart to visualize protein-protein and protein-DNA interactions.

(E) Deepen international cooperation and coordination:

Members of the subcommittee are in the process of raising funds to organize the first International Plant Systems Biology (iPSB) meeting. The iPSB organizing committee includes S. Brady (USA), P. Braun (DE), G. Coruzzi (US), R. Gutierrez (CH), G. Krouk (FR). Help to raise funds is also kindly provided by the co-organizers M. Gifford (UK) and R. Bastow (UK). The meeting is planned to be held in France. The dates and location of the 1st iPSB will depend on the success of diverse grant applications. The GARNet2016 meeting (www.GARNet2016.weebly.com) includes a session and a workshop focussed on 'Plant Synthetic Biology' and 'Usage and Application development within Araport' and will engage with an international group of researchers, the majority of which work in Arabidopsis.

Future Goals

Develop and establish improved approaches to translate network connectivity into directional and signed causality edges. There is an increasing determination within the worldwide community to add value, both in terms of discovery and translational outputs, to the knowledge on gene networks developed through systems biology approaches.

The natural pipeline for these outputs is in the development of synthetic biology tools that will enable the predictable expression of molecular components. This has been aided by the generation of a range of molecular tools that will reduce the time that has been historically taken to make lab-specific expression constructs and encourage the use of standardised tools that have been thoroughly tested by the community. This is aided by the current revolution in DNA synthesis and in turn allows for more efficient knowledge transfer from idea to product that avoided time-consuming characterisation of regulatory elements. Work in Arabidopsis remains an important component of this pipeline given the remaining bottlenecks that exist with the transformation of many other plant species. Therefore the testing of genetic elements in Arabidopsis will remain attractive before moving work into more challenging plant chassis'. The relationship between discovery in Arabidopsis and subsequent use of transient expression in *Nicotiana benthamiana* offers an excellent example of why Arabidopsis will remain a key element in plant science research in both systems and synthetic biology.

This will also involve development of both bioinformatic and experimental approaches, and requires expanded database representations. Towards this goal discussions among community members and interaction database representatives will be conducted at the HUPO-Proteomics Standards Initiative (PSI) meeting (April 18-20, 2016, Ghent, BE). The planning of a scientific meeting on the translation of network connectivity to mechanisms to quantitative models is currently in an early phase of preparation (P. Braun). The systems biology community aims to establish closer links to the phenotyping and standardization efforts and this subcommittee aims to facilitate the establishment of links through the aforementioned meetings and other venues.

Conferences and Workshops

- NSF-RCN Workshop: "Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology" ICAR 2015 Paris, France, Paris, France, July 5-9
- Thematic Session on Systems Biology and New Approaches - ICAR 2015, Paris, France July 5-9
- "From Systems Biology to Synthetic Biology in Plants", organized by R. Gutierrez, G. Coruzzi, G. Krouk; ICAR 2015, Paris France, July 5-9
- Gene Regulation and Regulatory Networks Session; FASEB Mechanisms in Plant Development, Saxton River, Vermont, USA August 2-7
- Stefan Altmann, Siobhan Brady and Fumiaki Katagiri spoke at the Cold Spring Harbor Systems Biology: Networks Meeting, March 17-21, Cold Spring Harbor, NY, USA (co-organizer: Pascal Braun)
- X Plant Biology Meeting, Chile, December 1-4; the first symposium of this meeting was on Systems and Synthetic biology.
- Havana Winter School: Statistical Physics Approaches to Systems Biology, Cuba, February 23 - March 7, the School focused on the use of Statistical Physics techniques to the study of complex biological systems, with special emphasis in the understanding of metabolic, regulatory and neural networks.
- Argentinian Conference on Bioinformatics and Computational Biology, Argentina, October 14-16; The CAB2C is a multidisciplinary forum for the presentation and discussion of research in computational biology, bioinformatics and their applications. The CAB2C welcomes academic and professional contributions, from various scientific disciplines between those Systems Biology and Networks.
- Inaugural OpenPlant Meeting: University of Cambridge, July 27-28. This meeting brought together a worldwide selection of experts in Synthetic Biology to discuss the use of plant chassis including Arabidopsis in the growing area of plant synthetic biology.
- Biochemical Society Meeting: Synthetic Biology UK, London, September 1-3. This general meeting included significant contributions from plant synthetic biologists.

Selected Publications

- *Li Y, Varala K and Coruzzi GM (2015) From milliseconds to lifetimes: Tracking the dynamic behavior of transcription factors in gene networks. Trends in Genet. 31(9):509-15.* Dynamic Transcriptional Networks/Hit-and-Run transcription: Transcriptional networks operate dynamically in vivo, but capturing and modeling these dynamics is an experimental and computational challenge. This piece, together with two BioEssay pieces on "ideas that push the boundaries" (Varala et al., 2015 and Charoensawan et al.,

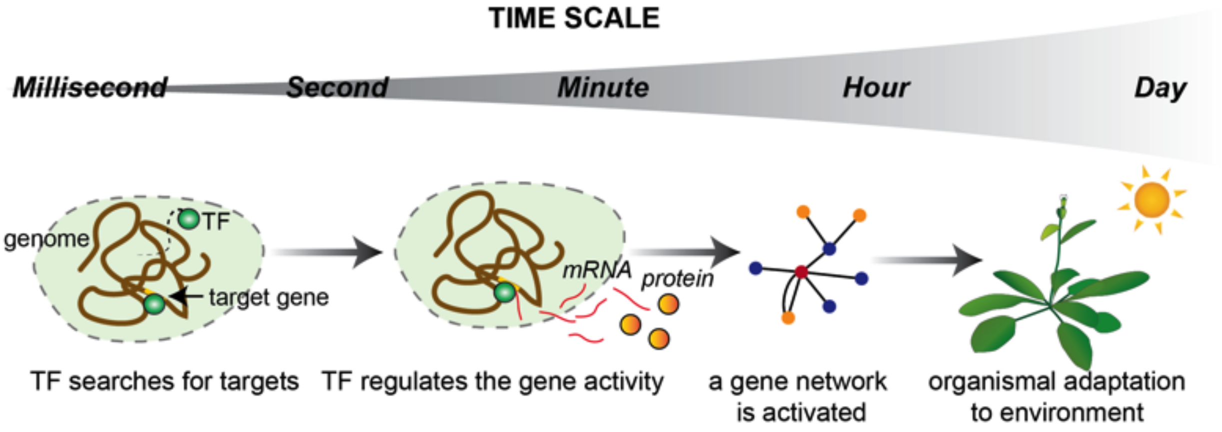

Figure 3. From milliseconds to lifetimes: dynamic behavior of transcription factors in gene networks Link to Summary: http://atlasofscience.org/from-milliseconds-to-lifetimes/

2015) highlight the importance of transient interactions between transcription factors (TFs), including Hit-and-Run transcription, and their genome-wide targets in rapid signaling in plants (Figure 3).

- Special Issue on Transcriptional Networks in Current Plant Biology, edited by Siobhan Brady and Nicholas Provart (http://www.sciencedirect.com/science journal/22146628/3-4)
- Lavenus J, Goh T, Guyomarc'h S, Hill K, Lucas M, VoB U, Kenobi K, Wilson MH, Farcot E, Hagen G, Guilfoyle TJ, Fukaki H, Laplaze L, Bennett MJ. (2015) Inference of the Arabidopsis lateral root gene regulatory network suggests a bifurcation mechanism that defines primordia flanking and central zones. Plant Cell. 27(5):1368-88
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Additional Information

Members of the sub-committee are particularly excited about several new approaches and discoveries in 2015/2016. First CRISPR-Cas9 gene editing methods have greatly advanced and thus will likely enable increase our ability to functionally test hypotheses derived from network analyses and systems approaches. Our ability to delete or modifiy cis-regulatory elements in their natural genomic context, to alter interactions between known dimerization domains of proteins and to make systematic gene knockouts are all examples of how this approach can be utilized to perturb a biological system. Additionally, the findings from Craig Venter's institute describing a minimal synthetic bacterial genome in Science (Hutchison et al., Science 2016) also leads us to consider the next steps with respect to considering the minimal synthetic plant genome.

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TOC

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 decadal plans, which alongside 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 thaliana* Functional Genomics Project (2002-2011) led to the functional annotation of most of the *Arabidopsis thaliana* genes. Alongside, The Arabidopsis Information Resource (TAIR) was founded in 2001 to meet the needs of the growing Arabidopsis research community.
- From Bench to Bountiful Harvests (2012-2021) aims to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, to be able to build a predictive model of an Arabidopsis plant. In order to provide a flexible platform to enable open sharing of the vast amount of data generated by today's omics approaches, the International Arabidopsis Informatics Consortium (IAIC, page 29) founded the Arabidopsis Information Portal, Araport, in 2013 (page 30).

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. This year the following projects and resources contributed:

Resource and Stock Centers

- Arabidopsis Biological Resource Center (ABRC) (page 28)
- Nottingham Arabidopsis Stock Center (uNASC) (page 28)
- RIKEN BioResource Center (BRC) (page 28)

Arabidopsis Informatics and Data Sharing Resources

- International Arabidopsis Informatics Consortium (IAIC) (page 29)
- Arabidopsis Information Portal (Araport) (page 30)
- The Arabidopsis Information Resource (TAIR) (page 32)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

- Bio-Analytic Resource for Plant Biology (BAR) (page 33)
- BrassiBase (page 34)
- Cyverse (page 34)
- European Plant Phenotyping Network (EPPN - ended in 2015) & EMPHASIS (page 35)
- Gramene (page 35)

Besides the above listed projects and resources, there are many other international and multinational initiatives with major contributions from Arabidopsis researchers, e.g. the 1001 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/) and the International Plant Phenotyping Network (http://www.plant-phenotyping.org/).

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Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC) www.abrc.osu.edu

By Erich Grotewold (Director) and Jelena Brkljacic (Associate Director)

The community continues to donate novel types of resources, along with some previously published, highly requested mutant and transgenic stocks. Genome editing resources are among the most highly requested new resources and are comprised of multiple sets of CRISPR/Cas9 vectors suitable for multiplexed genome editing in monocots and dicots, including the ones with egg cell-specific promoters to facilitate generation of homozygous mutants. Traffic lines, a set of lines used as a tool to identify homozygous mutants, have also recently been added to the collection. ABRC continues to solicit donations of genome editing and other novel and high-throughput resources, and donating is encouraged through the Stocks for Stocks Rewards program and by providing paid shipping to those who donate. The new policy allows us to accept donations of DNA and seed stocks from other organisms, depending on available space, growth requirements and other criteria. We continue to perform rigorous testing on newly donated and reproduced stocks, as well as on the stocks that users report as problematic. Our latest quality control statistics can be found at http://abrc.osu.edu/quality-control. In collaboration with the Nottingham Arabidopsis Stock Centre (NASC), ABRC is working on the development of a robust, expandable and fully sustainable Stock Center Module that will be integrated with the Arabidopsis Information Portal (Araport). We distributed 178,000 samples (including sets) in 2015/2016, with over 2,000 stocks sent as part of our education kits.

News

We are happy to announce that our new custom-made robotic system (Seed Aliquoting Machine, SAM) was able to dispense more than 250,000 seed stock samples in the first year. This enabled the preparation of eight large sets of T-DNA insertion lines, the distribution of which has increased 2.5-fold compared with the same period last year.

The Center is introducing a new category of stocks to the collection - antibodies and their corresponding antigens. Current inventory includes about 100 different antibodies, most of which were generated against Arabidopsis proteins, while the rest includes antibodies generated against antigens of other plant species or plant viruses. Ordering will be available starting in the summer of 2016.

ABRC continues being supported by the NSF for the 25th consecutive year. Our newest NSF grant will support the activities of the Center from 2016-2019.

The Nottingham Arabidopsis Stock Centre (uNASC) http://www.arabidopsis.info

By Sean May, Director and Marcos Castellanos-Uribe, Operations Manager.

Ordering statistics at NASC continue to be healthy and high for our seed service with well over 140,000 individual stocks sent this year (April 2015-16). Increased distribution stats alongside regular new donations of seed show that the Arabidopsis community continues to flourish and expand. Please do remember that we can save you time, effort and strengthen your research impact by distributing seed on your behalf to the wider plant community.

Feel free to drop into our booth at the ICAR and browse our freebies – shared with ABRC – we really do appreciate seeing you and solving any problems that you may have (with stocks). We are happy to answer your questions (in English or Spanish) then or at any time throughout the year (including emails to curators@arabidopsis.info).

Please see our site for a comprehensive and up-to-date list of new stocks, collections and lines (as always) and consider viewing @NascArabidopsis (http://twitter.com/#!/NASCArabidopsis).

See you in Korea!

RIKEN BioResource Center (RIKEN BRC) http://epd.brc.riken.jp/en/

By Masatomo Kobayashi (coordinator)

Since established in 2001, RIKEN BioResource Center (RIKEN BRC) has provided resources of plant, animal, human and microorganisms to the international research community. Our aim is the promotion of life sciences to contribute to food, health and environment problems that are urgent global issues for the human being. Since 2002, we join the National BioResource Project (NBRP) funded by the Japanese Government (http://www.nbrp.jp/index.jsp). The Experimental Plant Division is selected as the Core Facility of Arabidopsis/Cultured plant cells and genes from NBRP, and is responsible for distributing plant resources from RIKEN BRC. Approximately, 830,000 materials are preserved, and they have been distributed to ca. 1,900 laboratories and research groups in 45 countries.

We focus our efforts to collect, preserve and distribute Arabidopsis resources that have been established by Japanese researchers. Among them, RIKEN Arabidopsis full-length cDNA (RAFL) clone is the most famous resource. The total number of the clone is ca. 250,000. Among them, ca. 20,000 clones were fully sequenced. Another well-known resource is the RIKEN Transposon-tagged Mutant (RATM) line. More than 17,000 lines are on our catalogue, and homozygous seed stock is available for ca. 3,000 lines. Both RAFL clones and RATM lines are especially useful for reverse genetics approach. For forward genetics approach, we provide seed pools constructed from various types of Arabidopsis seed lines for screening purpose. They include activation(T-DNA)-tagged lines, FOX hunting lines, RATM lines and natural accessions. We also provide Arabidopsis T87 cells and At wt cells that are useful in various research purposes. In 2015, we started distributing TAC clone library deposited from Kazusa DNA Research Institute.

In order to establish and support the pipeline "from bench to bountiful harvests", RIKEN BRC also provides model plant resources such as Tobacco BY-2 cells, Rice Oc cells, and full-length cDNA clones of various plant species including *Brachypodium distachyon*, an experimental plant of monocot. The DNA materials are shipped within 2 weeks after the arrival of ordering documents, while shipment of plant cells to abroad requires additional period due to the preparation of the culture that is tolerant to transportation and documentations necessary for customs clearance.

We believe that quality control is the most important issue for resource project. Before shipment, end-sequence of every DNA material is obtained and compared with the data on our database. Insertion site of Ds transposable element in the RATM line is examined by PCR for confirmation. The results are provided to the recipients before or at the time of shipment. Other information necessary to utilize the resources are provided via website and/or e-mail. Any questions and comments from the community are appreciated.

Arabidopsis Informatics and Data Sharing Resources

International Arabidopsis Informatics Consortium (IAIC)

http://www.arabidopsisinformatics.org/

By Blake C. Meyers (Interim Director) and Joanna D. Friesner (Assistant)

The IAIC was initiated by Arabidopsis community members in 2009 and formally established in 2011 via a US National Science Foundation RCN award (Award #1062348) to PI Blake Meyers (Danforth Center). The RCN award is set to conclude this year (2016); however, mechanisms for sustaining IAIC are currently being explored. Key community coordination overlap exists between the IAIC steering committee and the steering committee of a recent NSF award to Siobhan Brady (PI) and Joanna Friesner (co-PI) entitled 'RCN Arabidopsis Research and Training for the 21st century (ART-21)'; NSF Award #1518280 (http://www.nsf.gov/awardsearch/showAward?AWD_ID=1518280). The ART-21 steering committee consists of the 8 member North American Arabidopsis Steering Committee (NAASC), key IAIC liaisons (Blake Meyers and Nick Provart), and Terri Long (USA), Jim Murray (UK), and Ute Kraemer (Germany).

The purpose of establishing the IAIC was to facilitate a coordinated global Arabidopsis informatics efforts 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. Arabidopsis community members, led largely by elected NAASC members, have participated in all stages of Consortium development and activities. In addition, a Scientific Advisory Board was elected by the Multinational Arabidopsis Steering Committee (MASC) and community participation was solicited in ten workshops including several organized specifically to enable IAIC design and development, and others at public conferences such as the annual International Conference on Arabidopsis Research (ICAR) and the Plant and Animal Genomes (PAG) meetings.

Two key project goals that have been achieved were (1) to facilitate a collaborative effort to establish and fund a new web-based "Arabidopsis Information Portal" for the global plant biology community (now entitled 'Araport', see NSF Award #1262414: ABI Development: The Arabidopsis Information Portal, http://1.usa.gov/1P5IB09) and (2) to develop a public platform via an IAIC web page to coordinate activities and serve as a community resource.
(http://www.arabidopsisinformatics.org/)

Recent activity

Joint sponsorship of a community workshop (with Araport) at the 2016 Plant and Animal Genomes (PAG) meeting in San Diego, California this past January. On behalf of the IAIC and NAASC, Joanna Friesner gave a presentation entitled "Community Collaborations: Advancing Arabidopsis Research and Training (ART-21) and the International Arabidopsis Informatics Consortium (IAIC)". The publicly-available presentation can be downloaded and viewed at: http://bit.ly/1QfMh4V.

Additional presentations on Araport were given by Araport staff including "A Tour of the Arabidopsis Information Portal (Agnes P Chan, J. Craig Venter Institute) and Module Development for Araport (Jason R. Miller, J. Craig Venter Institute).

Future activities

(1) NAASC recently received a 5 year NSF award for a collaborative project entitled 'Arabidopsis Research and Training for the 21st Century (ART-21)', mentioned above. This coordinated program has these three core objectives: (1) identify emerging technologies where using Arabidopsis as a model organism will provide fundamental discoveries and enable translational research in crop species; (2) enhance interdisciplinary training of scientists for academia and extra-academic careers; and (3) increase the diversity of Arabidopsis research scientists. The IAIC project has overlapping steering committee members with ART-21 and intends to partner with NAASC to expand its outreach to community members to enable analysis of future training needs and emerging bioinformatic and computational skills.

The proposed collaboration includes several activities:

(a) May 2016: A NAASC and IAIC co-organized Focus Group on "Computational training of biologists for academia and industry in the 21st Century" led by Blake Meyers, Nick Provart, Siobhan Brady and Joanna Friesner. The Focus Group will include 35 participants discussing these over-arching questions (1) What are the bioinformatics and computational skills needed by plant scientists of the 21st century to deal with more complex datasets (predictive, quantitative and theory-driven)? (2) What are the bottlenecks to providing students with the needed skills? (3) What do employers (of various types) need/want from employees; what are marketable skills in this area? Key topics include: (i) Training and Education: Skills needed for positions: Industry Positions; Faculty Positions; Undergraduate, Graduate and Postdoc Education (ii) Collaborations:Working with a biologist: a quantitative expert's perspective; Working with a quantitative expert: a biologist's perspective; Retraining: Yourself; From a funding perspective (iii) Training Arabidopsis Biologists for High-Throughput Phenotyping; and (iv) Translating from Arabidopsis to Crop Species, and Vice versa. A workshop white paper, led by IAIC members Blake Meyers and Nick Provart, will be produced and include recommendations and analysis.

(b) Another future IAIC goal is to incorporate the outcomes from the activity described above into a hands-on workshop prior to ICAR 2017, envisioned to span 4-5 days and encompass both wet-lab and computational and bioinformatic analysis and techniques. ICAR 2017 will be organized by NAASC in St. Louis, USA, June 19-23, 2017.

Conferences and Workshops

- Plant and Animal Genomes (PAG) meetings: IAIC presentation: January 2016: San Diego. Presentation available at: http://bit.ly/1QfMh4V
- International Conference on Arabidopsis Research (ICAR): July 2015 (Paris)

The Arabidopsis Information Portal (Araport)

www.araport.org

By Chris Town (Principal Investigator)

The Araport team extended its fully functional web portal by adding many data types to its ThaleMine data mining tool and many tracks to its JBrowse browser. The team delivered web site infrastructure that, even in its prototype stage, allows community participants to develop and deploy their own web services and data integration applications.

We have also completed the most up-to-date and complete re-annotation of the Col-0 genome to produce Araport11 that consists of 37,523 genes (27,688 protein-coding, 5,051 non-coding, 952 pseudogenic, and 3901 transposable element-related loci) and 58,149 transcripts. The annotation contains 738 new protein-coding loci and a further 508 novel transcribed loci. In addition, we retired 388 genes that encoded short (hypothetical) proteins for which there was no database or RNA-seq support. Araport11 is available on the Araport project site (http://www.araport.org) and has now been validated and accepted by GenBank for immediate release. A manuscript describing the annotation process and results is under review and can be found as a draft at http://biorxiv.org/content/early/2016/04/05/047308.

JBrowse and ThaleMine continue to be central features of the portal's user interface

JBrowse now hosts over 100 data tracks, including the latest gene models from Araport11 and their supporting evidence, as well as many community sourced tracks including 1001 genomes SNP data. Methods to allow community members to post and share their data through JBrowse using either GitHub or the CyVerse data store are in active development.

ThaleMine is a data warehouse which hosts and integrates a large collection of Arabidopsis genomics data including gene expression, orthologs, pathways, interactions, publications and others. We have continued to add new content and functionalities to ThaleMine. These include GeneRIFs, together with a portal to NCBI's submission page that will allow community members to submit their own comments on gene function, and phenotype and stock data with links to ordering from ABRC and eNASC. The most recent addition is an RNA-seq-based expression module that allows users to view expression levels of their favorite genes across the 113 RNA-seq data sets used in the Araport11 re-annotation process.

Science Apps, Web Services and Modules

The Araport framework allows registered users to install runnable code. Users may install Science Apps (client-side JavaScript programs that display content) or web services (server-side Python programs that deliver data) or community modules (combinations of Science Apps and web services). At this time, Araport hosts 21 Science Apps (listed on Table 2) and over 100 web services (including services contributed by SUBA and FLOR-ID). The Provart Lab is in the process of installing ePlant, an extensive module that integrates many visualization techniques and a diversity of data types, which will be Araport's largest externally-developed module.

News

Despite its technical success and demonstrated ability to assimilate and integrate a wide range of data types, the site sees many fewer visitors than expected. Furthermore, although the attendees at the 2011 Design Workshop were enthusiastic about their vision of a federated data model with many community-contributed modules, their enthusiasm has so far not translated into the level of participation envisaged in the white paper. This is of concern to all of us, including our funders - the US National Science Foundation and the UK Biotechnology and Biological Sciences Research Council. As we develop a proposal for continued funding of the project, we will be pro-actively recruiting major data generators to the project to facilitate assimilation of their data into Araport and demonstrate the value of integration of multiple data types within the portal.

Conferences and Workshops

Project PIs attended the 25th ICAR in Paris in July 2015. In addition to a talk in a Plenary Session, there was a well-attended Araport workshop with contributions both from project PIs and from community contributors. We attended the ASPB meeting in Minneapolis, July 2015, presented a talk in the "Bioinformatics Resources for Plant Biology Research" and also staffed a booth in the Exhibitor area together with colleagues from other resources. Project staff presented posters and/or talks at the Mid-Atlantic ASPB meeting (April, 2015), University of Maryland Mini-symposium (May 2015), the Mid-Atlantic Plant Molecular Biology Society Meeting (August 2015). Two team members spent one and a half days at Purdue University in November 2015 giving talks, a hands-on workshop and having one-on-one discussions with various faculty members. We organized the IAIC/Araport workshop at PAG, San Diego in January 2016 that included presentations from project personnel and community members.

Araport gave a talk at the ASPB mid-Atlantic Regional Meeting at Swarthmore in April 2016 and has been invited to give talks at ICAR 2016 in Korea in July and at the "GARNet2016: Innovation in the Plant Sciences" meeting in Wales in September 2016. We also plan a presence at the ASPB meeting in Austin in July 2016.

Table 2. Araport Science Apps

Science App	Developer/PI and Institution	Data source
Araport File Browser	Araport	Araport
D3 Matrix Demo App	Araport	Araport
Atted Science Application	Araport, ATTED	ATTED, Tohoku University
EBI IntAct Viewer	Araport, EBI	European Bioinformatics Institute
AT Expression Profiling	Araport, J. Craig Venter Institute	JCVI
KEGG Pathway Table	Araport, KEGG	KEGGKyoto University
PhosPhAt App	Waltraud Schulze (PI) with Araport developers.	PhosPhAt, Hohenheim University
Gene App	Araport, interns	ThaleMine
Protein Table	Araport, interns	ThaleMine
Sequence Viewer App	Araport	ThaleMine
BLAST+	Araport	Araport Custom DBs
Scientist's Notebook	Araport	User input
Tree Demo Application	Araport, Ensembl	Ensembl Genomes or any Newick provider
50 Years of Arabidopsis Research	Provart(PI), Waese, University of Toronto	BioAnalytic Resource
BAR Expression Viewer	Provart(PI), Pasha, University of Toronto	BioAnalytic Resource
BAR Gene Slider	Provart(PI), Waese, University of Toronto	BioAnalytic Resource
BAR Interactions Viewer	Provart(PI), Pasha University of Toronto	BioAnalytic Resource
Hormone Response Network	Zhao(PI), Dai, Noble Foundation	Hormone Response Gene Regulatory Network
phasiRNA loci	Meyers(PI), Nakano, Vemaraju , Delaware Bioinformatics Institute	DBI Small RNA Database
Plant Metabolite Plotter	Wurtele(PI), Hur, Iowa State University	Plant Metabolic Resource
Plant Ontology Lookup	Jaiswal(PI), Preece, Oregon State University	Plant Ontology

The Arabidopsis Information Resource (TAIR)

www.arabidopsis.org

By Tanya Berardini (TAIR curator) and Eva Huala (Director)

TAIR has been supported by community contributions in the form of non-profit subscriptions since April 2014. We are grateful for the strong show of support from the worldwide Arabidopsis and plant community and continue to strive to provide data and analysis tools that will help drive scientific discovery in the field of plant biology forward.

Curation and New Features

Approximately 2100 new Arabidopsis gene-related research articles are published each year. TAIR continues to mine this rich trove of new experimental results to provide researchers with continuously updated information about Arabidopsis gene function, expression and mutant phenotypes. Newly published gene function information is manually extracted from experimental results reported in the research literature by TAIR curators and authors who curate their own publications, thereby bringing more visibility to their work. This new experimentally derived knowledge is captured in the form of Gene Ontology (GO) and Plant Ontology (PO) annotations, individually composed gene summaries and phenotype descriptions, and new links between articles and genes, which are added to TAIR on a weekly basis. Within TAIR, the new experimental data are integrated with annotations made by UniProt, the Gene Ontology consortium, the IntAct effort and computational predictions about Arabidopsis genes, proteins, and RNAs to present a comprehensive overview of gene function.

In 2015, we added nearly 600 new gene symbols and full names, created new and updated gene summaries for many genes and integrated new GO and PO annotations for 8835 genes (including experiment-based annotations from almost 770 research articles to 2996 genes). We have also put additional effort into integrating more allele and phenotype information. To increase the visibility of new Arabidopsis research, we have begun featuring a Paper of the Month on our home page and we have also added a browsable list of recently published Arabidopsis papers. In the coming year, we will be integrating gene family data including orthologs from other species to facilitate the translation of Arabidopsis research results to other plants.

Subscriptions and Free Access

TAIR is financially supported by contributions from individual researchers, academic institutions and consortia, companies and country-level subscriptions that together represent 29 countries. As of March 2016, subscribers included: 2 countries (China and Switzerland), 4 academic consortia, 165 individual institutions (list at http://bit.ly/1RPlaeu), and approximately 340 individuals. Corporate subscribers include 4 major agricultural companies and 4 smaller companies. We have provided free access for undergraduate and graduate classes at 13 non-subscribing academic institutions, enabling teachers and students to use TAIR as part of their curriculum.

Data Releases

To foster data reuse in accordance with our data sharing policy, TAIR has produced four data releases in the past year (http://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases).The releases included all Gene Ontology and Plant Ontology annotations, gene symbols and names, links between genes and publications, and updated gene descriptions added to TAIR through 12/31/2014. We will continue to distribute TAIR data releases containing year-old data on a quarterly schedule. Access to the quarterly release files does not require a subscription and we do not impose any restrictions on reuse or redistribution of data contained in these year-old data releases. Subscribers have immediate access to all new information in TAIR through the website, which is updated on a weekly basis, and they may also request custom data sets via our helpdesk (curator@arabidopsis.org).

Outreach: Conferences, Workshops, Social Media

TAIR staff presented posters, gave talks, and were available for one-on-one interactions at exhibit booths at the following meetings: ICAR 2015 (Paris), ASPB 2015 (Minneapolis), and PAG 2016 (San Diego). TAIR curators will be attending both ICAR 2016 in Korea and ASPB 2016 in Austin, TX to spread the word about our continuing efforts to provide up-to-date literature-based functional annotation and analysis tools to the research community.

In addition, TAIR interacts with its online community through our HelpDesk (curator@arabidopsis.org), fielding over 1500 questions in 2015, 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).

Publications

- The Arabidopsis Information Resource: Making and mining the “gold standard” annotated reference plant genome. Berardini TZ, Reiser L, Li D, Mezheritsky Y, Muller R, Strait E and Huala E (2015) genesis 53: 474-85. DOI: 10.1002/dvg.22877
- Sustainable funding for biocuration: The Arabidopsis Information Resource (TAIR) as a case study of a subscription-based funding model. Reiser L, Berardini TZ, Li D, Muller R, Strait EM, Li Q, Mezheritsky Y, Vetushko A, and Huala E (2016) Database baw018. DOI: 10.1093/database/baw018

Plant Projects and Resources with Strong Participation of Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR)

http://bar.utoronto.ca

By Nicholas Provart (Director)

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) reseacher in mind. Data sets include:

- 150 million gene expression measurements (75 million from A.th.), plus "expressologs" (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser.
- 70,944 predicted protein-protein interactions plus 36,306 documented PPIs (rice interologs also available!).
- 29,180 predicted protein tertiary structures and 885 experimentally-determined structures.
- Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee's site at 1001proteomes.masc-proteomics.org.
- Documented subcellular localizations for 9.3k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

News

The BAR released a new, easier to navigate homepage in honour of its 10th birthday! Check it out at http://bar.utoronto.ca/. Thanks for citing papers in which our tools have been published, and for liking us on Facebook at https://www.facebook.com/BioAnalyticResource/. Hopefully this will help with getting funding to support our efforts.

Two new tools were released on the BAR - first, our Expression Angler tool has been updated to easily identify genes with any desired pattern of expression, simply by painting that pattern onto "eFP"-like pictographs of a plant's anatomy (or you can search with a desired gene of interest). Second, with the set of genes identified in this manner (or your own, by e.g. expression profiling) you can easily explore the promoters of those genes for known motifs from JASPAR, Weirauch et al. 2014, PLACE and other sources, using Cistome. See http://bar.utoronto.ca/ExpressionAngler/ and http://bar.utoronto.ca/cistome.

We also released high resolution expression data for the Shoot Apical Meristem from Yadav et al. 2014 in the Tissue Specific Data Source of the Arabidopsis eFP Browser. New Lateral Root Initiation data sets from the Gifford, Muday and Bennett groups will be added in the 2nd quarter of 2016 to the Lateral Root Initiation Data Source.

We have added a linkout icon to a Genevestigator-developed resource, "Genevisible", in the outputs of our eFP Browser. Now you can easily see the expression levels of your gene of interest in the top 10 tissues or perturbations (environmental stresses or mutations). In the latter instance, the top 10 also include cases where your gene exhibits the greatest decrease in expression. Another linkout icon to your gene of interest's information at Araport.org was also added to the eFP Browser outputs.

The BAR is also pleased to announce the release of three new tools for exploring three gene expression atlases from two plant species and from human: a Moss (*Physcomitrella patens*) eFP Browser, a *Camelina sativa* eFP Browser and a Human eFP Browser. The Moss eFP Browser was developed by Joerg Becker's group at the IGC in Portugal and may be accessed at http://bar.utoronto.ca/efp_physcomitrella/cgi-bin/efpWeb.cgi. The *Camelina sativa* eFP Browser was developed in conjunction with Isobel Parkin's group at Agriculture and AgriFood Canada in Saskatoon and may be accessed at http://bar.utoronto.ca/efp_camelina/cgi-bin/efpWeb.cgi. The BAR's own group created the Human eFP Browser (Patel et al., 2016, PLoS ONE, http://dx.doi.org/10.1371/journal.pone.0150982), and this may be accessed at http://bar.utoronto.ca/efp_human/cgi-bin/efpWeb.cgi.

Conferences and Workshops

The BAR partcipated in the 2015 ASPB Plant Biology conference in Minneapolis at the Plant Genome Resource Outreach booth. We were also conducting user testing for our new "ePlant" app for exploring Arabidopsis data integratively from the kilometre to nanometre scales at the 2015 International Conference on Arabidopsis Research - thanks for your feedback!

Additional Information

26 co-authors, 308 references, 17 sections and a brief survey of 54033 Arabidopsis articles ;-) Our review of 50 Years of Arabidopsis Research in honour of the 1st International Conference on Arabidopsis Research in 1965 is out now! See http://onlinelibrary.wiley.com/doi/10.1111/nph.13687/full. The Arabidopsis publications and their citations may be explored interactively at http://bar.utoronto.ca/50YearsOfArabidopsis/.

BrassiBase: A knowledge database on Brassicaceae taxonomy, systematics and evolution

http://brassibase.cos.uni-heidelberg.de/

By Marcus A. Koch (director)

BrassiBase is continously developed into a comprehensive Brassicaceae-knowledge-database system. During 2015/2016 a first family-wide species check-list has been created. In total, more than 15,000 taxonomic entities ("names" of species, subspecies, etc., including synonyms) have been collected, checked and cross-referenced. We are now in the process to use this most actual and accurate species check-list as "backbone" for BrassiBase and link given information whenever possible to this information.

Furthermore, morphological descriptions of characters of any genus are now finalized and implemented into an interactive key to the genera. We hope that this will help to identify cultivated and/or collected material more easily, particularly if used in combination with the "Phylogenetic placement tool" implemented with BassiBase.

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

Conferences and Workshops

BrassiBase workshop held in Heidelberg in October 2015.

CyVerse

http://www.cyverse.org/

By Parker Antin (principal investigator), Eric Lyons (co-principal investigator), Nirav Merchant (co-principal investigator), Matthew Vaughn (co-principal investigator) and Doreen Ware (co-principal investigator)

CyVerse is one of eight projects funded by the National Science Foundation (NSF) Directorate for Biological Sciences. CyVerse is a dynamic virtual organization led by the University of Arizona to fulfill a broad mission to design, deploy, and expand a national cyberinfrastructure for life sciences research and train scientists in its use. CyVerse partner institutions each contribute an important component to the endeavor: Texas Advanced Computing Center, Cold Spring Harbor Laboratory, and the University of North Carolina at Wilmington.

Developing the Science of the Future

CyVerse fills a niche created by the computing epoch and a rapidly evolving world. Developing solutions to today's grand scientific challenges means that we must understand how the organisms that contribute to our food, fuels, and ecosystem are shaped by interactions with their environment. CyVerse provides life scientists with powerful computational infrastructure to handle huge datasets and complex analyses, thus enabling data-driven discovery. CyVerse provides access to a comprehensive and cohesive suite of computational resources supporting data management, cloud computing, high-performance computing, high-throughput computing, identity management, and collaboration tools, all built from open source components. CyVerse resources are accessible using multiple methods, including web-accessible applications, command-line-based access and well-described Application Programming Interfaces (APIs) for ease of automation and performing scalable data analysis. The powerful extensible platforms provide data storage, bioinformatics tools, image analyses, cloud services, and more. Answering the need of an era of data science, CyVerse makes broadly applicable computational resources available across the life sciences.

Engaging the Data Science Community

CyVerse was launched in 2008 as the iPlant Collaborative, aiming to serve the plant science research community. From its inception, iPlant quickly grew into a mature organization providing powerful resources and offering scientific and technical support services to researchers nationally and internationally. Now rebranded to CyVerse, the project has expanded the mandate to provide CI support across the life sciences. CyVerse CI architecture and implementation is agnostic with regards to scientific domain and supports many different life science disciplines and their associated data types and analyses. CyVerse allows researchers to analyze their growing datasets more efficiently, with greater flexibility, and to address previously difficult or impossible questions. Together, CyVerse CI permits researchers to deposit and share new data, programmers to easily deploy new tools and analytical workflows, and researchers of all skill levels to easily use and reuse those data and tools. CyVerse has created a robust, widely used, and evolving CI that is profoundly impacting life sciences and bioinformatics. CyVerse also provides training, learning material, and best practice resources to help all researchers make the best use of their data, expand their computational skill set, and effectively manage their data and computation when working as distributed teams.

Creating Global Collaborations

CyVerse envisions a future where all biologists have access to, are able to use, and know how to extend CI to solve problems and advance scientific discovery in research and apply CI to education. Through partnerships and direct engagement, CyVerse has helped accelerate the pace of science for many labs and individual researchers by offering computational and data management solutions that meet the demands of modern scientific technologies. Going forward, CyVerse aims to promote computational thinking and empower researchers to new scientific discoveries by enabling global collaborations in data sharing, management, analysis, and visualization.

European Plant Phenotyping Network (EPPN) & EMPHASIS http://www.plant-phenotyping-network.eu/

By Roland Pieruschka and Ulrich Schurr

The European Plant Phenotyping Network is an EU funded project successfully managed to integrate the European plant phenotyping community by creating structural and functional collaborations between the leading plant phenotyping institutions in Europe and integrating the plant phenotyping community across Europe. EPPN followed the vision that the network of leading phenotyping infrastructures form the nucleus that provides a structured and efficient development of a persistently competitive plant phenotyping community in Europe.

EPPN addressed a wide stakeholder community from academia and industry in different levels of interaction. Joint Research Activities developed, adapted and benchmarked novel sensors and established experimental as well as IT standards for application in plant phenotyping. The standards were made available for the wider plant phenotyping community on the EPPN website and by publications in scientific journals. Networking Activities provided a link between phenotyping experts, user communities, and technology developers within Europe and beyond. EPPN realized communication, networking, and education throughout the duration of the project at different levels: i) between existing and newly developing phenotyping platforms; ii) between phenotyping platforms and users from academia and industry; iii) between platforms, developers, and users; iv) with other leading international phenotyping centres. This effort represented the basis for novel scientific approaches in the utilisation of the existing facilities through Transnational Access. The access was based on demand driven, transparent access procedure, which included independent reviewers from outside of EPPN. High demand from users across Europe for access to plant phenotyping facilities resulted in 66 experiments mostly from young scientists and new users of phenotyping facilities.

EPPN became an important nucleus for the integration of the plant phenotyping community by the establishment of cooperation with the user community and a number of national and international projects and initiatives. Successful EPPN activities have led to the creation of the EMPHASIS project, which was initiated by EPPN core members and has been listed in the ESFRI roadmap. EMPHASIS will facilitate structured development and use of plant phenotyping infrastructure in Europe based on the foundation of EPPN. Additionally, EPPN members represent the group of the International Plant Phenotyping Network (IPPN) which has been initiated as an association and an important hub for networking activities to successfully continue the integration of the plant phenotyping community on a global scale.

EMPHASIS

Phenotypic analysis has become a major limiting factor in genetic and physiological analyses in plant sciences as well as plant breeding. Molecular plant biology and molecular-based breeding techniques have developed rapidly within the last decade. In contrast, the understanding of the link between genotype and phenotype has progressed more slowly. Faster progress is currently hampered by insufficient technical and conceptual capacity in the plant science community to analyse the interaction between phenotypes of existing genetic resources and the environment. Improvement in phenotyping is a key factor for success in modern breeding as well as for advancement in basic plant research. Multi-scale plant phenotyping to analyse genotype performance under diverse environmental conditions is at the centre of the EMPHASIS project, a new large-scale European project coordinated by researchers at Forschungszentrum Jülich, Germany. EMPHASIS is part of the new ESFRI roadmap, in which the member states of the ESFRI Forums (European Strategy Forum for Research Infrastructures, http://www.esfri.eu) coordinate pan-European research strategies.

The current roadmap was made public on March 10th in Amsterdam, within the framework of the Dutch EU presidency. The project EMPHASIS – **European Multi-Environment Plant Phenomics and Simulation Infrastructure** – aims to create an integrated, European network of unique infrastructures for plant phenotyping. This includes research infrastructures bridging four dimensions (1) deep and high throughput research infrastructure in controlled environments (2) intense field site installations such as FACE facilities, field labs, etc., (3) lean phenotyping approaches with field sites across European climate zones and diverse soil conditions and (4) modelling platforms. The installations will be connected with common data management and standards and establish the competence to link the phenotypic with the genotypic data. EMPHASIS links national plant phenotyping platforms, such as the German Plant Phenotyping Network (DPPN, http://www.dppn.de/dppn/EN) and the French Plant Phenomic Network PHENOME (FPPN, https://www.phenome-fppn.fr/phenome_eng/) as well as the platforms in Great Britain (http://www.ukppn.org.uk/) and Belgium. EMPHASIS will also establish links with institutions, and include other European countries. The project will cooperate with users from industry such as technology developers and breeders and other international research organisations. After a preparatory phase funded by the European Union, EMPHASIS will be implemented and fully operational in the next few years with the goal to enable access to the key plant phenotyping facilities in Europe. Forschungszentrum Jülich will coordinate EMPHASIS in close cooperation with partners in France.

Gramene: A comparative resource for plants

http://www.gramene.org/

By Marcela Karey Tello-Ruiz (Project Manager) and Doreen Ware (PI)

The Gramene database (http://www.gramene.org) is an integrated resource for comparative genome and functional analysis in plants. The database provides agricultural researchers and plant breeders with valuable biological information on genomes and plant pathways of numerous crops and model species, thus enabling powerful comparisons across species.

The genomes component of the Gramene project is developed in collaboration with the Ensembl Genomes project (EMBL-EBI) in the Ensembl infrastructure. The main pathways component of the project is the Plant Reactome (http://plantreactome.gramene.org); it was built on the Reactome framework.

The Gramene project has had 7 data releases since January 2015. The current data release contains 39 reference genomes including *Arabidopsis thaliana* and *A. lyrata*, rice, maize, wheat, barley, soybean, Brassicas, poplar, medicago, tomato, potato, banana, cocoa, peach, grapevine, Amborella, spikemoss and algae. Evolutionary histories are provided in phylogenetic gene trees classifying orthologous and paralogous relationships as speciation and duplication events. Orthologous genes inform synteny maps that enable inter-species browsing across ancestral regions. In addition, genome browsers from multiple species can be viewed simultaneously, with links showing homologous gene and whole-genome alignment mappings (WGAs). Within the last year, we added WGAs for tomato (*Solanum lycopersicum*), potato (*S. tuberosum*), grape (*Vitis vinifera*), and cocoa (*Theobroma cacao*) to enrich our existing collection against *Arabidopsis thaliana* (dicot model crop) and *Oryza sativa* Japonica (monocot staple food crop). Since April of 2015, we are providing links to gene annotations from external sources like Araport and Expression ATLAS. SNP and structural diversity data, including individual genotypes, are available for 11 species including *A. thaliana*, and are displayed in the context of gene annotation, along with the consequence of variation (e.g. missense variant). The Arabidopsis variation database contains data from the screening of 1,179 strains using the Affymetrix 250k Arabidopsis SNP chip (Horton et al, 2012), and an updated data set produced through a BBSRC funded multi-institutional collaboration involving resequencing 18 Arabidopsis lines (Clark et al, 2007). It also contains 392 strains from the 1001 Genomes Project (80 strains from the Cao pilot study; 132 strains from a study by the Salk Institute; and 180 strains from a study by the Nordborg group at GMI). Phenotype data was also added from a GWAS study of 107 phenotypes in 95 inbred lines carried out by Atwell et al (2010). The 1001 Arabidopsis Genomes project released data freely in a pre-publication format from the Salk Institute, WTCHG, MPI, and GMI, under the Fort Lauderdale agreement. Visual displays can be downloaded as high-resolution, publication-ready, image files. Our Blast and BioMart interfaces enable complex queries of sequence, annotation, homology, and variation data. Also in the past year, a new search interface (http://search.gramene.org) was developed and built. It provides a simple interface for expressive comparative queries and tools to view large datasets. New detailed views for search results featuring gene trees, pathway, and expression data from Atlas (EMBL-EBI). In addition to ~240 curated rice pathways, the Plant Reactome incorporates orthology-based pathway projections to 58 plant species including both, *Arabidopsis thaliana* and *A. lyrata*.

As we aim to reach out to a larger audience, we have held a monthly webinar series since November of 2014. For this, we purposely created an e-mail address [webinars@gramene.org] and use the service of Campaign Monitor to most efficiently reach and track the responses of at least 1,000 e-mail recipients that we invite to each monthly webinar. To broadcast Arabidopsis specific resources, we also submit an invitation to the arab-gen@net.bio.net mailing list. We adopted the use of Adobe Connect software and are using the TV studio facility at the CSHL DNA Learning Center which facilitates direct interaction between users and the Gramene Team. Recorded webinars are available for public view from Gramene's YouTube channel.

Outreach, Conferences & Workshops

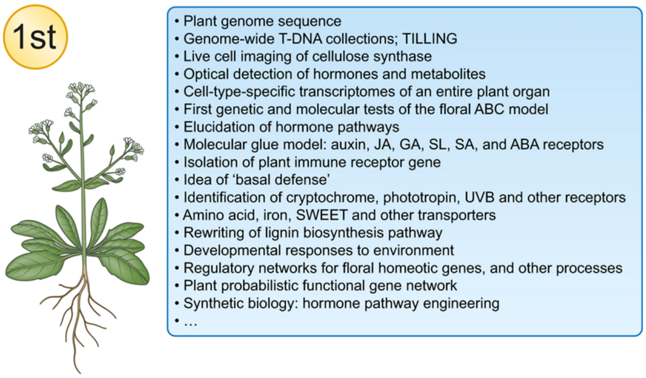
During the reporting period, Gramene staff attended 1 international and 7 domestic conferences with a total of 15 oral presentations and 9 posters. Project workshops with live demos were presented at the Plant & Animal Genome (PAG 2015 & 2016) & another one will be presented at the 2016 Maize Genetic Conference. At the PAG conferences, we also co-organized a community outreach booth with the participation of the following Arabidopsis bioinformatics resources: Araport, BAR & NASC. Published 7 peer-reviewed articles and 5 book chapters, and another 2 manuscripts are under review. Delivered 12 monthly webinars between February 2015 & February 2016, including one devoted to Arabidopsis resources on Gramene (July 14, 2015) that is available on the Gramene YouTube channel. We are in the process of generating video-tutorials from the 6 talks offered during the Gramene Project Workshop at the 2016 Plant and Animal Genome Conference. We continue to foster ~55 international collaborations. Between CSHL & OSU, we trained 7 post-doctorates, 3 graduate students, 2 undergraduate students (summer only), 1 high-school student & 1 visiting scholar at OSU (Oct 2014-Oct 2015).

Arabidopsis Basic Research and Translational Prospects

Scientific Highlights in 2015/16

The last UN projections revised in 2015 indicate that the world population will continue to grow within the next decades, reaching 8.5 billion in 2030. Particularly important is the fact that the highest rates of population growth are concentrated in less developed countries, in which hunger and malnutrition still prevail. The challenge of providing food, feed, fiber and energy to a growing population is further amplified by the impacts of climate changes, especially in regions with restricted water availability and constraints in arable land (e.g. due to lack of infrastructure, pests, diseases, etc). In order to tackle such issues, there is an urgent need for the efficient development of crops with higher yield and/or improved performance under unfavorable environmental conditions. Modern agriculture is undoubtedly the main beneficiary of the discoveries in plant research. The understanding of fundamental biological processes, from molecules to the whole plant and populations, is essential for sustainable crop production. Besides, advances in technology have and will provide new tools not only to study these biological processes, but also to apply the knowledge in the field, for instance via new genome editing techniques.

Although sometimes not clear to the major public and funding bodies, basic research approaches using model plants such as *Arabidopsis thaliana* considerably accelerate the progress in plant science, providing solid foundation for applications in the field. Researchers have for several decades exploited Arabidopsis' small size, small genome and short reproductive cycle to solve fundamental questions that led to key breakthroughs in plant biology. This matter was remarkably approached by members of the Arabidopsis community, who joined to publish an extensive compilation of highlights of Arabidopsis publications, as a commemoration for the 50th anniversary of the first conference on Arabidopsis research, held in Germany in 1965. The Tansley review, entitled "*50 years of Arabidopsis research: highlights and future directions*" (by Provart et al. New Phytol. 209(3):921-44, 2015), outlines how Arabidopsis became the model organism of choice for many of us, by dissecting the >54,000 Arabidopsis-related papers published in the last half-century (an interactive portal is available at http://bar.utoronto.ca/50YearsOfArabidopsis/). For instance, many 'firsts' in science that were discovered in or benefitted by Arabidopsis studies are highlighted (Figure 4). The importance of sharing biological resources and data via e.g. stock centers and databases/online tools is also therein appraised as one of the major strengths of the Arabidopsis community. Finally, the authors discuss the newer research directions that will drive plant biology forward in the future, not without at the end demonstrating concern about the criticisms surrounding the use of Arabidopsis in plant research.



- Plant genome sequence
- Genome-wide T-DNA collections; TILLING
- Live cell imaging of cellulose synthase
- Optical detection of hormones and metabolites
- Cell-type-specific transcriptomes of an entire plant organ
- First genetic and molecular tests of the floral ABC model
- Elucidation of hormone pathways
- Molecular glue model: auxin, JA, GA, SL, SA, and ABA receptors
- Isolation of plant immune receptor gene
- Idea of 'basal defense'
- Identification of cryptochrome, phototropin, UVB and other receptors
- Amino acid, iron, SWEET and other transporters
- Rewriting of lignin biosynthesis pathway
- Developmental responses to environment
- Regulatory networks for floral homeotic genes, and other processes
- Plant probabilistic functional gene network
- Synthetic biology: hormone pathway engineering
- ...

Figure 4. Arabidopsis 'firsts'. ABA, abscisic acid; JA, jasmonic acid; SL, strigolactones; SA, salicyclic acid. Source: Provart et al. New Phytol. 209(3):921-44, 2015 (http://onlinelibrary.wiley.com/doi/10.1111/nph.13687/full).

The fact that basic research is underfunded at expenses of projects with more applied approaches may have reflected on the drop in number of Arabidopsis publications in 2015, while papers referring to crop species, e.g. rice and maize, continued to increase (Figure 5). Nevertheless, several labs around the globe have and will continue to perform cutting-edge research using Arabidopsis, highlighted in this section of the MASC report. Notably, many of the selected publications discuss potential biotechnological applications, and all resulted from collaborations within 3 or more countries, featuring the international scope of the Arabidopsis community.

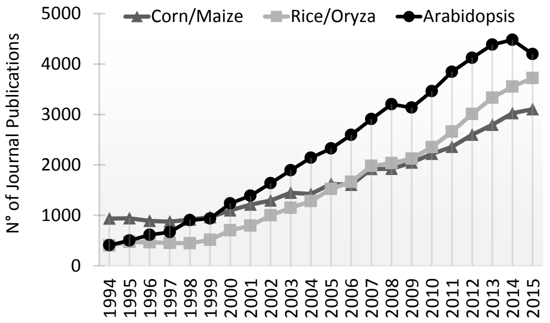


Figure 5. Number of Journal Publications from 1994-2015 citing corn, rice or Arabidopsis. Source: www.ncbi.nlm.nih.gov/pubmed

Nutrient-induced plasticity of endodermal differentiation

By Marie Barberon and Niko Geldner (DBMV, University of Lausanne, Lausanne, Switzerland)

Barberon M, Vermeer JEM, De Bellis D, Wang P, Naseer S, Andersen TG, Humbel BM, Nawrath C, Takano J, Salt DE, Geldner N (2016) Adaptation of Root Function by Nutrient-Induced Plasticity of Endodermal Differentiation. Cell 164: 447–59.

On their way from the soil to the plant's vascular system, water and nutrients are transported through the concentric root cell layers of epidermis, cortex and endodermis. The endodermis is the innermost cortical cell layer that surrounds the vasculature. It undergoes two states of differentiation (Casparian strip and suberin lamellae) differentially affecting its permeability. The Casparian strips correspond to lignin impregnations between adjacent endodermal cells, forming an apoplastic diffusion barrier. Suberin lamellae correspond to a secondary cell wall deposition, forming at the inner surfaces of endodermal cell walls and serve as a barrier for the uptake from the apoplastic space into the endodermis.

In our recent work we found that endodermal state I to state II transition is modulated by a wide range of nutritional stresses: salt treatment, sulfur and potassium deficiencies enhance suberization while iron, manganese and zinc deficiencies reduce suberization. This plasticity is controlled by the antagonistic activities of abscisic acid and ethylene, respectively. Interestingly, we could provide evidence that suberin plasticity is an adaptive strategy to cope with changing nutrient availability. Reduced suberization leads to salt hyperaccumulation and hypersensitivity, yet it alleviates iron-deficiency phenotypes. In addition, it causes potassium deficiency and exacerbates sulfur-deficiency phenotypes. Thus, changes in suberization have a broad impact on many nutrients, enhancing accumulation of some while reducing that of others. Our findings might provide a straightforward explanation for the often unexplained, complex "cross-talk" between different nutrients.

The particular significance of this work is that it re-defines the physiological role of endodermal suberization and its interplay with the environment. The suberin plasticity in response to nutrients is bound to be of central importance for plant's adaptation to their environment. It will be particularly interesting to study to which degree this plasticity is conserved among different plant's species and if endodermal suberization could be use as a trait for improving crops.

DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation

By J. Matthew Watson (Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria)

Dubin MJ, Zhang P, Meng D, Remigereau MS, Osborne EJ, Casale FP, Drewe P, Kahles A,Jean G, Vilhjálmsson B, Jagoda J, Irez S, Voronin V, Song Q, Long Q, Rätsch G, Stegle O,Clark RM, Nordborg M (2015) eLife 4:e05255.

Adaptation to changing environments can occur genetically over multiple generations. It has also been proposed that epigenetic changes, such as DNA methylation, can facilitate adaptation within a single generation. However, neither the extent to which this occurs nor the underlying mechanisms are known. In this study, researchers at 6 institutions from Austria, Germany, the US, and the UK used Genome Wide Association Studies (GWAS) to examine differences in genome wide DNA methylation in a Swedish Arabidopsis population, and demonstrated the first direct link between DNA methylation and environmental adaptation.

The authors grew 150 Swedish accessions at 10°C and 16°C and used Illumina sequencing to generate a transcriptome and methylome of each accession. They found that growth temperature was significantly correlated with CHH methylation, while there was no significant relationship with CG or CHG methylation. Using methylation as the phenotype, they performed GWAS and identified two SNPs specifically correlated with CHH methylation levels. These SNPs are located upstream of CMT2, a methylase involved in CHH and CHG methylation at transposable elements (TEs). Indeed, when they examined which loci showed increased levels of CHH methylation at higher temperatures, nearly 80% of the loci were associated with a small fraction of TEs that were highly expressed, located in euchromatic regions, and had recently inserted.

While CHH methylation varied with temperature, they found that CG methylation was highly correlated with the latitude of origin of the individual accessions. Plants that came from Northern Sweden had higher levels of CG methylation within gene bodies (GBM for Gene Body Methylation) across the entire genome. They performed GWAS for each gene with GBM and identified 15 SNPs that were associated with increased methylation levels at multiple genes. These SNPs were largely limited to Northern Sweden, and were located in genomic regions that had undergone strong selection in plants in the North.

Taken together, these data indicate that methylation levels are genetically regulated, and that the loci controlling this regulation have undergone selection in Northern Sweden, likely to help plants there adapt to the colder environment.

Control of root stem cells by microRNAs

By Javier Palatnik and Ramiro Rodríguez (Instituto de Biología Molecular y Celular de Rosario, CONICET, Universidad Nacional de Rosario, Argentina)

Rodriguez RE, Ercoli MF, Debernardi JM, Breakfield NW, Mecchia MA, Sabatini M, Cools T, De Veylder L, Benfey PN, Palatnik JF (2015) MicroRNA miR396 regulates the switch between stem cells and transit-amplifying cells in Arabidopsis roots. The Plant Cell 27: 3354–66.

Stem cells are ultimately responsible for the generation of the different cell types that constitute the body parts of plants and animals. They are located within specific environments referred to as stem-cell niches. In plants, the root stem cell niche is located at the distal part of the root apical meristem and is formed by the quiescent center and the adjacent stem cell initials. The stem cells divide slowly while generating new cell types and renewing themselves. Their progeny in turn generally undergoes rapid, transient amplifying cell divisions before differentiation. These actively dividing cells are referred to as transient amplifying cells, and provide enough cells to sustain the root growth.

MicroRNA miR396 is an evolutionary conserved small RNA that regulates GROWTH-REGULATING FACTORs (GRFs), which encode plant specific transcription factors. We found that miR396 is highly expressed in root stem cells, where it actively represses the expression of GRF transcription factors. In turn, the GRFs are specifically expressed in transit amplifying cells. When unchecked, the expression of the GRFs in the stem cell niche distorts the organization of the quiescent center. In contrast, overexpression of miR396 and a decreased activity of the GRFs affected the transit amplifying cells, which acquired properties of stem cells: cell division proceeded at a slower pace, and often through periclinal cell division planes instead of the usual anticlinal planes. In addition, miR396 overexpression caused an expansion of stem cell markers.

PLETHORA (PLT) transcription factors are master regulators of root development. Their expression gradient along the longitudinal axis of the root determines the different developmental zones of the organ: PLT proteins accumulate to their highest level in the stem cell niche specifying stem cell identity, while they are expressed at lower levels in transient amplifying cells where they promote rapid cell division cycles. We have shown that PLT family members activate miR396 in the stem cell niche to repress the GRFs. In turn, the GRFs repress PLT and other stem cell-associated genes in the transit amplifying cells.

These findings uncovered a regulatory mechanism that contributes to establish the sharp limit between the stem- and transient amplifying cells, a transition that ensures both correct organ patterning and the provision of a critical number of cells to sustain organ growth.

The role of inositol pyrophosphates in the perception of the plant defense hormone jasmonate

By Debabrata Laha, Philipp Johnen and Gabriel Schaaf (ZMBP, University of Tuebingen, Germany)

Laha D, Johnen P, Azevedo C, Dynowski M, Weiss M, Capolicchio S, Mao H, Iven T, Steenbergen M, Freyer M, Gaugler P, de Campos MKF, Zheng N, Feussner I, Jessen HJ, Van Wees SC, Saiardi A, and Schaaf G (2015) VIH2 Regulates the Synthesis of Inositol Pyrophosphate $InsP_8$ *and Jasmonate-Dependent Defenses in Arabidopsis. The Plant Cell 27: 1082-97.*

Inositol hexakisphosphate ($InsP_6$), also known as phytic acid, is abundant in eukaryotes and serves as a major phosphate storage molecule in plants during seed germination. Importantly, $InsP_6$ is the precursor of a novel class of signaling molecules, inositol pyrophosphates, which contain high energy diphosphate or pyrophosphate moieties. To date the best characterized inositol pyrophosphate species are $InsP_7$ and $InsP_8$, which play important cellular functions in several physiological processes including telomere length maintenance, vesicular trafficking, apoptosis, phosphate sensing and energy homeostasis in amoebae, yeast and mammalian cells. In yeast and mammals, $InsP_6$ is phosphorylated by Kcs1/IP6K to generate 5-$InsP_7$ and Vip1/PPIP5K-like proteins then further phosphorylate 5-$InsP_7$ to generate 1,5-$InsP_8$. Recent work in our lab shows that Vip1/PPIP5K homologs are widely distributed in plants, that inositol pyrophosphates can be readily detected in Arabidopsis seedling extracts, and that Arabidopsis VIH1 and VIH2 are functional $InsP_8$ synthetases. Our findings further show that *VIH2* is expressed ubiquitously and that jasmonate causes a specific and VIH2-dependent increase in $InsP_8$. $InsP_8$-deficient *vih2* mutant lines are significantly compromised in JA perception and defenses against insect herbivores and fungal necrotrophs. *In silico* docking experiments and structure-based functional interaction assays in yeast suggest that $InsP_8$ is superior ligand of the jasmonate receptor complex than lower inositol phosphate $InsP_5$. In a direct approach, we show furthermore that inositol pyrophosphates can bind to the COI1–JAZ jasmonate co-receptor complex with high affinity, suggesting that coincidence detection of $InsP_8$ ***and*** jasmonate is a critical step in the activation of plant defenses. These findings extend the spectrum of inositol phosphate signaling in plants and unravel a new regulatory mechanism of F-box protein COI1 function by two unrelated molecules jasmonate and $InsP_8$. To improve our current understanding about inositol phosphate signaling, future works needs to decode the isomeric nature of plant inositol pyrophosphates as well as to identify plant $InsP_6$ kinases(s) responsible for $InsP_7$ biosynthesis *in planta*.

Interplay of endoplasmic reticulum protein quality control and cytokinin activity

By Tomáš Werner and Michael Niemann (Dahlem Center of Plants Sciences, Freie Universität Berlin, Germany)

Niemann MCE, Bartrina I, Ashikov A, Weber H, Novák O, Spíchal L, Strnad M, Strasser R, Bakker H, Schmülling T, Werner T (2015) Arabidopsis ROCK1 transports UDP-GlcNAc/UDPGalNAc and regulates ER protein quality control and cytokinin activity. PNAS 1(112):291-6.

The plant hormone cytokinin coordinates a wide range of processes key to plant development including cell proliferation and differentiation, tissue patterning, meristem maintenance and organ initiation. Although central components of cytokinin metabolism and signal transduction pathways have been identified over the past years, the importance of additional regulatory mechanisms such as posttranslational modification of the core regulatory proteins is only starting to emerge. In a search for new factors controlling the cytokinin activity in Arabidopsis, Niemann et al. described the identification of *REPRESSOR OF CYTOKININ DEFICIENCY1* (*ROCK1*) through a genetic screen for suppressors of cytokinin deficiency caused by overexpression of cytokinin-degrading, CKX, proteins. *ROCK1* encodes a protein belonging to a family of nucleotide-sugar transporters which function in translocating cytosolically synthesized nucleotide sugars across the endoplasmic reticulum (ER) and Golgi membrane. In these organelles, nucleotide sugars are required for glycosylation reactions essential for modifications of proteins and lipids, and for cell wall biosynthesis. In cooperation with colleagues from Germany, Czech Republic and Austria, the group of Tomáš Werner demonstrated that ROCK1 localizes specifically to ER and represents the first transporter of UDP-GlcNAc and UDP-GalNAc identified in plants. How can nucleotide-sugar availability in the ER influence cytokinin activity? The authors showed that the *rock1* mutation strongly reduces CKX activity by affecting the protein levels, indicating that ROCK1 plays a role in maintaining the CKX function. Importantly, CKX proteins are mainly localized within the secretory pathway controlling thus cytokinin concentrations directly sensed by the hormone receptors in the ER and apoplast. They further demonstrated that the predominantly ER-localized CKX1 protein is degraded in a proteasome-dependent way in a process called ER-associated protein degradation; a conserved cellular route to withdraw non-native proteins recognized by ER quality control. Results of this work led to conclude that ROCK1 represents an important component of ER quality control and the nucleotide sugars transported by ROCK1 are substrates for hypothetical posttranslational modifications determining cellular fate of target proteins, such as CKXs. It will be interesting to study the nature of these glycan modifications and their role in controlling plant developmental programs. In this regard, the study provided evidence that *ROCK1* is a vital regulator of the cytokinin signal in the shoot apical meristem determining its organogenic activity.

The circadian clock: A developmental metronome for lateral root development

By Ute Voß and Malcolm J. Bennett (Centre for Plant Integrative Biology, University of Nottingham, UK)

Voß U, Wilson MH, Kenobi K, Gould PD, Robertson FC, Peer WA, Lucas M, Swarup K, Casimiro I, Holman TJ, Wells DM, Péret B, Goh T, Fukaki H, Hodgman TC, Laplaze L, Halliday KJ, Ljung K, Murphy AS, Hall AJ, Webb AA, Bennett MJ (2015) The circadian clock rephases during lateral root organ initiation in Arabidopsis thaliana. Nature Communications 6;6:7641.

Root systems architecture determines the efficiency with which plants can take up water and nutrient resources. In Arabidopsis lateral roots (LRs) are derived from pairs of xylem pole pericycle cells and after several rounds of cell divisions break through overlying tissues to emerge into the soil. Auxin is the major regulator of this process and determines the position of LR initiation as well as reprograms cells overlying LR primordia to undergo cell separation, thereby facilitating the emergence of the new organ.

To identify new mechanisms regulating root branching, we generated an unique time course transcriptomic dataset that profiled each individual stage of LR development (which is available via the Arabidopsis eFP browser at http://bar.utoronto.ca/). Rather surprisingly, transcriptomic analysis (and backed up with circadian regulated reporters) revealed that the clock rephases during LR development and is independent of other shoot tissues and root zones. Genetic experiments later confirmed that a fully operating circadian clock appears essential for normal LR development; since LR emergence was disrupted in circadian clock mutants.

The key question is, why does a new LR need to rephase the clock? Transcript analysis revealed that during LR development the expression of auxin signalling genes are gated by the circadian clock. In particular IAA14/SLR1, a major regulator of the LR auxin response pathway, is expressed in a circadian manner and which is functionally important since constitutive expression of IAA14 blocks lateral root emergence. Within our transcriptomic dataset we also identified a novel auxin degrading enzyme, AtDAO2. Intriguingly, metabolic profiling revealed that root auxin levels display strong circadian oscillations, and was in anti-phase to AtDAO2. We concluded by proposing that the circadian clock functions akin to a developmental metronome during LR development, helping coordinate organ emergence by gating auxin homeostasis and signalling in cells overlying LR primordia.

TOC

Contributions to Applied Research and Industry

Arabidopsis has been for many years the reference plant used in basic and applied research due to not only its previously mentioned features, but also due to the great efforts of the scientific community, strongly supported by the funding bodies. During the last decades, the Arabidopsis community leveraged the applied research fields with their achievements like the first sequenced plant genome, followed by functional genomics studies, today's prosperity of omics and network approaches and the concomitant development of a plethora of new technologies. The prevalent focus of applied research is on the development of products with commercial value, which requires studies in crops like rice, corn, soybean, tomato and legumes, just to name a few. In contrast, basic research is mainly curiosity-driven and allows higher freedom to explore a broader range of hypothesis and develop new techniques and approaches. Additionally, companies rely on confidentiality, whereas basic research depends on an open exchange of information and resources. In the previous decades, the division of labor between the public and private sector has proven to be tremendously successful in case of Arabidopsis and plant biology in general.

Measuring the impact and evaluating the future potential of Arabidopsis research on applied research and industry is rather difficult, which is essentially due to the complementary information policies and the fact that a minimum ten years elapse is required between the discovery and the subsequent successful application. Therefore, in most cases the actual origins of real world applications remain obscure to a large extent, unless published e.g. in peer-reviewed journals or mentioned in patent submissions. Figure 6 illustrates a 20-year trend of patent applications referring to model and crop species (represented by maize and rice) in the United States, Europe and worldwide. In the US, since 1994 more than 15,000 utility patents referring to Arabidopsis were published compared to almost 55,000 on rice and 112,200 on maize (Figure 6A). Considering that Arabidopsis is a non-agricultural plant, its number of patents is rather impressive, and has been stable over the years. The trend in published applications in Europe was comparable to the US until 2011, when the restrictions towards genetically modified crops became more prominent in European countries. In the last year, the number of rice and maize applications in Europe dropped to the levels of 2008 (830 and 1230, respectively),while those referring to Arabidopsis stabilized in around 120 applications (Figure 6B). A decrease in international patent applications was also observed in 2012 and 2013 (PCT-WIPO, 187 contracting states, Figure 6C). In 2014 this trend seemed to be positively reverted for rice and corn, decreasing again in the last year. As expected, patents on corn and rice far exceed those citing Arabidopsis, but the translation of basic knowledge and technologies to crop species should not be underestimated. Several labs around

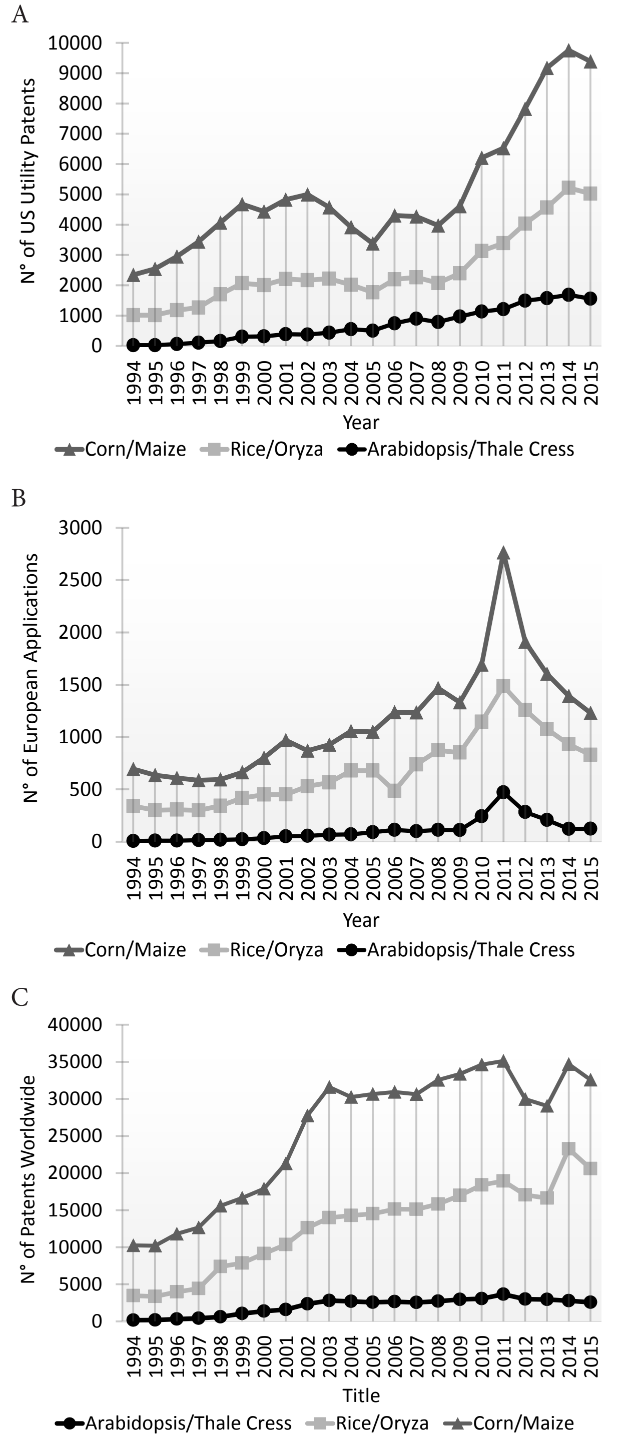


Figure 6. Trends of patents referencing model organisms (maize, oryza, Arabidopsis) from 1994-2015; (A) number of utility patents in the United States; (B) number of published applications in Europe; (C) number of patents worldwide, Patent and Cooperation Treaty applications (PCT) according to the World Intellectual Property Organization (WIPO, 187 contracting states).

Searches were performed (2016-03-01): A) http://patft.uspto.gov/netahtml/PTO/search-adv.htm, e.g. query: SPEC/rice OR SPEC/oryza AND ISD/20150101->20151231; B) http://worldwide.espacenet.com/advancedSearch?locale=en_EP, select EP collection, e.g.: Keyword(s) in full text: rice OR oryza, Publication date: 2015; C) http://patentscope.wipo.int/search/en/structuredSearch.jsf, select any field, e.g. English all: rice OR oryza, Publication date: 2015.

the world study Arabidopsis and crop species in parallel, being Arabidopsis often the first choice for plant researchers to test hypothesis and develop new methods. The continuous funding of basic research is crucial to further develop a basic understanding of plant processes in order to leverage applied studies with other plant species to in the end face the current challenges in agriculture. In this section, a selection of recently published studies in different crop species is summarized. It is important to note that little (if not none) progress would have been possible without previous knowledge obtained from Arabidopsis research.

The last selected publication summarized here exemplifies the usage of genome editing (GE) technology for the generation of crops with improved traits. The potential applications of CRISPR/Cas9, TALENs and ZFNs technologies in plant research and crop production are immensurable, and could overcome several of the current issues imposed by goverments and the general public regarding the regulation and acceptance of GMOs. In a commentary at Nature Genetics published earlier this year, Sanwen Huang et al. call for changes in the regulatory framework for crops generated with GE technologies, following a product-based rather than technology-based regulation (Nature Genetics 48:109–11, 2016. doi:10.1038/ng.3484). The authors propose that, as long as the GE trait could have been introduced by natural mutation or conventional breeding, the plant should not be assessed within GMO legislations, a view that is already shared by governments such as the US and Germany. Importantly, plant researchers should continue to follow this path and transparently discuss the pros and cons of their research with the general public and policy makers, in order to tackle important misconceptions that hinder the progress of plant science and agriculture.

Genetic diversity in cassava unraveled

Bredeson JV, Lyons JB, Prochnik SE, Wu GA, Ha CM, Edsinger-Gonzales E, Grimwood J, Schmutz J, Rabbi IY, Egesi C, Nauluvula P, Lebot V, Ndunguru J, Mkamilo G, Bart RS, Setter TL, Gleadow RM, Kulakow P, Ferguson ME, Rounsley S, Rokhsar DS (2016) Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. Nature Biotechnology, DOI:10.1038/nbt.3535.

Cassava is one of the major staple crops cultivated in tropical regions, providing food for more than half a billion people in the world. The domestication of cassava dates up to 6,000 years ago in regions of the Amazon basin. Being further distributed during colonial times, today cassava is produced worldwide along the tropics. The low genetic variation of many cultivars, combined with clonal propagation methods, confer to cassava high susceptibility to diseases and environmental stresses, representing a great threat to food security. Conventional breeding techniques in cassava are challenging due to several aspects, including a long reproductive cycle with asynchronous flowering. Therefore, a better understanding of the gene pools of cultivated cassava and its wild relatives is expected to facilitate genetic improvement. With this in mind, Bredeson and colleagues took a deeper look into the genomes of various cassava accessions, which led to very interesting findings. The authors used shotgun sequencing and genotyping-by-sequencing to analyze the genetic variation within cultivated and wild accessions from Africa and several regions of the globe, as well as two rubber tree species employed in breeding programs aiming at exploiting the species' natural resistance to cassava pathogens. A high-quality reference genome for cassava was provided by augmenting the earlier draft sequence of the reference genotype AM560-2. Their findings revealed that its genome comprises of over 33,000 predicted protein-coding genes out of which 96.6% are anchored to chromosomes. Comparative analyses showed that cassava and the rubber tree Hevea share paleotetraploidy, and that there is widespread interspecific introgressions in the nucleus, providing an interesting hint into the genetic signature of past cassava breeding programs. The authors expect that the knowledge of the relationships among cultivars will help developing diverse germplasm and will guide breeding decisions to restore genetic variation, ultimately contributing to improve disease resistance and yield in this very important crop.

Protecting our breakfast orange juice

Dutt M, Barthe G, Irey M, Grosser J (2015) Transgenic Citrus Expressing an Arabidopsis NPR1 Gene Exhibit Enhanced Resistance against Huanglongbing (HLB; Citrus Greening). PLoS ONE, DOI:10.1371/journal.pone.0137134.

Huanglongbing (HLB; Citrus Greening) is a serious disease affecting citrus production worldwide. It is caused by phloem infection of the bacterium *Candidatus* Liberibacter asiaticus (CLas), limiting resource distribution throughout the tree, ultimately leading to plant decline. The commercial cultivars lack resistance to HLB, therefore the disease spread is currently managed by preventing trees from being infected, either by controlling the transmitting psyllid or destroying infected trees. One possible disease management strategy is to identify and introduce traits from tolerant Citrus spp., which is limited by the fact that conventional breeding techniques in citrus crops are difficult and lengthy. Genetic engineering represents the fastest and most efficient strategy to improve resistance, an approach that researchers from the University of Florida have been successfully employing. In an attempt to stimulate plant defense pathways, Dutt and colleagues transformed two important sweet orange cultivars with the Arabidopsis *AtNPR1* gene expressed under either constitutive CaMV35S or the phloem-specific *AtSUC2* promoters. AtNPR1 is a key regulator of the salicylic acid (SA)-mediated systemic acquired resistance pathway, and its expression have been implicated in fungal disease resistance in several crops such as rice, wheat and cotton, and other bacterial disease resistance in citrus. Although orthologs of *NPR1* are present in sweet orange's genome, the authors chose to express an Arabidopsis gene in order to avoid homology-dependent gene silencing. Indeed, several of the independent lines expressed high levels of AtNPR1, as well as of its endogenous targets PR1, PR2 and WRKY70, suggesting a better activation of plant-defense genes in transgenic plants. Most importantly, when submitted to HLB susceptibility assays, the majority of the lines tested were more resistant to HLB infection. In a no-choice greenhouse assay in which plants were cultivated in the presence of CLas-contaminated psyllids, most of the transgenic plants were tested negative for bacterial infection even after several months of exposure. In contrast, control plants died in the same or even lower periods of time, similarly to results obtained under field conditions. In this work, the authors discuss that a plant-derived transgene would represent a more consumer-friendly GM crop, even though one should consider the additional components of the T-DNA cassette that are not plant-derived. In addition, they suggest that transgenic rootstocks might confer resistance to non-transgenic scion, an approach that would certainly be more appealing to the general public, since the final product would be GM-free. In any case, crop improvement via genetic engineering represents an example of (possibly the only) potential strategies to overcome HLB and other devastating citrus diseases.

Biofuel production from Switchgrass: can genetic engineering improve sustainability?

Yang J, Worley E, Torres-Jerez I, Miller R, Wang M, Fu C, Wang Z, Tang Y, Udvardi M (2015) PvNAC1 and PvNAC2 Are Associated with Leaf Senescence and Nitrogen Use Efficiency in Switchgrass. Bioenerg. Res. 8:868–880.

Switchgrass (*Panicum virgatum* L.) is a perennial C4 plant whose high biomass yield, robustness and ability to grow in marginal soils make it an important alternative crop targeted for biofuel. The sustainability of switchgrass production depends in part on the nutrient conservation in the soil-plant system, since economic and environmental costs of synthesis and usage of fertilizers (particularly Nitrogen) are very high. One strategy to address this concern is to decrease nutrient concentration in the harvested shoots, while keeping higher contents belowground. Following this line, Yang and colleagues explored the control of leave senescence on the regulation of nutrient remobilization within plant parts. It is known that during early senescence of switchgrass, N is remobilized to seeds and roots with an efficiency of 20-61%, however the genetic regulation of this process is unknown. In this work, the authors identified two switchgrass genes, *PvNAC1* and *PvNAC2*, which were phylogenetically grouped with NAC transcription factors (TFs), known to be involved in senescence of annual plant species. By using expression analyses, subcellular localization, as well as phenotypic complementation of an Arabidopsis *atnap* mutant with *PvNAC1*, they concluded that these genes are indeed master regulators of leaf senescence. When expressing *PvNAC1* in Arabidopsis, senescence was triggered in whole plants, resulting in chlorophyll degradation and N translocation out of the leaves. The authors further investigated how PvNAC1 mediates leaf senescence and N remobilization via transcriptomic analysis of the transgenic Arabidopsis plants, therefore determining important targets of *PvNAC1* activation (e.g. transcription regulators, protein degradation genes and genes involved in ammonium metabolism). Finally, the authors overexpressed *PvNAC2* in switchgrass and found that transgenic plants had higher aboveground biomass and N content than the controls, particularly in stem tissues. They found evidences to support that the high N levels in transgenic plants may have resulted from upregulation of genes encoding ammonium transporters in the roots and N metabolism in leaves. Taken together, the results therein presented place *PvNAC*s as potential tools to manipulate senescence aiming at improved N use efficiency in switchgrass. This will certainly contribute to the development of plants with higher yield and nutrient efficiency, a promising outlook for the sustainable production of bioenergy crops.

Get to the point: targeted gene-editing in Maize

Svitashev S, Young JK, Schwartz C, Gao H, Falco SC, Cigan AM (2015) Targeted Mutagenesis, Precise Gene Editing, and Site-Specific Gene Insertion in Maize Using Cas9 and Guide RNA. Plant Physiology 169: 931-45.

Modern gene-editing (GE) technologies e.g. TALENs, ZFNs and Crispr/Cas9 have revolutionized the way genetic engineering is approached, due to their ability to generate site-specific DNA breaks and to introduce desirable traits in a more controlled fashion. The Cas9-guide RNA (gRNA) was recently discovered as a bacterial adaptive defense system against plasmid and viral infection, via an RNA-guided Cas9 protein that recognizes and cleaves the invading DNA. Most promptly, scientists from all research areas have manipulated the components of the system aiming at applications that range from basic tools to study gene function, to biotechnological uses in human health and agriculture. In the last case, GE have been used to generate targeted mutations in several crop species, including orange, tomato, potato, sorghum, soybean and maize, among others. Many of those studies have employed non-homologous end joining (NHEJ), which mainly generates gene knockouts, limiting the vast potential of the technology. Svitashev and colleagues were able to exploit additional applications of Cas9-gRNA in maize, using cutting-edge resources e.g. amplicon deep sequencing to optimize the time and efficiency in obtaining GE plant material. By using multiplexed targeted mutagenesis, they could introduce, in a single transformation experiment, NHEJ-mediated knockouts with a high success rate in multiple loci, i.e. upstream the *liguleless1 LIG1* gene, the male fertility genes *Ms26* and *Ms45* and acetolactate synthase genes *ALS1* and *ALS2*. This approach has been used in other plant species, and is particularly promising for the manipulation of several genes from a pathway, gene families and homologues in polyploid species, such as maize. Targeted mutations were also obtained via direct delivery of gRNA in the form of in vitro synthesized RNA molecules in maize embryos containing pre-integrated Cas9, representing a viable alternative to generate mutagenized plant cells. Moreover, targeted editing of native maize genes, as well as gene integration at specific genome locations were successfully achieved via homology-directed repair (HDR). In the first case, the authors chose to edit ALS genes to introduce known mutations that confer plant resistance to sulfonylurea herbicides. By designing an ALS2-specific ALS-CR4 gRNA, they could target DNA cleavage to one of the two homologues and test different repair templates to introduce the desired P165S mutation. Importantly, the recovered edited plants were resistant to the chlorsulfuron herbicide, and the trait was inherited in the subsequent generation. The last approach aimed to overcome the issues of random integration of trait genes, which potentially leads e.g. to disruption of native gene functions. Two distinct methods of DNA cleavage (Cas9-gRNA and meganuclease), as well as different delivery systems (*Agrobacterium*-mediated and biolistic) and different combinations of vectors were tested to introduce a *UBI* promoter-driven *MoPAT* gene near the *LIG1* locus. A maize-optimized system was successfully established and the progeny of gene-edited plants also showed Mendelian segregation of targeted gene insertions. The results presented by Svitashev and colleagues exemplify important applications of Cas9-gRNA for introducing desirable traits in economically important plants such as maize. They and other plant researchers all over the world are not sparing efforts in further developing this and other GE technologies, which will certainly contribute to future demands of agriculture.

Country Reports of the International Arabidopsis Community

Country Highlights

Argentina

- Rodriguez et al. (2015) MicroRNA miR396 Regulates the Switch between Stem Cells and Transit-Amplifying Cells in Arabidopsis Roots. Plant Cell, highlighted in the cover of the journal.
- The 11th International Plant Molecular Biology Congress, with strong participation of Arabidopsis researchers, was held in Iguazú Falls, at the border of Argentina and Brazil.

Austria

- 10th TNAM, Tri-National Arabidopsis Meeting. Sept 14-16, 2016, Vienna.
- Martens & Bachmair (2015) How cells coordinate waste removal through their major proteolytic pathways. Nat Cell Biol.

Belgium

- Xuan et al. (2016) Cyclic programmed cell death stimulates hormone signaling and root development in Arabidopsis. Science.
- PLAZA, an access point for plant comparative genomics (http://bioinformatics.psb.ugent.be/plaza/).

Brazil

- Zorzatto et al. (2015) NIK1-mediated translation suppression functions as a plant antiviral immunity mechanism. Nature.
- Daloso et al. (2015) Thioredoxin, a master regulator of the tricarboxylic acid cycle in plant mitochondria. PNAS.

Canada

- Provart et al. (2016) 50 years of Arabidopsis research: highlights and future directions. New Phytologist.
- Toh et al. (2015) Structure-function analysis identifies highly sensitive strigolactone receptors in Striga. Science.

Chile

- The Chilean Society for Plant Biologists was founded. Rodrigo A. Gutiérrez is the first elected president.

Czech Republic

- Kulich et al (2015) Cell Wall Maturation of Arabidopsis Trichomes Is Dependent on Exocyst Subunit EXO70H4 and Involves Callose Deposition. Plant Physiology.
- Muchova et al (2015) Homology-dependent repair is involved in 45S rDNA loss in plant CAF-1 mutants. Plant Journal.

Denmark

- Poulsen et al. (2015) A phospholipid uptake system in the model plant *Arabidopsis thaliana*. Nature Communications.
- Munch et al. (2015) Retromer contributes to immunity-associated cell death in Arabidopsis. Plant Cell.

Finland

- Siligato et al. (2016) MultiSite Gateway compatible cell type-specific gene inducible system for plants. Plant Physiology.
- A new phenomics facility built at the University of Helsinki (http://blogs.helsinki.fi/nappi-blog).

France

- Over 1000 participants attended the 26th ICAR at the Palais des Congrès in Paris, 5th-9th July 2015.
- Lauressergue et al. (2015) Primary transcripts of microRNAs encode regulatory peptides. Nature.

Germany

- Newly designed and updated AFGN website is now online at http://www.dbg-afgn.de/.
- Endler et al. (2015) A Mechanism for Sustained Cellulose Synthesis during Salt Stress. Cell.

Greece

- Beris et al. (2016) RNAi-mediated silencing of the *Arabidopsis thaliana* ULCS1 gene, encoding a WDR protein, results in cell wall modification impairment and plant infertility. Plant Science.
- Daras et al. (2015) Potassium transporter TRH1 subunits assemble regulating root-hair elongation autonomously from the cell fate determination pathway. Plant Science.

India

- Prof. M.K. Mathew's lab at NCBS, Bangalore, has shown that saline stress reconfigures clathrin-independent endocytosis and remodels endomembrane systems, forming large vacuoles in the inner cell layers of Arabidopsis roots.
- Dr. Utpal Nath's group at IISc, Bangalore, has surveyed 75 eudicot species and proposed that the leaf growth polarity is of divergent nature. The expression gradient of miR396-GROWTH-REGULATING FACTOR module has a strong association with the polarity of leaf growth in Arabidopsis.

Israel

- Dr. Roy Weinstain (Tel Aviv University) and Dr. Assaf Zemach (Tel Aviv University) were awarded the ERC starting grant (ERC-2015-StG).

Italy

- Benedetti et al. (2015) Plant immunity triggered by engineered in vivo release of oligogalacturonides, damage-associated molecular patterns. PNAS (USA).

Japan

- Takeuchi & Higashiyama (2016) Tip-localized receptors control pollen tube growth and LURE sensing in Arabidopsis. Nature.

Netherlands

- Long et al. (2015) Arabidopsis BIRD zinc finger proteins jointly stabilize tissue boundaries by confining the cell fate regulator SHORT-ROOT and contributing to fate specification. The Plant Cell.
- Vera-Sirera et al. (2015) A bHLH-based feedback loop restricts vascular cell proliferation in plants. Dev Cell.

New Zealand

- Dr Nick Roberts from AgResearch won the NZBIO Biotechnologist of the year 2015 for work that included Arabidopsis.

South Korea

- 27th ICAR will be hosted by Inhwan Hwang and the local organizing committee in GyeongJu in June 29th-July 3rd, 2016.
- Woo et al. (2015) DNA-free genome editing in plants with preassembled CRISPR-Cas9 ribonucleoproteins. Nat Biotechnol.

Spain

- Takahashi et al. (2015) A hierarchical multi-oscillator network orchestrates the Arabidopsis circadian system. Cell.

Sweden

- Will genome edited plants have to be treated as GMOs? The current response from The Swedish Board of Agriculture suggest that they might not.

Switzerland

- Switzerland has had a strong focus on Arabidopsis research. Swiss plant scientists regularly meet at the SwissPlant Symposium. SERI and Swiss Institute of Bioinformatics gratefully covered TAIR database subscription in Switzerland.

United Kingdom

- Neil Bruce demonstrates the potential of Arabidopsis to lead to translatable research with their TNT study published in Science.
- GARNet and OpenPlant organised a two-day workshop at the John Innes Centre that brought together an international group of 150 researchers to learn about the potential of using CRISPR gene-editing technology in plant science.

United States

- Siobhan Brady (PI) and Joanna Friesner (co-PI), NAASC member and Coordinator, respectively, received a 5 year NSF award entitled 'Research Coordination Network: Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology.'
- Notable community publication led by Nick Provart: open-access review "50 years of Arabidopsis research: highlights and future directions" with 26 co-authors, 308 references, 17 sections and a concise overview of 54033 Arabidopsis articles.

Argentina

Marcelo J. Yanovsky (myanovsky@leloir.org.ar) Instituto Leloir (FIL and CONICET)

General Activities

Arabidopsis Research Facilities

There are more than 30 groups conducting varied research with Arabidopsis in Argentina. They work in different Institutes and Universities scattered throughout the country in cities such as Buenos Aires, Rosario, Mar del Plata, Santa Fe, Córdoba, Mendoza and Bariloche.

Current Arabidopsis Projects

The research topics and research groups include, among others, water transport (Gabriela Amodeo), responses to water deficit (Raquel Chan, Norberto Iusem), light signaling and photomorphogenesis (Jorge Casal, Carlos Ballaré, Javier Botto), responses to UV-B light (Paula Casati, Carlos Ballaré, Raúl Cassia), 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), carbohydrate metabolism (Graciela Salerno, Fernando Carrari), root growth and development (José Estevez) biotic stress responses (Sebastián Azurmendi, Mariana del Vas, María Elena Alvarez), gene expression, micro RNAs and alternative splicing (Pablo Manavella, Javier Palatnik, Marcelo Yanovsky, Alberto Kornblihtt).

Conferences and Workshops

- The 11th International Plant Molecular Biology Congress, with strong participation of Arabidopsis researchers, was held in Iguazú Falls, at the border of Argentina and Brazil, and was organized by a bi-national Argentine-Brazilian Committee.

Selected Publications

- MicroRNA miR396 Regulates the Switch between Stem Cells and Transit-Amplifying Cells in Arabidopsis Roots. Rodriguez RE, Ercoli MF, Debernardi JM, Breakfield NW, Mecchia MA, Sabatini M, Cools T, De Veylder L, Benfey PN, Palatnik JF (2015) Plant Cell 27(12):3354-66.
- KH domain protein RCF3 is a tissue-biased regulator of the plant miRNA biogenesis cofactor HYL1. Karlsson P, Christie MD, Seymour DK, Wang H, Wang X, Hagmann J, Kulcheski F, Manavella PA (2015) Proc Natl Acad Sci U S A. 112(45):14096-101.
- The spliceosome assembly factor GEMIN2 attenuates the effects of temperature on alternative splicing and circadian rhythms. Schlaen RG, Mancini E, Sanchez SE, Perez-Santángelo S, Rugnone ML, Simpson CG, Brown JW, Zhang X, Chernomoretz A, Yanovsky MJ (2015) Proc Natl Acad Sci U S A. 112(30):9382-7.
- Induced folding in RNA recognition by *Arabidopsis thaliana* DCL1. Suarez IP, Burdisso P, Benoit MP, Boisbouvier J, Rasia RM (2015) Nucleic Acids Res. 43(13):6607-19.

Major Funding Sources

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

Austria

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

General Activities

Arabidopsis Research Facilities

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) (www.ist.ac.at/en/)

AIT Austrian Institute of Technology (www.ait.ac.at/)

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/)

Research Groups

- 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/): Stress signal transduction and cellular responses; Markus Teige (www.univie.ac.at/mosys/markus_teige_cv.html): signaling in acclimation to stress, organellar signaling; Irute Meskiene (www.univie.ac.at/mosys/groups.html): stress signaling and protein phosphatases

- Chromosome Biology

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

- Epigenetics

Frederic Berger (www.gmi.oeaw.ac.at/research-groups/frederic-berger): Chromatin architecture and function; Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/research-groups/mittelsten-scheid): Epigenetic changes in plants

- Development

Wolfgang Busch (www.gmi.oeaw.ac.at/research-groups/wolfgang-busch): Regulation of root development in Arabidopsis; Michael Nodine (http://www.gmi.oeaw.ac.at/research-groups/michael-nodine): Small RNA functions in plant embryos; Eva Benkova (http://ist.ac.at/en/research/research-groups/benkova-group): Hormonal regulation of plant development; Jiri Friml (http://ist.ac.at/research/research-groups/friml-group): Auxin transport, cell polarity and endocytic trafficking

- Molecular Genetics & Cell Biology

Marie-Theres Hauser (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-hauser): development, stress; Jürgen Kleine Vehn (http://www.dagz.boku.ac.at/arbeitsgruppen/team-kleine-vehn/): phytohormonal crosstalk, differential growth regulation; Barbara Korbei (http://www.dagz.boku.ac.at/pgz/korbei): Elucidating the role of TOL proteins in post-Golgi trafficking

- Glycobiology

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

- RNA Metabolism

Mariya Kalyna (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-hauser/projekt-kalyna): Alternative splicing

- Plant Pathogen Interaction

Youssef Belkhadir (www.gmi.oeaw.ac.at/research-groups/youssef-belkhadir): Plant cell signalling at the interface of growth and defences; Armin Djamei (http://www.gmi.oeaw.ac.at/research-groups/armin-djamei): Effectomics - exploring the toolbox of plant pathogens

Current Arabidopsis Projects

Doctoral programmes financed by the FWF

- 2012-2020 “Chromosome Dynamics” (gscd.gmi.oeaw.ac.at:8080/Plone)
- 2010-2018 “Population Genetics” (www.popgen-vienna.at/)
- 2014-2016 “RNA Biology” (www.mfpl.ac.at/rna-biology/)

ITN (international training network)

- 2013-2017 “CALIPSO - Calcium and Light Signals in Photosynthetic Organisms” (itn-calipso.univie.ac.at/)
- 2013-2017 “COMREC: Control of Meiotic Recombination: Arabidopsis to Crops” (www.birmingham.ac.uk/comrec)

ERC

- 2011-2016 “MAXMAP: Developing maximum-resolution genotype-phenotype maps using whole-genome polymorphism data”

- 2012-2017 “PSDP: Polarity and subcellular dynamics in plants”
- 2014-2019 “EFFECTOMICS- elucidating the toolbox of biotrophic pathogens”
- 2015-2020 “sRNA-EMB: Small RNA regulation of the body plan and epigenome in Arabidopsis embryos”
- 2015-2020 “AuxinER: Mechanism of Auxin-dependent Signaling in the Endoplasmatic Reticulum”

ERA-CAPS projects

- 2014-2017 “Dimorphic fruits, seed and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments (SeedAdapt)”
- 2014-2017 “EURO-PEC - European Plant Embryology Consortium”
- 2015-2018 “Evolution of sexual reproduction in plants (EVOREPRO)”
- 2014-2017 “The role of the N-end rule pathway in controlling plant response to the environment (N-vironment)”
- 2014-2017 "Delineating the crossover control networks in plants (DeCOP)"

WWTF projects

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

FWF projects

- 2008-2019 “Chromosome Dynamics“ SFB 34
- 2013-2016 “SINUDYN – Stress-induced nucleosome dynamics in plants”
- 2014-2017 “Impact of a new histone H2A variant on chromatin structure and dynamics”
- 2014-2017 “N-vironment - The role of the N-end rule in plant response to the environment”
- 2014-2017 “In vivo Protein Interaction during Cell Signaling”
- 2014-2017 “N-vironment - The role of the N-end rule in plant response to the environment”
- 2014-2019 “TOL Proteins in post-Golgi Trafficking in Plants”
- 2015-2016 “Epigenetic Reprogramming of the Plant Paternal Genome”
- 2015-2017 “Root growth Control and Epistasis”
- 2015-2017 “Elucidating Salicylic Acid Sensing in Biotrophic Smut Fungi”
- 2015-2017 “Hormone cross-talk drives nutrient-dependent root development”
- 2015-2017 “Pectin signaling in responses to heavy metals and pathogens”
- 2015-2018 “Dissecting the glycan-dependent ERAD pathway in plants”
- 2015-2018 “Signaling Salt Stress to the chromatin”
- 2015-2018 “Characterization of an essential virulence factor in the maize pathogen Ustilago maydis”
- 2015-2018 “EXO70 exocyst subunits in morphogenesis and adaptation”
- 2015-2019 “Small RNAdirected reprogramming of lineage-specific epigenomes in plant embryos”
- 2016-2017 “The histone variant H2A.W: a novel component that structures chromatin domains”
- 2016-2018 “Evolution of the chromatin organization in plants”
- 2016-2018 “The role of PLD zeta1 in iron dependent root growth regulation”
- 2016-2019 “Importance of Lewis A Epitopes for Pseudomonas syringae Infection of Arabidopsis”

DFG

2011-2017 “Evolutionary plant solutions to ecological challenges: Molecular mechanisms underlying adaptive traits in the Brassicaceae s.l. (Adaptomics)”

APART fellowship of the Austrian Academie of Sciences

2014-2018 “O-GlcNAc Modification of Plant Proteins“

Road Map Related Activities

Arabidopsis Tools and Resources

Fred Berger: Several antibodies against Arabidopsis histones

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

VBCF ProTech facility: offering made-to-order CRISPR/Cas9 transgenics

Andreas Bachmair: Mutants in ubiquitin conjugation, in vitro SUMO conjugation assay

IST Austria: root chip tracking system, light sheet (SPIM) microscope for Arabidopsis roots, lateral roots, apical hook (not published), vertical confocal microscope allowing automatic tracking of the root growth (not published), platform for specific cell ablation combined with real-time imaging in plants

Outreach Activities

Fascination of plant day, May 18, 2016. (http://www.plantday12.eu/home.htm)

European Researchers Night, Sept 25, 2016 (http://www.fit-for-future.at/calipso)

Long night of Research, April 22, 2016 (http://www.langenachtderforschung.at/)

Open campus day IST Austria presenting, May 31, 2015

Open campus day IST Austria presenting, June 5, 2015

Conferences and Workshops

- Vienna Region Plant Network Meeting, Feb 2015, Vienna, University of Natural Resources and Life Sciences
- Symposium "Pair, Share and Care: Chromosomes throughout Life", Vienna, Sept 2015
- VBC PhD Symposium "Communication: let's talk about it", Nov 2015 Vienna Austria
- Vienna Region Plant Network Meeting, Nov 2015, Vienna Biocenter Campus
- "11th Microsymposium on Small RNAs" May 2016 Vienna Austria
- EMBO Workshop "New Model systems for early land plant evolution" June 2016 Vienna Austria
- "Tri-National Arabidopsis Meeting (TNAM)" Sept 2016 Vienna, Austria
- International Conference "Plant Organellar Signaling 2016" (http://www.plant-organellar-signaling.eu/)

Selected Publications

- DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. Dubin MJ, Zhang P, Meng D, Remigereau MS, Osborne EJ, Paolo Casale F, Drewe P, Kahles A, Jean G, Vilhjálmsson B, Jagoda J, Irez S, Voronin V, Song Q, Long Q, Rätsch G, Stegle O, Clark RM, Nordborg M (2015) Elife 4:e05255.
- "SnRK1-triggered switch of bZIP63 dimerization mediates the low-energy response in plants. Mair A, Pedrotti L, Wurzinger B, Anrather D, Simeunovic A, Weiste C, Valerio C, Dietrich K, Kirchler T, Nägele T, Vicente Carbajosa J, Hanson J, Baena-González E, Chaban C, Weckwerth W, Dröge-Laser W, Teige M (2015) Elife 05828.
- How cells coordinate waste removal through their major proteolytic pathways. Martens S, Bachmair A (2015) Nat Cell Biol. 17(7):841-2.
- Actin-dependent vacuolar occupancy of the cell determines auxin-induced growth repression. Scheuring D, Löfke C, Krüger F, Kittelmann M, Eisa A, Hughes L, Smith RS, Hawes C, Schumacher K, Kleine-Vehn J (2016) Proc Natl Acad Sci U S A. 113(2):452-7.
- Auxin regulates SNARE-dependent vacuolar morphology restricting cell size. Löfke C, Dünser K, Scheuring D, Kleine-Vehn J (2015) Elife 4. doi: 10.7554/eLife.05868.

Major Funding Sources

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

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

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

European Union:

Seventh Framework Programme (FP7) http://ec.europa.eu/research/fp7/index_en.cfm

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

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

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

OeAD http://www.oead.at/projects_cooperations/EN/

Belgium

Moritz K. Nowack (moritz.nowack@vib.be) VIB-Ghent University, Plant Systems Biology

General Activities

Arabidopsis Research Facilities

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

Current Arabidopsis Projects

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

A Belgian national research project (IAP), coordinated by D. Inzé, focuses on how root and shoot influence each other and how this interaction contributes to the development of the plant. This program also involves T. Beeckman, F. Van Breusegem G. Beemster, L. De Veylder, M. Boutry, X. Draye, N. F. Chaumont, and C. Périlleux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project. For more information, see http://www.iuap-mars.be/.

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

An F.R.S.-FNRS grant was appointed to C. Hermans to study mineral influences on root architecture.

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

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

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

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

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

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/).

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

Conferences and Workshops

- 2nd meeting of The International Society for Plant Molecular Farming. Gent, Belgium. May 25-26, 2016 (http://societyformolecularfarming.org/node/34)
- Genome Engineering and Synthetic Biology. Gent, Belgium. January 28-29, 2016 #GESB (http://www.vib-conferences.be/)
- International PSE Symposium Plant Omics and Biotechnology for Human Health. Gent, Belgium. November 21-24, 2016 (http://www.psb.ugent.be/news/430-international-pse-symposium/)
- 14th Euro Fed Lipid Congress - Fats, Oils and Lipids: Innovative Approaches towards a Sustainable Future. Gent, Belgium. September 18-21, 2016 (http://www.eurofedlipid.org/meetings/ghent2016//), hosted by the Benelux Lipid Network

Selected Publications

- Cyclic programmed cell death stimulates hormone signaling and root development in Arabidopsis. Xuan W, Band LR, Kumpf RP, Van Damme D, Parizot B, De Rop G, Opdenacker D, Möller BK, Skorzinski N, Njo MF, De Rybel B, Audenaert D, Nowack MK, Vanneste S, Beeckman T (2016) Science 351(6271):384-7.
- ROTUNDA3 function in plant development by phosphatase 2A-mediated regulation of auxin transporter recycling. Karampelias M, Neyt P, De Groeve S, Aesaert S, Coussens G, Rolčík J, Bruno L, De Winne N, Van Minnebruggen A, Van Montagu M, Ponce MR, Micol JL, Friml J, De Jaeger G, Van Lijsebettens M (2016) Proc Natl Acad Sci U S A. 113(10):2768-73.
- The DELLA protein SLR1 integrates and amplifies salicylic acid- and jasmonic acid-dependent innate immunity in rice. de Vleesschauwer D, Seifi S, Filipe O, Haeck A, Nguyen Huu S, Demeestere K, Höfte MM (2016) Plant Physiol. pii: pp.01515.2015.
- It's Time for Some "Site"-Seeing: Novel Tools to Monitor the Ubiquitin Landscape in *Arabidopsis thaliana*. Walton A, Stes E, Cybulski N, Van Bel M, Iñigo S, Durand AN, Timmerman E, Heyman J, Pauwels L, De Veylder L, Goossens A, De Smet I, Coppens F, Goormachtig S, Gevaert K (2016) Plant Cell 28(1):6-16.
- An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. Van Leene J, Eeckhout D, Cannoot B, De Winne N, Persiau G, Van De Slijke E, Vercruysse L, Dedecker M, Verkest A, Vandepoele K, Martens L, Witters E, Gevaert K, De Jaeger G (2015) Nat Protoc. 10(1):169-87.

Major Funding Sources

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework Programs (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/)

TOC

Brazil

Wagner Araújo (wlaraujo@ufv.br); Adriano Nunes-Nesi (nunesnesi@ufv.br) Universidade Federal de Viçosa, Viçosa

General Activities

Arabidopsis Research Facilities

There is currently a growing interest in using Arabidopsis as a model plant for research in Brazil.

The groups working with Arabidopsis are distributed throughout the country in cities such as Brasília, Campinas, Fortaleza, Porto Alegre, Piracicaba, Rio de Janeiro, São Paulo, Viçosa and Fortaleza.

There is currently no dedicated Arabidopsis consortia or centers in Brazil, but Arabidopsis is commonly used by plant biologists as a model organism. Brazilian funding agencies funds a number of projects in which Arabidopsis is employed as a model; however, most of those projects presents also an applied version using crops of interest in Brazil.

Research topics and research groups in Brazil include, among others: plant growth and development, biotic and abiotic stress responses, phytohormonal crosstalk and biology, cell signalling mechanisms, circadian rhythms, carbohydrate metabolism, micro RNA, plant-insect-pathogen interactions, mitochondrial metabolism and transport, plant senescence and chlorophyll catabolism, system biology, oxidative stress, plant cell wall,

Current Arabidopsis Research Projects

- *Camila Caldana, CTBE/CNPEM, Campinas*: Regulation of plant growth by the target of rapamycin (TOR) pathway.
- *Michel Georges Albert Vincentz, CBMEG-UNICAMP, Campinas:* Define the architecture of the gene regulatory network related to AtbZIP63: an *Arabidopsis thaliana* bZIP type transcriptional factor invovled in the control of energetic homeostasis.
- *Maria Magdalena Rossi, IB-USP, São Paulo:* Manipulation of senescence and chlorophyll catabolism for yield and nutritional quality improvement.
- *Márcio de Castro Silva Filho, ESALQ-USP, Piracicaba:* Deciphering the molecular mechanisms involved in the localization of organelar proteins as well as the complex plant-insect-pathogen interactions.
- *Daniel Scherer de Moura, ESALQ-USP, Piracicaba:* AtRALF1 perception mechanisms: its receptors and the dissociation between ion fluxes and the negative regulation of celular expansion.
- *Alessandra Alves de Souza, IAC, APTA, Cordeirópolis:* Functional study of genes associated with plant defense to pathogens: focus on the control of *Xylella fastidiosa*, the causal agent of citrus variegated chlorosis
- *Ivan de Godoy Maia, IB-Unesp, Botucatu:* Plant uncoupling mitochondrial proteins: functional analysis employing RNA-seq and knockout mutants.
- *Marcelo Mendes Brandao, CBMEG-UNICAMP, Campinas:* System biology techniques applied to the agriculture: transcriptomes and interactomes analyses.
- *Juan Armando Casas Mollano, IQ-USP, São Paulo:* Functional characterization of the newly discovered family of MUT9 kinases in *Arabidopsis thaliana* and sugarcane.

There are other researchers involved in several Arabidopsis projects that should be also mentioned:

Paulo Mazzafera, IB-UNICAMP, Campinas

Celso Benedetti, LNBio/CNPEM, Campinas

Fabio Tebaldi Nogueira, ESALQ-USP, Piracicaba

Hana Masuda, UFABC, São Bernardo

Marcelo Menossi, IB/UNICAMP, Campinas

Marco Aurelio Zezzi Arruda, IQ-UNICAMP, Campinas

Marcelo Dornelas, IB- UNICAMP, Campinas

Ione Salgado, IB- UNICAMP, Campinas

Carlos Hotta, IQ-USP, São Paulo

Adriano Nunes-Nesi (UFV, Viçosa)

Elizabeth B. Fontes (UFV, Viçosa)

Wagner L. Araújo (UFV, Viçosa)

Thomas Willians (UnB, Brasília)

Márcia Margis (UFRGS, Porto Alegre)

Luis Fernando Revers (EMBRAPA, Bento Gonçalves)

Paulo Cavalcanti Gomes Ferreira (UFRJ, Rio de Janeiro)

Adriana Hemerly (UFRJ, Rio de Janeiro)

Outlook on Arabidopsis Research

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 Arabidopis 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.

Road Map Related Activities

Arabidopsis Tools and Resources

This is still an area that needs to be developed in Brazil.

Conferences and Workshops

- The International Plant Molecular Biology Congress was held in Iguazu Falls, Brazil, in October 25th - 30th, 2015

- XV Brazilian Congress of Plant Physiology/I Brazil-Israel Plant Science Conference, was held in Iguazu Falls, Brazil in September 28th - October 2nd 2015

Selected Publications

- AIP1 is a novel Agenet/Tudor domain protein from Arabidopsis that interacts with regulators of DNA replication, transcription and chromatin remodeling. Brasil JN, Cabral LM, Eloy NB, Primo LMF, Barroso-Neto IL, Grangeiro LPP, Gonzalez N, Inzé D, Ferreira PCG, Hemerly AS (2015) BMC Plant Biology 15: 1-21
- Overexpression of mitochondrial uncoupling protein 1 (UCP1) induces a hypoxic response in Nicotiana tabacum leaves. Barreto P, Okura V, Pena IA, Maia R, Maia IG, Arruda P (2016) Journal of Experimental Botany 67: 301-13
- Revisiting the Non-Animal Peroxidase Superfamily. Trends in Plant Science. Lazzarotto F, Turchetto-Zolet AC, Margis-Pinheiro M (2015) 20: 807-13
- The ASYMMETRIC LEAVES Complex Employs Multiple Modes of Regulation to Affect Adaxial-Abaxial Patterning and Leaf Complexity. Husbands AY, Benkovics AH, Nogueira FTS, Lodha M, Timmermans MCP (2015) The Plant Cell 27: 3321-35
- TOR Signaling and Nutrient Sensing. Dobrenel T, Caldana C, Hanson J, Robaglia C, Vincentz M, Veit B, Meyer C (2016) Annual Review of Plant Biology 67: 261-85

Major Funding Sources

Major fundings agencies in Brazil include:

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

Canada

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

General Activities

Arabidopsis Research Facilities

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

Outlook on Arabidopsis Research

Funding for Arabidopsis research is largely from NSERC, one of the three federal funding agencies in Canada. Basic research in plant biology continues to be underfunded. Indeed, compared to non-plant applicants to NSERC, plant biology has seen a steady decrease in funding since 2009 (personal communication David Guttman, University of Toronto).

Road Map Related Activities

Arabidopsis Tools and Resources

- Bio-Analytic Resource for Plant Biology (BAR; http://bar.utoronto.ca) hosted by the Department of Cell and Systems Biology, University of Toronto.
- Centre for the Analysis of Genome Evolution and Function (CAGEF), Department of Cell and Systems Biology, University of Toronto.

Selected Publications

- 50 years of Arabidopsis research: highlights and future directions. Provart NJ, Alonso J, Assmann SM, Bergmann D, Brady SM, Brkljacic J, Browse J, Chapple C, Colot V, Cutler S, Dangl J, Ehrhardt D, Friesner JD, Frommer WB, Grotewold E, Meyerowitz E, Nemhauser J, Nordborg M, Pikaard C, Shanklin J, Somerville C, Stitt M, Torii KU, Waese J, Wagner D, McCourt P (2016) New Phytol. 209(3):921-44.
- Structure-function analysis identifies highly sensitive strigolactone receptors in Striga. Toh S, Holbrook-Smith D, Stogios PJ, Onopriyenko O, Lumba S, Tsuchiya Y, Savchenko A, McCourt P (2015) Science. 350(6257):203-7.
- PARASITIC PLANTS. Probing strigolactone receptors in Striga hermonthica with fluorescence. Tsuchiya Y, Yoshimura M, Sato Y, Kuwata K, Toh S, Holbrook-Smith D, Zhang H, McCourt P, Itami K, Kinoshita T, Hagihara S (2015) Science. 349(6250):864-8.

Major Funding Sources

Natural 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, Santiago;
Rodrigo Gutiérrez (rgutierrez@bio.puc.cl) Pontificia Universidad Católica de Chile, Santiago

General Activities

Arabidopsis Research Facilities

- Centro de Biotecnología Vegetal, UNAB, Santiago (http://cbv.unab.cl/)
- Centro de Biotecnología Vegetal, Universidad de Chile, Santiago
- Centro de Ciencia y Biotecnología Vegetal PUC, P. Universidad Católica de Chile, Santiago (http://agronomia.uc.cl/centros-unidades-y-laboratorios/cecibuc)
- Millennium Nucleus in Plant Systems and Synthetic Biology, P. Universidad Católica de Chile, Santiago (http://www.genomicavegetal.cl/)
- Department of Molecular Genetics and Microbiology, P. Universidad Católica de Chile, Santiago
- Laboratorio de Bioingeniería, Facultad de Ingeniería y Ciencias, Universidad Adolfo Ibáñez, Santiago
- Center for Applied Ecology and Sustainability, Santiago
- Instituto de Ciencias Biológicas, Universidad de Talca, Talca (http://biologia.utalca.cl/index.html)

Patricio Arce's lab is interested in viral spread and the effect of viral infections in plants, employing Arabidopsis and the most important fruit plant in Chile, *Vitis vinifera*. Using functional genetics methods they could identify genes affected by the infection, and are currently looking for the key regulators of the plant response.

Holuigue's lab goal is to better understand plant defense mechanisms in response to stress, particularly Salicylic Acid (SA) functions using Arabidopsis. They could identify and functionally characterize SA-induced defense genes, and study the mechanism how SA induces their expression.

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

Xavier Jordana's lab studies mitochondrial RNA editing. Their goal is to contribute to the characterization of a large gene family encoding nuclear factors (PPR proteins) controlling the specificity of the 400 Arabidopsis editing sites, via isolation of mutant plants and analysis of editing defects.

Josefina Poupin's group focuses in obtaining new insights into the mechanisms underlying the enhancement of salt-stress tolerance in the salt-sensitive Arabidopsis Col-0 plants, when inoculated with the PGPR strain *Burkholderia phytofirmans* PsJN.

Felipe Aquea's lab focuses on GCN5, an important histone acetyltransferase required for gene expression involved in many developmental pathways in plants and animals. They could identify a set of potential direct target genes of AtGCN5 through a combination of ChIP-Seq and genome-wide transcriptional profiling usingRNA-seq.

Francisca Blanco's lab studies signaling pathways associated to endoplasmic reticulum stress during plant-pathogen interaction. They are especially focused on SA signaling pathways involved in plant responses to bacterial infection.

Ariel Orellana's lab studies regulation of polysaccharides biosynthesis in the Golgi Apparatus. They could identify some Arabidopsis proteins sharing molecular characteristics with Nucleotide Sugar Transporters (NSTs) from other organisms, transporting GDP sugars. They focus on determining the substrate specificity of these NSTs via transient expression in plants, stable over-expression in Arabidopsis and insertional mutant lines.

Gabriel León's lab studies the molecular mechanisms that regulate the development and function of pollen grain.

Lorena Norambuena's lab focuses on endocytosis. Using chemical biology, they have described a lateral root formation mechanism in Arabidopsis induced by endocytic trafficking via a mechanism distinctive from auxin-driven promotion of lateral root formation.

Michael Handford's lab is interested in the study of Arabidopsis sugar alcohol metabolism. By using reverse genetics, they identified AtSDH, which oxidizes sorbitol, and characterized *atsdh*- mutants to be more resistant to drought stress.

Pablo Figueroa's lab studies the connection between Jasmonate and abiotic stress such as high salinity, a relationship not well understood at cellular and molecular levels. They investigated JA signaling activation by NaCl and its effect on primary root growth, and found that JA-responsive JAZ genes were upregulated by salt stress in a COI1-dependent manner.

Javier Canales' lab focuses on the molecular mechanisms underlying plant response to nutrients, specifically on their complex interactions in metabolic pathways.

Current Arabidopsis Projects

Rodrigo Gutiérrez. Howard Hughes Medical Institute International Early Career Scientist. Fondecyt grant (2014-2018), funded by Conicyt. FONDAP Center for Genome Regulation (http://www.genomacrg.cl/), funded by Conicyt (2016-2020). Millennium Nucleus Center for Plant Systems and Synthetic Biology (www.genomicavegetal.cl), funded by ICM (2015-2017).

Michael Handford. "Sorbitol synthesis and its role in abiotic stress tolerance in non-Rosaceae species". Sponsored by Fondecyt 1140527, Anillo ACT-1110 (2014-2018).

Francisca Blanco. "Adaptive response to salt stress, mediated by salicylic acid in *Arabidopsis thaliana*". Funded by Núcleo UNAB 590 DI-590-14/N (2014-2016).

Felipe Aquea. Sponsored by FONDECYT 11130567, CAPES FB-002-2014, Millennium Nucleus NC130030 (2014-2017).

Gabriel León. Funded by Fondecyt 1120766 and UNAB DI-74-12/R (2013-2016).

Loreto Holuigue. "Study of the Mechanisms that Regulate Salicylic Acid Levels and Functions in the Redox Modulation of Defense Responses Against Biotic and Abiotic Stress in Arabidopsis". Funded by Conicyt FONDECYT 1141202, (2014-2018).

Xavier Jordana. "Mitochondrial Biogenesis and Function in Plants: Insights into the Role of Respiratory Complex II, Sirtuins and Pentatricopeptide Repeat Proteins". Funded by Conicyt (2014-2018).

Pablo Figueroa. "Elucidating Molecular Links Involved in the Crosstalk Between Salt-Elicited Responses and Jasmonate Signaling Pathway in *Arabidopsis thaliana* Roots". Funded by Conicyt (2012-2016).

Ariel Orellana. "The role of the UDP-rhamnose transporters in the biosynthesis of rhamnogalacturonan -I and -II in *Arabidopsis thaliana*". FONDECYT 1151335. Funded by Conicyt (2014-2018).

Javier Canales. "Uncovering gene regulatory networks involved in the crosstalk between sulfur and nitrogen nutrition in *Arabidopsis thaliana*". FONDECYT 11150070. Funded by Conicyt (2015-2019).

Outlook on Arabidopsis Research

Our research community is very small as can be easily deduced from the previous section. However, the few groups are very active in research and training. The main research focus is on metabolism and responses to environmental cues (abiotic and biotic). In many instances, there are close ties to the Chilean industry and research groups use Arabidopsis and some other plant model systems that are of interest to the local economy (e.g. grapes, fruit trees). We believe this will continue to be the case in coming years with not much space to grow in terms of number of independent groups or topics. The recent changes in funding higher education (plan for gratuity in most Universities) has created much uncertainty and major research Universities in the country are not investing or expanding at the moment. Chile is also suffering major changes in the way Science and Technology is conducted at the government level, which introduces uncertainties. It is difficult to foresee how research will change in the upcoming years as a result of these changes. For example, the President recently announced creation of the Ministry for Science and Technology. How this will impact science research direction and funding possibilities is unknown at this stage, but we certainly all hope it will be for the best.

Road Map Related Activities

Arabidopsis Tools and Resources

Constructing simple biological networks for understanding complex high-throughput data in plants Moyano TC, Vidal EA, Contreras-López O, Gutiérrez RA (2015) Methods Mol Biol. 1284:503-26.

In this chapter, the authors provide detailed methods for users without prior knowledge of bioinformatics to construct gene networks and derive hypotheses that can be experimentally verified. Step-by-step instructions for acquiring, integrating, analyzing, and visualizing genome-wide data are provided for two widely used open source platforms, R and Cytoscape. The examples provided are based on Arabidopsis data, but the protocols presented should be readily applicable to any organism for which similar data can be obtained.

Outreach Activities

- "Lectures On the Cell Wall". Guests: Dr. Helen North (INRA de Versailles, France), Dr Marie- Christine Ralet (INRA de Nantes, France). Organizers: Dr. Ariel Orellana, Dr. Susana Saez-Aguayo (Universidad Andres Bello), 24-26 November, 2015.
- International Meeting "Plant Stress and Sustainable Agriculture". Guests: Dr. Serge Delrot, Dr. Tierry Candresse, Dr. Philippe Galluschi, Dr. Dominique Rolin, Dr. Alain Blanchard (University of Bordeaux), Dr. Alan Bennett, Dr. Dario Cantú (University OF CALIFORNIA – DAVIS). Organizers: Dr. Patricio Arce (Pontificia Universidad Católica de Chile), 30 June, 2015.
- Seminar "A systems approach to improved root traits". Guest: Dr. Philip Benfey (DUKE University, USA). Organizer: Dr. Rodrigo Gutierrez (Pontificia Universidad Católica de Chile), 21 January, 2016.
- Seminar "Diversity Seek (Divseek): An International Partnership to Harness the Genetic Potential of Crop Diversity". Guest: Dr. Ruth Bastow (Director of The Global Plant Council). Organizer: Dr. Rodrigo Gutierrez (Pontificia Universidad Católica de Chile), 3 November, 2015.

Conferences and Workshops

First Meeting of the Chilean Society of Plant Biologist (X Chilean Plant Biology Meeting). Valdivia, Chile, 2-5 December, 2015.

As it is now a tradition, the conference consists of sessions ranging across plant sciences: Systems and Synthetic Biology, Cell and Developmental Biology, Breeding and Genetics, Biotic/Abiotic Stress, Ecophysiology and Metabolism. Attendees comprise primarily students, young scientists and faculty from major Universities and research institutes in Chile. Nearly 180 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.

Guests: Natasha Raikhel (UC Riverside, USA), Zhenbiao Yang (UC Riverside, USA), Dan Klessig (Cornell University, USA), Ian Fergusson (Plant and Food Research, New Zeland), Jose Quero Garcia (INRA, France)

Organizers: Chilean Society of Plant Biologist

Selected Publications

- The Calcium Ion Is a Second Messenger in the Nitrate Signaling Pathway of Arabidopsis. Riveras E, Alvarez JM, Vidal EA, Oses C, Vega A, Gutiérrez RA (2015) Plant Physiology169(2):1397-404.
- Transcriptional networks in the nitrate response of *Arabidopsis thaliana*. Vidal EA, Álvarez JM, Moyano TC, Gutiérrez RA (2015) Curr Opin Plant Biol. 27:125-32.
- The UDP-glucose: glycoprotein glucosyltransferase (UGGT), a key enzyme in ER quality control, plays a significant role in plant growth as well as biotic and abiotic stress in *Arabidopsis thaliana*. Blanco-Herrera F, Moreno AA, Tapia R, Reyes F, Araya M, D'Alessio C, Parodi A, Orellana A (2015) BMC Plant Biol. 15:127.
- The dynamic of the splicing of bZIP60 and the proteins encoded by the spliced and unspliced mRNAs reveals some unique features during the activation of UPR in *Arabidopsis thaliana*. Parra-Rojas J, Moreno AA, Mitina I, Orellana A (2015) PLoS One 10(4):e0122936.
- Male sterility in Arabidopsis induced by overexpression of a MYC5-SRDX chimeric repressor. Figueroa P, Browse J (2015) Plant J. 2015 Mar;81(6):849-60. doi: 10.1111/tpj.12776.

Major Funding Sources

http://www.conicyt.cl/

http://www.iniciativamilenio.cl/

http://www.corfo.cl/

http://www.fia.cl/

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

General Activities

Arabidopsis Research Facilities

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

- In Brno:

Masaryk University - https://www.muni.cz/sci/314010

Mendel University - http://ubfr.af.mendelu.cz/en/?lang=en

Institute of Biophysics - http://www.ibp.cz/en/

"Central European Institute of Technology (CEITEC)" (http://www.ceitec.eu/) in Brno includes big units devoted to genomics and proteomics of plant systems used for studies in cell and developmental biology and cytogenomics.

- In Olomouc:

Palacky university in Olomouc - http://www.prf.upol.cz/en/menu/departments/

Institute of Experimental Botany - http://www.ueb.cas.cz/en

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

- In České Budějovice:

Institute of Plant Molecular Biology - http://www.umbr.cas.cz/

- In Prague:

Institute of Experimental Botany - http://www.ueb.cas.cz/en

Charles University in Prague - http://kfrserver.natur.cuni.cz/english/index.html

Current Arabidopsis Projects

Arabidopsis research in the Czech Republic is funded mostly on the individual grants basis. In 2014 the Department of Experimental Plant Biology at the Charles University was granted a "Centre of plant experimental biology, Charles University" project supported by the Ministry of Education of the Czech Republic. In 2015 twenty seven projects using Arabidopsis as a model were funded by the Czech Science Foundation (GACR). Among the biggest ones there were:

- "Study of the phosphorylation in Katanin1 and microtubules severing in Arabidopsis"

- "Molecular mechanisms controlling homeostasis of plant growth regulatory compound auxin"
- "Global proteomic analysis of temperature perception in Arabidopsis and its interaction with cytokinin signalling"
- "Role of gama-tubulin in the coordination of microtubuli nucleation and cytokinesis with the DNA damage in plants"
- "Role of formins in plant cell morphogenesis"
- "Structural and functional components of plant telomeres"
- "Elucidating molecular mechanisms of cytokinin-ethylene crosstalk in the plant development"
- "Impact of temperature and photosynthetically active radiation on dynamics of regulation of photosystem II function in higher plants"
- "Deciphering of molecular mechanisms of light and hormonal signalling integration in plant development".

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

BRNO - CEITEC - Central European Institute of Technology

Proteomics Core Facility

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

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

Outreach Activities

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

Selected Publications

- Lack of Phosphatidylglycerol Inhibits Chlorophyll Biosynthesis at Multiple Sites and Limits Chlorophyllide Reutilization in Synechocystis sp Strain PCC 6803. Kopecna J, Pilny J, Krynicka V, Tomcala A, Kis M, Gombos Z, Komenda J, Sobotka R (2015) Plant Physiology 169(2): 1307-17
- Genome Structure of the Heavy Metal Hyperaccumulator Noccaea caerulescens and Its Stability on Metalliferous and Nonmetalliferous Soils. Mandakova T, Singh V, Kramer U, Lysak MA (2015) Plant Physiology 169(1): 674-89
- The Arabidopsis mitogen-activated protein kinase 6 is associated with -tubulin on microtubules, phosphorylates EB1c and maintains spindle orientation under nitrosative stress. Kohoutova L, Kourova H, Nagy SK, Volc J, Halada P, Meszaros T, Meskiene I, Bogre L, Binarova P (2015) New Phytologist 207(4):1061-74
- Cell Wall Maturation of Arabidopsis Trichomes Is Dependent on Exocyst Subunit EXO70H4 and Involves Callose Deposition. Kulich I, Vojtikova, Z, Glanc M, Ortmannova J, Rasmann S, Zarsky V (2015) Plant Physiology 168(1):120-31
- Homology-dependent repair is involved in 45S rDNA loss in plant CAF-1 mutants. Muchova V, Amiard S, Mozgova I, Dvorackova M, Gallego ME, White C, Fajkus J (2015) Plant Journal 81(2):198-209

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. Both institutions support also bilateral projects with selected countries.

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

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.

- Technology Agency of the Czech Republic (http://www.tacr.cz/english/)

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

Denmark

Michael Palmgren (palmgren@plen.ku.dk) University of Copenhagen, Department of Plant and Environmental Sciences

General Activities

Arabidopsis Research Facilities

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 completed 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 two such centers Arabidopsis is employed as a model organism: Centre for Membrane Pumps in Cells and disease (Pumpkin; plant work directed by Prof. Michael Palmgren) and Center for Dynamic Molecular Interactions (Dynamo; directed by Prof. Barbara Ann Halkier).

Outlook on Arabidopsis Research

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

- A phospholipid uptake system in the model plant *Arabidopsis thaliana*. Poulsen LR, López-Marqués RL, Pedas PR, McDowell SC, Brown E, Kunze R, Harper JF, Pomorski TG, Palmgren M (2015) Nat Commun. 6:7649
- Retromer contributes to immunity-associated cell death in Arabidopsis. Munch D, Teh OK, Malinovsky FG, Liu Q, Vetukuri RR, El Kasmi F, Brodersen P, Hara-Nishimura I, Dangl JL, Petersen M, Mundy J, Hofius D (2015) Plant Cell 27(2):463-79
- The bifurcation of the cyanogenic glucoside and glucosinolate biosynthetic pathways. Clausen M, Kannangara RM, Olsen CE, Blomstedt CK, Gleadow RM, Jørgensen K, Bak S, Motawie MS, Møller BL (2015) Plant J. 84(3):558-73
- The glucosinolate biosynthetic gene AOP2 mediates feed-back regulation of jasmonic acid signaling in Arabidopsis. Burow M, Atwell S, Francisco M, Kerwin RE, Halkier BA, Kliebenstein DJ (2015) Mol Plant. 8(8):1201-12

- Simple and robust determination of the activity signature of key carbohydrate metabolism enzymes for physiological phenotyping in model and crop plants. Jammer A, Gasperl A, Luschin-Ebengreuth N, Heyneke E, Chu H, Cantero-Navarro E, Großkinsky DK, Albacete AA, Stabentheiner E, Franzaring J, Fangmeier A, van der Graaff E, Roitsch T (2015) J Exp Bot. 66(18):5531-42

Finland

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

General Activities

Arabidopsis Research Facilities

Research concentrating on Arabidopsis is carried out at several universities in Finland with two main centres at the Universities of Helsinki and Turku.

Research at the University of Helsinki focuses on plant stress responses and plant development. Research projects address the role of reactive oxygen species (ROS) as signaling molecules in plants, the role of transcription factors in the stress response, receptor and receptor-like kinase signaling, plant stem cell maintenance, root development, plant-pathogen interactions, as well as the role of the proteasome in the regulation of flowering. Groups in Helsinki are also exploiting the natural variation of *Arabidopsis thaliana* to identify new regulators of stress tolerance. A saturating mutant screen is currently being carried out with the goal to identify components in early stomatal signaling downstream of apoplastic ROS. Identification of ozone-sensitive mutants is followed by analysis of their gas-exchange parameters. Causative mutations are being identified by genome resequencing. The flower-related ubiquitin proteasome system project is currently characterizing a collection of about 100 Arabidopsis T-DNA mutants using the new phenotyping facility (http://blogs.helsinki.fi/nappi-blog/). In the future the research will be extended towards plant pathogen interactions in the flower and also towards translational approaches using crop species. The receptor-ligand signaling group is aiming to integrate plant biochemistry and physiology with evolutionary analysis to facilitate translational research using Arabidopsis as a tool to provide insights into complex gene families for subsequent application in crops.

Research at the University of Turku is centered on stress signaling and photosynthesis. Projects address the role of protein kinases and protein phosphatases as well as the regulation of photosynthesis and the integration of the chloroplastic light harvesting machinery into cell- and plant-wide signaling networks.

The Centre of Excellence (CoE) “Molecular Biology of Primary Producers” (2014-2019) funded by the Academy of Finland brings together groups from Turku and Helsinki in order to combine expertise on plant development, stress signaling and photosynthesis. While several plant species and also cyanobacteria are being used Arabidopsis continues to be the most important model for the fundamental research carried out within the Centre of Excellence.

Current Arabidopsis Projects

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

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

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

Outlook on Arabidopsis Research

In Helsinki, the Viikki Plant Science Centre (ViPS) has been established with 31 PIs, 208 researchers and 9.1 million € funding in 2015. While ViPS encompasses research on plants in general, Arabidopsis is one of the core tools used by most research teams to address fundamental questions and unravel molecular mechanisms. Plant Science has been named as a focus and marketing area of the new HiLife centre, with ViPS used as an example of an excellent and successful research program. A plant biology master's degree with heavy involvement of ViPS will begin in the autumn of 2017. The vision of ViPS is to attract internationally visible top level researchers; to stimulate multidisciplinary research environments; to participate in research and infrastructure core facilities also outside the University; to take an active role in post-graduate education. Research on Arabidopsis or using Arabidopsis as a tool continues to be a major factor in Finnish plant science. Efforts include translation of knowledge from Arabidopsis towards tree research. As many research groups at ViPS use Arabidopsis as their model species there is a heavy emphasis on Arabidopsis research in the Doctoral Programme in Plant Sciences and Arabidopsis continues to be the primary model system to address fundamental research questions in all levels of education.

Road Map Related Activities

Arabidopsis Tools and Resources

A community resource based on the saturating mutant screen for novel components in early stomatal signaling downstream of apoplastic ROS will available by the end of 2016.

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

Work on the phenotypic analysis of a mutant collection for cysteine-rich receptor-like kinases (Bourdais et al., 2015) has led to the creation of a software package for the analysis of heterogenous phenotypic data. This will be available as a package for the programming language R during 2016 from Dr. Jarkko Salojärvi (Salojärvi & Wrzaczek, in preparation).

A phenomics facility has been built at the Viikki campus of the University of Helsinki (http://blogs.helsinki.fi/nappi-blog). This high throughput facility is part of a National Plant Phenotyping Infrastructure that also includes a high precision unit at the University of Eastern Finland. The Viikki facility will accommodate tools for morphological and physiological analysis of Arabidopsis by imaging (fluorescence and thermal).

Outreach Activities

Plant biology groups working with Arabidopsis at the University of Helsinki have started to introduce school classes to molecular plant biology in spring 2016.

Outreach activities have been done towards high school students on scientific career choice and towards general public on genetically improved organisms.

Conferences and Workshops

- The 11th Finnish Plant Science Days (Kasvitieteen Päivät). University of Turku, Turku, Finland. May 25-26, 2016
- The biannual Finnish-Japanese plant science meeting will be held in autumn 2016 in Finland
- The National Plant Phenotyping Infrastructure will arrange Nordic meetings and a winter school in "Current challenges in plant phenotyping"

Selected Publications

Finnish researchers contributed to 36 publications referring to Arabidopsis from 2015 according to Pubmed.

- MultiSite Gateway compatible cell type-specific gene inducible system for plants. Siligato R, Yadav SR, Ma G, Lehesranta S, Ma G, Ursache R, Sevilem I, Zhang J, Gorte M, Prasad K, Wrzaczek M, Heidstra R, Murphy A, Scheres B, Mähönen AP (2016) Plant Physiology 170(2):627-641.
- Integration of photosynthesis, development and stress as an opportunity for plant biology. Allahverdiyeva Y, Battchikova N, Brosché M, Fujii H, Kangasjärvi S, Mulo P, Mähönen AP, Nieminen K, Overmyer K, Salojärvi J, Wrzaczek M (2015) New Phytologist 208(3):647-655.
- Large-scale phenomics identifies primary and fine-tuning roles for CRKs in responses related to oxidative stress. Bourdais G, Burdiak P, Gauthier A, Nitsch L, Salojärvi J, Rayapuram C, Idänheimo N, Hunter K, Kimura S, Merilo E, Vaattovaara A, Oracz K, Kaufholdt D, Pallon

A, Anggoro DT, Glów D, Lowe J, Zhou J, Mohammadi O, Puukko T, Albert A, Lang H, Ernst D, Kollist H, Brosché M, Durner J, Borst JW, Collinge DB, Karpinski S, Lyngkjaer M, Robatzek S, Wrzaczek M, Kangasjärvi J (2015) PLoS Genetics 7(11):e1005373.

- Quantitative trait loci mapping and transcriptome analysis reveal candidate genes regulating the response to ozone in *Arabidopsis thaliana*. Xu E, Vaahtera L, Horak H, Hincha DK, Heyer AG, Brosché M (2015) Plant Cell & Environment 38(7):1418-33.
- Light acclimation involves dynamic re-organization of the pigment-protein megacomplexes in non-appressed thylakoid domains. Suorsa M, Rantala M, Mamedov F, Lespinasse M, Trotta A, Grieco M, Vuorio E, Tikkanen M, Järvi S, Aro EM (2015) Plant Journal 84(2):360-373.

Major Funding Sources

Academy of Finland (http://www.aka.fi)

University of Helsinki (http://www.helsinki.fi/university)

Finnish Cultural Foundation (http://www.skr.fi)

France

Catherine Perrot-Rechenmann (catherine.rechenmann@cnrs-dir.fr), CNRS Saclay Plant Sciences Labex, Gif sur Yvette; Loïc Lepiniec (Loic.Lepiniec@versailles.inra.fr) Saclay Plant Sciences LaBex, Institut Jean-Pierre Bourgin, INRA, Versailles

General Activities

Current Arabidopsis Projects

The Institute of Plant Sciences Paris-Saclay, IPS2, located in Orsay France, was created by restructuring several Plant Biology Institutes associated with 3 universities (Paris-Sud, University of Evry and Paris-Diderot), the CNRS and INRA. IPS2 aims to better understand the molecular mechanisms controlling plant growth and their responses to biotic and abiotic stresses while developing a continuum from fundamental to translational research in Plant Sciences.

Current research focuses on the analysis of model plants using multidisciplinary approaches (from genomics, bioinformatics to biochemistry, genetics and physiology) and 3 plant-dedicated platforms with expertise in transcriptomics and RNA sequencing, metabolomics, and translational biology, including TILLING mutant collections of diverse crop species (tomato, *Brachypodium distachyon*, melon and cucumber). Among the projects to transfer the knowledge obtained from Arabidopsis to crop species are: improving biomass by manipulating metabolic pathways/rate-limiting enzymes, improving root architecture to improve nutrient uptake and drought resistance, improving pathogen resistance by manipulating MAPK signalling.

We wish all the best to this newly created Plant Institute.

Outlook on Arabidopsis Research

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

The French national research agency, ANR (http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency/), provides funding for project-based research. Main applications based on social issues are not appropriate to support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is constantly decreasing, which severely affects research activities of French labs.

Fundamental research might, however, be taken into account again for coming grants as announced by the French government.

Road Map Related Activities

Arabidopsis Tools and Resources

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

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

Outreach Activities

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

Conferences and Workshops

- The 26th edition of the International Conference on Arabidopsis Research (ICAR 2015) took place in Paris from 5th to 9th of July 2015. The meeting was organized by the French Society of Plant Biologists (SFBV, http://sfbv.snv.jussieu.fr/) with the scientific and organisational assistance of members of the Saclay Plant Sciences Laboratory network of excellence (SPS LabEx, http://www6.inra.fr/saclay-plant-sciences). ICAR 2015 was a great success with up to 1054 registrations, scientists coming from 38 distinct countries from all over the world.

Selected Publications

- Primary transcripts of microRNAs encode regulatory peptides. Lauressergues D, Couzigou JM, Clemente HS, Martinez Y, Dunand C, Bécard G, Combier JP (2015) Nature 520(7545):90-3. doi: 10.1038/nature14346.
- Plants Encode a General siRNA Suppressor That Is Induced and Suppressed by Viruses. Shamandi N, Zytnicki M, Charbonnel C, Elvira-Matelot E, Bochnakian A, Comella P, Mallory AC, Lepere G, Saez-Vasquez J, and Vaucheret H (2015) PLoS Biol 13, e1002326.
- A receptor pair with an integrated decoy converts pathogen disabling of transcription factors to immunity. Le Roux C, Huet G, Jauneau A, Camborde L, Trémousaygue D, Kraut A, Zhou B, Levaillant M, Adachi H, Yoshioka H, Raffaele S, Berthomé R, Couté Y, Parker JE, Deslandes L (2015) Cell 161(5):1074-88. doi: 10.1016/j.cell.2015.04.025.
- A mechanically sensitive cell layer regulates the physical properties of the Arabidopsis seed coat. Creff A, Brocard L, Ingram G (2015) Nat Commun. 6:6382. doi: 10.1038/ncomms7382.
- OCTOPUS Negatively Regulates BIN2 to Control Phloem Differentiation in *Arabidopsis thaliana*. Anne P, Azzopardi M, Gissot L, Beaubiat S, Hématy K, Palauqui JC. (2015) Curr Biol. 25(19):2584-90. doi: 10.1016/j.cub.2015.08.033.

Major Funding Sources

ANR, thematic calls organized in societal issues (http://www.agence-nationale-recherche.fr/en/funding-opportunities/)

Investissement d'avenir (PIA 1 and 2 in progress) by Ministère de l'Education nationale, de l'enseignement supérieur et de la recherche (http://www.enseignementsup-recherche.gouv.fr/cid55892/comprendre-le-programme-investissements-d-avenir.html)

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

Germany

Klaus Harter (klaus.harter@zmbp.uni-tuebingen.de); Marília K. F. de Campos (marilia.campos@zmbp.uni-tuebingen.de) University of Tübingen, Tübingen

General Activities

Arabidopsis Research Facilities

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

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

Current Arabidopsis Projects

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

Individual Funding

Currently the DFG provides funding to a total of 191 individual projects concerning Arabidopsis research. Of these, 7 are funded by the Emmy Noether Programme, 2 by the Heisenberg Programme, 7 are research fellowships and 175 are individual research grants.

Priority Programmes

Arabidopsis researchers are involved in 3 priority programmes.

- SPP 1710 (since 2014) Dynamics of thiol-based redox switches in cellular physiology
- SPP 1529 (since 2011) Evolutionary plant solutions to ecological challenges: molecular mechanisms underlying adaptive traits in the Brassicaceae s.l.
- SPP 1530 (since 2011) Flowering time control: from natural variation to crop improvement

Collaborative Research Centers

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

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

Research Training Groups

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

Research Units

- FOR 948 (since 2009) Nitrogen uptake, metabolism and remobilization in leaves during plant senescence
- FOR 1186 (since 2009) Photorespiration: Origins and metabolic integration in interacting compartments
- FOR 964 (since 2008) Calcium signaling via protein phosphorylation in plant model cell types during environmental stress adaption
- FOR 1061 (since 2008) Dynamic storage functions of plant vacuoles during cold and osmotic stress
- FOR 804 (since 2007) Retrograde signalling in plants

European Research Council

The ERC currently funds 11 Arabidopsis research projects in Germany, comprising of 4 Advanced Grants, 2 Consolidator Grants and 5 Starting Grants

Road Map Related Activities

Arabidopsis Tools and Resources

- Arabidopsis Functional Genomics Network (www.dbg-afgn.de)
- 1001 genomes platform (http://1001genomes.org/)
- German Plant Phenotyping Network (DPPN, http://www.dppn.de/en)
- The Arabidopsis Protein Phosphorylation Site Database (PhosPhAt, http://phosphat.uni-hohenheim.de/)
- GABI Primary Database (GabiPD, http://www.gabipd.org/)

- Plant Genome and Systems Biology Databases (http://pgsb.helmholtz-muenchen.de/plant/plantsdb.jsp)
- The Plant Transcription Factor Database (http://plntfdb.bio.uni-potsdam.de/v3.0/)

Outreach Activities

The PLANT2030 initiative from the German Federal Ministry of Education and Research (BMBF) fosters research projects within public-private partnerships. Two Arabidopsis related projects are listed below.

- PLANT-KBBE IV NESTOR (2014-2017): Nematode susceptibility targets for a durable resistance
- PLANT-KBBE IV (2014-2017): Control of the abiotic stress response in plants by DELLA proteins and chemicals

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

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

Conferences and Workshops

- Deutsche Botanikertagung

  Munich, 30 August - 3 September, 2015 (http://botanikertagung2015.de/)
- Tri-National Arabidopsis Meeting (TNAM) biannual conference, hosted by colleagues from Germany, Austria and Switzerland. 10th TNAM, Vienna, Austria, 14-16 September, 2016
- Conference Molecular Biology of Plants, Dabringhausen (http://pflanzen-molekularbiologie.de/):

  29th Conference, 23-26 February 2016

  28th Conference, 24-27 February 2015
- 22nd International Symposium on Plant Lipids. Göttingen, 03-08 July, 2016
- 1st SFB 1101 Symposium, 04-06 April 2016, Tübingen (https://www.uni-tuebingen.de/en/research/core-research/collaborative-research-centers/sfb-1101/sfb-1101-1st-symposium.html)
- PhD School in Plant Development. Retzbach-Zellingen, 07-09 October, 2015
- 36th New Phytologist Symposium: Cell biology at the plant-microbe interface. Munich, 29 November- 1 December, 2015 (https://www.newphytologist.org/symposiums/view/38)
- 2nd Summer Academy in Plant Molecular Biology, 13-15 July 2015, Freudenstadt (http://www.summer-academy-pmb.com/)

Selected Publications

German Arabidopsis researchers were involved in 494 publications since last year's report (search at NCBI using "Arabidopsis"[All Fields] AND "Germany"[Affiliation] AND "2015/05/01"[Date - Publication] : "3000"[Date - Publication]). Highlights are listed below.

- Endler A, Kesten C, Schneider R, Zhang Y, Ivakov A, Froehlich A, Funke N, Persson (2015) A Mechanism for Sustained Cellulose Synthesis during Salt Stress. Cell 162(6):1353-64.
- Albert I, Böhm H, Albert M, Feiler CE, Imkampe J, Wallmeroth N, Brancato C, Raaymakers TM, Oome S, Zhang H, Krol E, Grefen C, Gust AA, Chai J, Hedrich R, Van den Ackerveken G, Nürnberger T (2015) An RLP23-SOBIR1-BAK1 complex mediates NLP-triggered immunity. Nature Plants 1(10):15140.
- Wagner S, Behera S, De Bortoli S, Logan DC, Fuchs P, Carraretto L, Teardo E, Cendron L, Nietzel T, Füßl M, Doccula FG, Navazio L, Fricker MD, Van Aken O, Finkemeier I, Meyer AJ, Szabò I, Costa A, Schwarzländer M (2015) The EF-Hand Ca^{2+} Binding Protein MICU Choreographs Mitochondrial Ca^{2+} Dynamics in Arabidopsis. Plant Cell 27:3190-212.
- Bai Y, Müller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, Dombrowski N, Münch PC, Spaepen S, Remus-Emsermann M, Hüttel B, McHardy AC, Vorholt JA, Schulze-Lefert P (2015) Functional overlap of the Arabidopsis leaf and root microbiota. Nature 528(7582):364-9
- Kriegel A, Andrés Z, Medzihradszky A, Krüger F, Scholl S, Delang S, Patir-Nebioglu MG, Gute G, Yang H, Murphy AS, Peer WA, Pfeiffer A, Krebs M, Lohmann JU, Schumacher K (2015) Job Sharing in the Endomembrane System: Vacuolar Acidification Requires the Combined Activity of V-ATPase and V-PPase. Plant Cell 27(12):3383-96.

Major Funding Sources

Major funding source for Arabidopsis research is the German Science Foundation (DFG) (http://www.dfg.de/en/). Contact: Catherine Kistner (catherine.kistner@dfg.de)

Greece

Polydefkis Hatzopoulos (phat@aua.gr), Agricultural University of Athens, Athens

General Activities

Arabidopsis Research Facilities

- Agricultural University of Athens, Athens, Greece

  Polydefkis Hatzopoulos (phat@aua.gr)
  Dimitra Milioni (dmilioni@aua.gr)
  Stamatis Rigas (srigas@aua.gr)
  Dimitris Tsitsigianis (dimtsi@aua.gr)

- Aristotle University of Thessaloniki, Thessaloniki, Greece

  Angelos Kanellis (kanellis@pharm.auth.gr)
  Konstantinos Vlachonasios (kvlachon@bio.auth.gr)
  Emmanouil Panteris (epanteris@bio.auth.gr)

- National and Kapodistrian University of Athens, Athens, Greece

  Kosmas Haralampidis (kharalamp@biol.uoa.gr)
  Andreas Rousiis (aroussis@biol.uoa.gr)

- University of Crete, Crete, Greece

  Kriton Kalantidis (kriton@imbb.forth.gr)

- Mediterannean Agronomic Institute of Chania, Chania, Crete, Greece

  Panagiotis Kalaitzis (panagiot@maich.gr)

- Technological University of Athens, Athens, Greece

  Georgios Banilas (gban@teiath.gr)

Current Arabidopsis Projects

Arabidopsis still remains the model species used as reference to validate gene regulatory networks of crop species that are difficult to work with. The knowledge gained from Arabidopsis can be applied on agronomically important crops like olive trees, tomato, grapes and peaches etc.

Arabidopsis research is mainly focused on the following topics:

- The role of HSP90 and Pescadillo-like proteins on plant development
- Organellar biogenesis
- Protein trafficking and signal transduction
- The interplay between potassium transport and auxin homeostasis
- Molecular and functional characterization of genes encoding WD40 and Armadillo domain proteins
- Role of selenium binding proteins in Arabidopsis development and during abiotic stress

Outlook on Arabidopsis Research

Funding resources for research activities are significantly reduced having a major impact on basic research grants related to Arabidopsis. However, there is a general trend to shift towards other model species apart from Arabidopsis that may attract the interest of industrial partners.

Conferences and Workshops

- 37th Hellenic Society for Biological Science (EEBE) meeting. Volos, Greece

Selected Publications

- Transcriptional profiling unravels potential metabolic activities of the olive leaf non glandular trichome. Koudounas K, Manioudaki ME, Kourti A, Banilas G, Hatzopoulos P (2015) Front Plant Sci. 6(633).
- A defence-related Olea europaea β-glucosidase hydrolyses and activates oleuropein into a potent protein cross-linking agent. Koudounas K, Banilas G, Michaelidis C, Demoliou C, Rigas S, Hatzopoulos P (2015) J Exp Bot. 66(7): 2093-106.
- RNAi-mediated silencing of the *Arabidopsis thaliana* ULCS1 gene, encoding a WDR protein, results in cell wall modification impairment and plant infertility. Beris D, Kapolas G, Livanos P, Roussis A, Milioni D, Haralampidis K (2016) Plant Sci. 245:71-83.
- Potassium transporter TRH1 subunits assemble regulating root-hair elongation autonomously from the cell fate determination pathway. Daras G, Rigas S, Tsitsekian D, Iacovides TA, Hatzopoulos P (2015) Plant Sci. 231:131-7.
- Brassinosteroid nuclear signaling recruits HSP90 activity. Samakovli D, Margaritopoulou T, Prassinos C, Milioni D, Hatzopoulos P. (2014) New Phytol. 203(3):743-57.

Major Funding Sources

Grants from the European Union

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

General Secretariat for Research and Development (GSRT),
HELLENIC REPUBLIC MINISTRY OF EDUCATION
AND RELIGIOUS AFFAIRS (www.gsrt.gr)

National and Kapodistrian University of Athens, Special
Account for Research Grants, (http://www.elke.uoa.gr/)

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

General Activities

Arabidopsis Research Facilities

In India, the number of groups working on Arabidopsis is steadily increasing. The major areas of research include regulation of organ development, patterning, plant pathogen interaction, abiotic stress, light, hormone and sugar signaling. Some of the important centres working on Arabidopsis are CCMB, Hyderabad; IISc, Bangalore; NIT, Durgapur; University of Delhi South Campus; NIPGR, New Delhi; NRCPB, New Delhi; JNU, New Delhi; IHBT, Palampur; IISER, Thiruvanathapuram; IISER, Mohali; IISER, Bhopal; IIT, Roorkee; NCBS, Bangalore; NISER, Bhubaneswar.

Most of the funding for these projects comes in the form of competitive grants from Government agencies like the Department of Biotechnology, the Council for Scientific and Industrial Research, and the Department of Science and Technology, all based in New Delhi.

Current Arabidopsis Projects

There are several ongoing projects, most of them are sanctioned for a 3-year duration and in some cases for 5 years. Additionally, some ongoing projects are funded by the respective institutes in-house. Only the projects that have been approved in the past one year are listed below.

- Prof. Sudip Chattopadhyay (NIT, Durgapur); Investigation of functional interrelations of bZIP transcription factors: ZBF2/GBF1, HY5 and HYH of light signaling pathways in *Arabidopsis thaliana*. Funded by the Department of Science and Technology, Govt. of India; Under the scheme: JC Bose National Fellowship; 2016-2021.
- Dr. Sourav Datta (IISER, Bhopal); Molecular approach to enhance soil phosphate extraction by plants and reduce the application of fertilizers. Funded by the Department of Biotechnology, Govt. of India; Under the scheme: Innovative Young Biotechnologists Award (IYBA); 2015-2018.

Outlook on Arabidopsis Research

The future of Arabidopsis research in India looks bright. Looking at the influx of young faculty, availability of funds from different governmental agencies and the quality of publications in recent years, bodes well for Arabidopsis research in India.

Road Map Related Activities

Arabidopsis Tools and Resources

Ravi Maruthachalam at IISER, Thiruvanthapuram, is pursuing centromeric histone H3 (CEN H3) based haploid induction system to answer a variety of questions. He is exploiting natural variation in Arabidopsis accessions available for in vivo haploid induction. In *A. thaliana*, genome elimination frequently occurs in the offspring of two individuals that carry different versions of CEN H3. The genomic rearrangements observed in the Arabidopsis plants are similar to those observed in several human cancer and other genetic diseases. Ravi's group has shown that Arabidopsis could serve as a useful model system for studying these genome rearrangements and provide useful information on these human disorders.

Dr. Ananda Sarkar's group at NIPGR, New Delhi, has described a method to solate both high quality RNA and miRNAs from LCM-derived embryonic root apical meristematic tissue, which is both efficient as well as cost-effective. This has been accomplished by modifying and improving the tissue fixation, processing, sectioning and RNA isolation steps that involves minimal use of kits. (Sci Rep. 2016; 6:21577. doi: 10.1038/srep21577).

Outreach Activities

In addition to researchers working on Arabidopsis exclusively, there are many other laboratories that use Arabidopsis as a model system for gene function validation of the heterologous genes from crop plants like rice, wheat and pea. The resources available are shared with those who wish to start the programme a fresh using Arabidopsis as a system. Some of the genes identified based on work done on Arabidopsis for agronomically important traits like flowering time and root architecture are being tested in crop plants like tomato, rice and Brassica. The financial support for such projects is received from Governmental funding agencies.

A few of the college teachers engaged in imparting training to undergraduate students have also shown interest in using Arabidopsis mutants to explain their utility in understanding the regulation of plant development by endogenous cues like hormones and external signals like light.

Conferences and Workshops

One of the important conferences held in India where Arabidopsis research was discussed in many presentations was the "3rd International Plant Physiology Congress: Challenges and Strategies in Plant Biology Research" held at Jawaharlal Nehru University (JNU), New Delhi, India, during December 11-14; It was jointly organized by the Indian Society of Plant Physiologists, JNU and NIPGR, New Delhi, and also supported by the American Society of Plant Biologists, USA. A large number of foreign and Indian delegates participated;

number of participants in fact exceeded 600. Another meeting exclusively focused on Arabidopsis was the “Arabidopsis Research Conference 2016” that was held during March 20–22, 2016 at the IISER, Mohali. This meeting was attended by the majority of the researchers working on Arabidopsis in India. Presentations were made by the group leaders as well as young students and post-doctoral fellows. A couple of delegates from the UK and Australia also participated in this conference.

Selected Publications

- Salt-Induced remodeling of spatially restricted clathrin-independent endocytic pathways in Arabidopsis root. Baral A, Irani NG, Fujimoto M, Nakano A, Mayor S, Mathew MK (2015) Plant Cell 27: 1297-315.
- Divergence in patterns of leaf growth polarity is associated with the expression divergence of miR396. Das Gupta M, Nath U (2015) Plant Cell 27(10):2785-99.
- Interaction of MYC2 and GBF1 results in functional antagonism in blue light mediated Arabidopsis seedling development. Maurya JP, Sethi V, Gangappa SN, Gupta N, Chattopadhyay S (2015) Plant Journal 83:439-50.
- Multiple interactions between glucose and brassinosteroid signal transduction pathways in Arabidopsis are uncovered by whole-genome transcriptional profiling. Gupta A, Singh M, Laxmi A (2015) Plant Physiology 168(3): 1091-105.
- Calcineurin B-like protein-interacting protein kinase CIPK21 regulates osmotic and salt stress responses in Arabidopsis. Pandey GK, Kanwar P, Singh A, Steinhorst L, Pandey A, Yadav AK, Tokas I, Sanyal SK, Kim BG, Lee SC, Cheong YH, Kudla J, Luan S (2015) Plant Physiology 169(1):780-92.

Major Funding Sources

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

Department of Science & Technology (DST), Government of India (http://www.dst.gov.in/scientific-programme/ser-index.htm)

Council of Scientific and Industrial Research (CSIR), New Delhi (http://www.csirhrdg.res.in/)

Indian Council of Agricultural Research (ICAR), New Delhi (http://www.icar.org.in/)

Additional Information

In addition to the information previously provided, below some of other work is highlighted.

Ashis Nandi’s lab at JNU, New Delhi works on salicylic acid (SA) signaling and systemic acquired resistance (SAR). Using transcriptome profile of a constitutive SA signaling mutant, his group has identified a zinc finger protein that promotes SA signaling in both NPR1-dependent and –independent pathways.

Ashverya Laxmi’s lab at NIPGR, New Delhi, has contributed towards understanding the role of sugars as a signaling molecule in regulating plant growth and development. In the past year, they have shown interaction between glucose and brassinosteroid in regulation of lateral root development in Arabidopsis.

Israel

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

General Activities

Arabidopsis Research Facilities

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

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

Three new Arabidopsis research labs were established by young PIs:

- Dr. Yariv Brotman, Ben-Gurion University (project leader, Max Planck Institute, Golm, Germany)
- Dr. Idan Efroni, The Hebrew University of Jerusalem (postdoctoral training: the lab of Kenneth Birnbaum, NYU, US)
- Dr. Roy Weinstain, Tel Aviv University (postdoctoral training: the lab of Roger Tsien, UCSD, US)
- Dr. Assaf Zemach , Tel Aviv University (postdoctoral training: the lab of Daniel Zilberman, UC Berkeley US)

Current 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:

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

Outlook on Arabidopsis Research

Tel Aviv University will establish a school for Plant Sciences and Food security, demonstrating the university commitment to the promotion of plant sciences research at the university.

Road Map Related Activities

Outreach Activities

- Summer Course 2015: Plant Signaling in Changing Environment

Conferences and Workshops

- Canada-Israel Workshop on Plant Biology and Agriculture in the 21st Century, Ottawa, 2-4 November, 2015
- Plant Stress: Student Organised Conference at the Weizmann Institute, 17 February, 2016

Selected Publications

About 60 research articles employing Arabidopsis were published since the beginning of 2015 and until March 2016.

Major Funding Sources

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

Chief Scientist. Israel Ministry of Agriculture.

Italy

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

General Activities

Arabidopsis Research Facilities

Several Italian groups continue to utilize Arabidopsis as a model organism for plant biology research and their results are published in high impact journals. Work is mainly performed in individual laboratories; however networks and collaborations are common. Facilities for growth, handling and analysis of Arabidopsis are often shared among groups. Research is mainly focused on root, flower and hypocotyl development, seed germination, characterization of the signalling pathways involved in oligogalacturonides-mediated resistance, ion homeostasis mechanisms and plant response to environment.

Current Arabidopsis Projects

The Italian Ministry of Education, University and Research has funded several Arabidopsis projects (2013-2016), including a large network project entitled "The control of plant root growth: a systems biology approach", whose partners are I. Ruberti (IBPM-CNR, Rome), C. Tonelli (University of Milan), Emanuele De Paoli (University of Udine), Luisa Di Paola (Università Campus Biomedico, Roma), Eugenia Schininà (Sapienza University, Rome), S. Sabatini/P. Costantino (Sapienza University, Rome). This project is coordinated by Paolo Costantino.

The Italian Ministry has funded a project (PRIN 2014-2017) on "Genetic and epigenetic control of ovule number and fertility in Arabidopsis". Coordinator: Lucia Colombo.

A collaboration funded by the Italian Ministry of Foreign Affairs is continuing between the Italian laboratories of M. Cardarelli/G. Serino/P. Costantino (CNR/Sapienza University) and the Japanese laboratories of T. Tsuge/M. Matsui (Kyoto Univ./Riken). The goal is to find common regulatory networks controlling stamen and hypocotyl growth in Arabidopsis.

A research project entitled: "Cross-talks between reactive Oxygen Species, jasmonates and lipid peroxidation during root formation in response to heavy metals and metalloids and fungus infection" is currently funded by Sapienza University of Rome.

Additional funding comes from the EU: ERC grants have been awarded to S. Sabatini/P. Costantino and F. Cervone/G. deLorenzo, and from MC-IRSES - International research staff exchange scheme (IRSES), "The physiology and genetics of fruit formation: from genes to networks" (FRUIT-look) FP7-PEOPLE-2013-IRSES, Coordinator: UNIMI Italy. Participants: Sweden (SVERIGES LANTBRUKSUNIVERSITET) and Spain (AGENCIA ESTATAL CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS). Period: 2014-2017.

Outlook on Arabidopsis Research

Several groups have participated in the call from the Italian Ministry of Education, University and Research (PRIN 2015) and are applying for international and national grants. However, Arabidopsis research in Italy is getting very limited support, as compared to research on crops. Future work will focus on the continuation of the main research projects while many groups are seeking fundings for applied research on species other than Arabidopsis.

Road Map Related Activities

Arabidopsis Tools and Resources

- S. Sabatini/P. Costantino group has developed a mathematical model simulating the role of the hormone cytokinin on the position of the transition zone, the boundary were root cell lose their capacity to divide and start differentiating.
- M. Kater/L. Colombo group have developed a protocol for laser micro-dissection of reproductive meristems coupled to RNA sequencing and for ChIP-sequencing of transcription factors related to flower development.
- M. Galbiati has developed synthetic promoters for the spatio-temporal control of gene expression in guard cells.

Outreach Activities

Several Arabidopsis researchers from Milan and Rome were involved in planning and organizing the 'Fascination of Plants' day under the umbrella of EPSO (European Plant Science Organisation) in May 18, 2015.

The group of Ida Ruberti participates in the project Promotion of consumer health of the National technological cluster Agrifood.

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

Conferences and Workshops

- 59th Annual Congress of the Italian Society of Agricultural Genetics "Feeding the planet: plant science and breeding for the future of agriculture". Milano, September 8-11, 2015, (included a session at World Expo 2015)
- 109th Conference of the Italian Society of Botany-International Plant Science Conference (IPSC) - with the patronage of World Expo 2015, Pavia, September 14-18, 2015

- C. Tonelli was the organizer of the International Conference "Water and Food Security. The role of Science in Food Security and Environmental Sustainability" held in Venice, May 6-7, 2015

Selected Publications

- Plant immunity triggered by engineered in vivo release of oligogalacturonides, damage-associated molecular patterns. Benedetti M, Pontiggia D, Raggi S, Cheng Z, Scaloni F, Ferrari S, Ausubel FM, Cervone F, De Lorenzo G (2015) PNAS (USA) 112 (17) 5533-8.
- The COP9 SIGNALOSOME is required for postembryonic meristem maintenance in *Arabidopsis thaliana*. Franciosini A, Moubayidin L, Du K, Matari NH, Boccaccini A, Butera S, Vittorioso P, Sabatini S, Jenik PD, Costantino P, Serino G (2015) Mol Plant 8:1623-34.
- Cadmium-inducible expression of the ABC-type transporter AtABCC3 increases phytochelatin-mediated Cd tolerance in Arabidopsis. Brunetti P, Zanella L, De Paolis A, Di Litta D, Cecchetti V, Falasca G, Barbieri M, Altamura MM, Costantino P, and Cardarelli M (2015) J Exp Bot 66(13):3815-29.
- Changing the spatial pattern of TFL1 expression reveals its key role in the shoot meristem in controlling Arabidopsis flowering architecture. Baumann K, Venail J, Berbel A, Domenech MJ, Money T, Conti L, Hanzawa Y, Madueno F, Bradley D (2015) J Exp Bot. 66(15):4769-80.
- The Arabidopsis RNA-binding protein AtRGGA regulates tolerance to salt and drought stress. Ambrosone A, Batelli G, Nurcato R, Aurilia V, Punzo P, Bangarusamy DK, Ruberti I, Sassi M, Leone A, Costa A, Grillo S (2015) Plant Physiol. 168(1):292-306.

Major Funding Sources

European Commision program "Horizon 2020" (https://ec.europa.eu/programmes/horizon2020/)

Italian Ministry of Agriculture (https://www.politicheagricole.it)

Italian Ministry of University and Scientific Research (www.istruzione.it)

Italian Ministry and Foreign Affairs (www.esteri.it)

CARIPLO Foundation (http://www.fondazionecariplo.it/it/index.html)

Institute Pasteur - Cenci Bolognetti Foundation (www.istitutopasteur.it)

Sapienza University, Rome (http://www.uniroma1.it)

Japan

Minami Matsui (minami@riken.jp) and Keiko Sugimoto (keiko.sugimoto@riken.jp) RIKEN Center for Sustainable Resource Science

General Activities

Arabidopsis Research Facilities

Coordinated projects continuing in 2015/2016:

Kazusa DNA Research Institute (http://www.kazusa.or.jp/e/) Laboratory of Plant Genomics and Genetics, Plant DNA Analysis Group, Metabolomics Team, Bioresources team, Biomass Team. Genome Informatics Group developed the portal site Plant Genome DataBase Japan PGDBj (http://pgdbj.jp) integrating databases related to plant omics studies. Manually curated literature information on DNA markers of 55 plants.

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) (http://www.csrs.riken.jp/en/) CSRS (Director Kazuo Shinozaki), established in 2013 to conduct basic research and also seek out, identify, and work for solutions for critical scientific, technical and social issues with special focus on Green Innovation, as well as sustainable production of energy and resources. CSRS integrates plant scientists, chemists and chemical biologists. Chemists and plant biologists from its Biomass Engineering Research Division (BMEP) (http://www.csrs.riken.jp/en/labs/bepcd/) focus on applied research through interdisciplinary innovation for plant biomass production and renewable chemical materials and bioplastics. Besides Arabidopsis, the program uses Brachypodium as a model of grass biomass.

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 and TAC clones), and cultured cells (T87 and At wt cell lines). The center also distributes full-length cDNA clones and cultured cells of model plants such as rice, Brachypodium distachyon and tobacco to the international research community.

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

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

Integrative system of autonomous environmental signal recognition and memorization for plant plasticity (http://www.rs.tus.ac.jp/plantmemory/en/) Project goal to clarify distributed response of cells and tissues of plants and determine how plants control such information through plant unique whole-organism dynamic signal transduction system in response to environmental stimuli. Scientific Research on Innovative Areas MEXT Grant-in Aid Project FY2015-2019. Multi-organization representative: Toshinori Kinoshita, ITbM/Nagoya University.

Multidimensional Exploration of Logics of Plant Development (MEXT) (2013-2017) (http://bit.ly/1TyA7Fg) Project to delineate systems coordinating intercellular and intracellular signals, functions of key differentiation genes, and control of metabolism, under combined efforts of 9 core research groups, 4 supporting facilities/teams, and 18 research groups (2013-2015) using multiple model species. Four facilities/teams assist in metabolomics, use of an *Arabidopsis thaliana* transcription factor library, development of a new model system, *Marchantia polymorpha*, and mathematical modeling. Multidisciplinary collaborative approach will explore unprecedented research directions. Led by Hirokazu Tsukaya.

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

Creation of fundamental technologies contribute to the elucidation and application for the robustness in plants against environmental changes" Started 2015, Core Research for Evolutional Science and Technology (JST-CREST) (http://bit.ly/1TyzoDT) coordinated with PRESTO (Sakigake). Goal to establish environmentally-adaptive-plant design systems for stable food supply in age of climate change via highly precise quantitative analysis of environmental response mechanisms of plants, modeling of plant environmental response mechanisms, and evaluation of plant characters modified by sophisticated reconstruction of genes or genotype. Led by Satoshi Tabata (Kasuza DNA Research Inst.).

Creation of essential technologies to utilize carbon dioxide as a resource through the enhancement of plant productivity and the exploitation of plant products. Started in 2011, Core Research for Evolutional Science and Technology (JST-CREST) (http://bit.ly/22I7neA). Goal to create basic technologies to use plant photosynthetic functions and biomass that will enable efficient carbon dioxide utilization. Led by Akira Isogai (Nara Institute of Science and Technology).

JST-ALCA Japan Science and Technology Agency - Advanced Low Carbon Technology Research and Development Program (http://www.jst.go.jp/alca/en/index.html) provides competitive funding for research up to ten year period in biotechnology, chemical and energy processes and systems, materials.

JST-NSF "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society" (http://1.usa.gov/1LVBpaI), research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and K. Saito (RIKEN), Oliver Fiehn (Univ. of California at Davis) and M. Arita (NIG).

ERATO Higashiyama Live-Holonics Project (2010-2016) (http://www.liveholonics.com/en/) headed by T. Higashiyama, Nagoya University. Project studies intercellular signaling in multicellular organisms with complete control of cells and molecules under microscope by developing new live-cell analysis technologies.

Japan Advanced Plant Science Research Network (http://www.psr-net.riken.jp/) started in 2011-2017. Program's nine centers of excellence in universities and research institutes support plant research for green innovation.

NC-CARP Network of Centers of Carbon Dioxide Resource Studies in Plants (http://nc-carp.org/index) Program in GRENE; Green Network of Excellence. Organizer: Hiroo Fukuda. Started in 2011, ending in 2016. Aims at innovation of plant biomass technology by collaboration among Plant Science, Agriculture, Engineering and Chemistry, and education of this new area.

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, 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.

East Asia Science and Innovation Area Joint Research Program (e-ASIA) (http://bit.ly/1P30g72) JST-NSTDA (Thailand)-MOST (Vietnam) on "Biomass and Plant Science". Research led by Motoaki Seki (RIKEN CSRS). Ham Huy Le (Institute of Agricultural Genetics) and Jarunya Narangajavana (Mahidol University).

Current Arabidopsis Projects

Kazusa DNA Research Institute

Kazusa Metabolomics Database (KOMICS) web portal to databases, tools and other information was developed through plant metabolomics studies of Daisuke Shibata, including integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, co-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 related TAIR gene models and annotations, by specifying a Resource ID, a TAIR AGI code or a keyword. All SABRE resources available from core facilities of Japan NBRP (National BioResource Project) (http://bit.ly/1RYOkI3)

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS)

- Metabolome platform using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi, Tetsuya Sakurai). CSRS established the Arabidopsis metabolomics platform (http://prime.psc.riken.jp/), consisting of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics.
- Hormonome platform and RIKEN Plant Hormone Research Network: (Hitoshi Sakakibara, Mitsunori Seo) CSRS established highly sensitive high-throughput phytohormone quantification platform consisting of mass spectrometry-based technology. Platform is conducting a wide range of collaborative research in plant hormone biology (http://hormones.psc.riken.jp/)
- Transcriptome platform using next generation sequencers. RIKEN ACCC and IMS (Motoaki Seki, Keiichi Mochida, Minami Matsui, Takaho Endo, Piero Carninci, Kazuo Shinozaki)
- Proteome platform: Plant Phosphoproteome Database (RIPP-DB) CSRS (Hirofumi Nakagami, Ken Shirasu) and Keio University (Yasushi Ishihama, Naoyuki Sugiyama) High-throughput shotgun phosphoproteomics tool for plants and phosphorylation site databases (http://bit.ly/224sjjk) (http://pepbase.iab.keio.ac.jp)
- Phenome platform RIKEN Activation tagging lines Database and Full-length-cDNA- overexpressing (FOX) Arabidopsis lines (M. Matsui) (http://bit.ly/1WdrX2Z), Rice FOX Arabidopsis line Database (http://ricefox.psc.riken.jp/), RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary (Takashi Kuromori, T. Sakurai, K. Shinozaki) (http://rarge-v2.psc.riken.jp/)
- The Chloroplast Function Database II (Fumiyoshi Myouga, K. Shinozaki) Comprehensive database analyzed by combining genotypic and phenotypic multiparametic analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins. (http://rarge.psc.riken.jp/chloroplast/)
- Analysis of small Open Reading Frame (Kousuke Hanada, M. Matsui, M. Seki) They identified ~8,000 sORFs with high coding potential in intergenic regions of the Arabidopsis genome (http://bit.ly/1P2YUt6)
- MassBank (Masanori Arita, Takaaki Nishioka, K. Saito) Public repository of mass spectral data for sharing spectra among research communities. The data is useful for chemical identification and structure elucidation of metabolites detected by mass spectrometers. (http://www.massbank.jp/en/about.html)
- PosMed Positional Medline (Y. Makita, N. Kobayashi, T. Toyoda) Semantic web association study (SWAS) search engine ranks resources including Arabidopsis genes and metabolites, using associations between user-specified phenotypic keywords and resources connected directly or inferentially via a semantic web of biological databases such as MEDLINE, OMIM, pathways, co-expressions, molecular interactions and ontology terms (http://omicspace.riken.jp/)

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- High-throughput genome-wide biochemical analysis using wheat germ cell-free-based protein array technology. The method developed by Proteo-Science Center of Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) (http://bit.ly/21ssVcQ) and RIKEN CSRS (M. Seki and K. Shinozaki) is useful for in vitro screening of substrate protein, interacting protein or chemical compound.
- RIPPS (RIKEN Plant Phenotyping System) (K. Shinozaki, Miki Fujita, Kaoru Urano) 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://pasmet.riken.jp/)
- Plant-PrAS (Plant-Protein Annotation Suite) (A. Kurotani, Y. Yamada, AA. Tokmakov, Y. Kuroda, Y. Fukami, K. Shinozaki, T. Sakurai) Analyzed predicted multiple physicochemical and secondary structural parameters using over 20 analysis tools with whole amino acid sequences from genomes of representative plant species (*Arabidopsis 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/)
- "Development of Synthetic Promoters for Acceleration of Biomass Production" JST-ALCA project (http://bit.ly/1SRr7de) led by Yoshiharu Yamamoto (Gifu Univ.).
- Plant Promoter Database, ppdb (http://ppdb.agr.gifu-u.ac.jp) (Yoshiharu Yamamoto, Gifu Univ.) http://bit.ly/1LVwnep was updated to ver. 3.0. Large TSS data of a NGS incorporated into the database.

Road Map Related Activities

Arabidopsis Tools and Resources

Kazusa DNA Research Institute

- PGDBj Plant Genome DataBase Japan (http://pgdbj.jp/?ln=en)
- Arabidopsis EST Index (http://bit.ly/22I7EhI)
- KATANA Kazusa *Arabidopsis thaliana* Annotation Abstract (http://bit.ly/1M6noqN)
- TACWeb Database of the transformation-competent bacterial artificial chromosome (TAC) vectors for *Arabidopsis thaliana* (http://bit.ly/22kE5CY)
- KOMICS Kazusa Metabolomics Database portal (http://bit.ly/1QWjzok)
- KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (http://kpv.kazusa.or.jp/)
- MassBase: a plant metabolome database (http://bit.ly/1Rlf9Dd)
- KomicMarket Kazusa omics data market: metabolite eaks annotations database (http://bit.ly/1YY8dly)
- MS-MS Fragment Viewer (http://bit.ly/1QWjPUm)
- KAGIANA co-expressed gene search tool (http://bit.ly/253kFEO)
- CoP co-expressed gene search tool (http://bit.ly/1nMWuso)
- RnR regulatory network research (http://bit.ly/1WpdQaU).
- MFSearcher molecular formula searcher (http://bit.ly/1RN2BFp)

RIKEN BRC

- Resources from RIKEN BRC including seed catalogs (http://epd.brc.riken.jp/en/)
- Phenotype database of natural accessions (Beta) (http://bit.ly/1YY8PYk)
- The ABRANA (Arabidopsis-Brassica Network Access) DB. Resources related with TAIR cDNAs and annotations through sequences (http://www.abrana.jp/)
- SABRE2: Database connecting plant EST/Full-Length cDNA clones with Arabidopsis information. (http://sabre.epd.brc.riken.jp/)

RIKEN CSRS

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

- Widely-targeted metabolomics (http://bit.ly/227pkDi)
- LC-MCS Branch (http://bit.ly/1P2Zhnt)
- AtMetExpress Arabidopsis metabolome expression database (http://bit.ly/1P2YByw)

PRIMe Web Applications

- Standard Spectrum Search (http://bit.ly/1TyDxaT)
- MS2T Arabidopsis MS/MS spectral tag viewer (http://bit.ly/1XgNdot)
- ReSpect RIKEN MSn Spectral database for phytochemicals (http://bit.ly/1P2ZaIv)
- PRIMeLink integrates 3 above databases (AtMetExpress, MS2T and ReSpect) for bi-directional search from gene or metabolite (http://bit.ly/1RCX4Bc)
- HiFi Heteroatom-containing Ion Finder (http://bit.ly/1nBxjJ6)

- MeKO Metabolomic characterization of knock-out mutants of Arabidopsis (http://bit.ly/1QQBWYl)
- SpinAssign annotation of metabolites by NMR from 13C-HSQC peaks (http://bit.ly/1LVE58h)
- Correlated Gene Search (http://bit.ly/1RCXbwn)
- Cluster Cutting (http://bit.ly/227pNoU)

Distribution and Redistribution

- MetBoard standard compounds (http://bit.ly/24U5A8B)
- Drop Met mass-spec based metabolome analyses (http://bit.ly/1LVEfwq)
- Simple BL-SOM (http://bit.ly/1TyE10E)

Other RIKEN CSRS developed tools and resources:

- Plant Hormone Research Network (http://hormones.psc.riken.jp/)
- UniVIO Uniformed Viewer for Integrative Omics (http://univio.psc.riken.jp/)
- RARGE II Arabidopsis Genome Encyclopedia II (http://rarge-v2.psc.riken.jp/)
- The Chloroplast Function Database II (http://bit.ly/1P2YMty)
- RAPID Phenome Analysis of Ds transposon-tagging line in Arabidopsis (http://bit.ly/1TQBVdb)
- RARTF RIKEN Arabidopsis Transcription Factor database (http://bit.ly/1P2YO4N)
- Arabidopsis Activation Tagging Line Database (http://bit.ly/1WdrX2Z)
- RIPP-DB Plant Phosphoproteome Database (http://bit.ly/224sjjk)
- AtGenExpress Arabidopsis Gene Expression profile database (http://bit.ly/1P2YT8v)
- (HANADB-AT) Analysis of small open reading frame (sORF) (http://bit.ly/1P2YUt6)
- (sORFfinder) tool program package to identify high coding potential sORF (http://bit.ly/1P2Z2bX)
- KNApSacK Comprehensive species-metabolite relationship database (http://bit.ly/1LfFkyZ) (NAIST)

Conferences and Workshops

- Nov. 29-Dec. 2, 2016: Cold Spring Harbor Asia Conference in Japan, "Latest Advances in Plant Development and Environmental Response" Awaji Island, Kobe (http://bit.ly/1TKqqDK) Mar. 18-10, 2016: 57th Annual Meeting of Japanese Society of Plant Physiologists (http://bit.ly/1RNsULu)
- Nov. 30-Dec. 4, 2015: 8th Plant Biomechanics International Conference, Nagoya (http://bit.ly/1TKsATT)
- Nov. 24-25, 2015: International Symposium "Towards Increased Plant Productivity through Understanding of Environmental Responses and Epigenetic Regulation" RIKEN, Yokohama Campus. Sponsorship: RIKEN CSRS; Bioscience and Biotechnology Center, Nagoya Univ.; JST CREST (http://bit.ly/1TKqm6O)
- Oct. 8-9, 2015: ICPES 2015: 17th International Conference on Plant and Environment Sciences, Osaka (http://bit.ly/1TKrtU9)

Selected Publications

- Tip-localized receptors control pollen tube growth and LURE sensing in Arabidopsis. Takeuchi H, Higashiyama T (2016) Nature 531:245-8.
- Rapid Elimination of the Persistent Synergid through a Cell Fusion Mechanism. Maruyama et al. (2015) Cell 161(4):907-18.
- PARASITIC PLANTS. Probing strigolactone receptors in Striga hermonthica with fluorescence. Tsuchiya Y et al. (2015) Science. 349(6250):864-8.
- Decentralized circadian clocks process thermal and photoperiodic cues in specific tissues. Hanako et al. (2015) Nature Plants 1, Article number: 15163 doi:10.1038/nplants.2015.163
- PRC2 represses dedifferentiation of mature somatic cells in Arabidopsis. Ikeuchi et al. (2015) Nature Plants 1, Article number: 15089 doi:10.1038/nplants.2015.89

Major Funding Sources

RIKEN is supported by MEXT.

Kazusa projects are supported by Chiba-Prefecture.

Grants-in-Aid for Science from MEXT, (http://www.jsps.go.jp/english/e-grants/)

CREST of Japan Science and Technology Corporation (http://bit.ly/22I8avZ)

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)

Netherlands

Ben Scheres (ben.scheres@wur.nl) Wageningen UR, Plant Developmental Biology, Wageningen; Sacco de Vries (sacco.devries@wur.nl) Wageningen UR, Laboratory of Biochemistry, Wageningen

General Activities

Arabidopsis Research Facilities

Leiden University: Auxin and pattern formation (Offringa), DNA repair and recombination (Hooykaas). Metabolomics facility for plant defence compounds (Klinkhamer).

Utrecht University: Sugar sensing networks and phase transitions (Smeekens), Flooding stress and light avoidance (Pierik/Voesenek), Plant-Microbe interactions (Pieterse), Multi-scale modelling (ten Tusscher).

Wageningen University: Floral transcription factor networks (Angenent), Strigolactone signalling (Bouwmeester), Root development and stem cells (Scheres), Receptor kinase biology and Embryogenesis (De Vries/Weijers).

University of Amsterdam/VU: Abiotic stress response, lipid signalling, volatile signaling (Testerink/Haring), Chromatin structure (Koes).

Current Arabidopsis Projects

- EU-ITN-MERIT: Metabolic Reprogramming by Induction of Transcription (2012-2015 Smeekens).
- ERA-CAPS: Plasticity of flowering time in response to environmental signals in *Arabidopsis thaliana* (FLOWPLAST) (2014-2017 Angenent)
- ERA-CAPS: European Plant Embryology Consortium (2014-2017, Weijers, Scheres)
- Dose-dependent BBM action (2015-2019-Boutilier)
- Role of TCP transcription factors in growth (2013-2017, Immink)
- NWO-VENI: Evolutionary aspects of the MADS domain transcription factor FUL (2014-2017, Bemer)
- NWO-GSU (2015-2020) Ronald Pierik. Moving from tip to base: how local far-red signalling regulates distant growth.
- NWO-ALW (2014-2017) Ronald Pierik. Unravelling molecular mechanisms of plant competition: the interplay between above- and belowground competitive responses in *Arabidopsis thaliana*.
- EMBO Long term fellowship (Oct2015-Oct2017) Scott Hayes, with Ronald Pierik. Mechanism and functional significance of salt-mediated inhibition of plant shade avoidance.
- NWO-VIDI (2013-2018) Ronald Pierik. When growing tall is not an option: down-regulation of shoot elongation in the shade.
- NWO-VIDI (2015-2019) Kirsten ten Tusscher. Lateral root patterning in plants: multi-scale modelling of complex feedbacks.
- NWO-ALW (Mar2013-Jan2016) Flooding stress tolerance: an ecomolecular approach using Arabidopsis and wild relatives.
- NWO-Veni (Jan2013-Jan2016) After the rains: unravelling the molecular mechanisms driving post flooding recovery in plants
- NWO-ALW (Sep2015-Sep2019) A novel role for ethylene in conferring anoxia tolerance: mechanism and significance
- NWO-GSU (Sep2015-Sep2019) NO problem: ethylene-induced regulation of nitric oxide confers flooding tolerance in plants
- NWO-DBT (Jan2016-Jan2020) Understanding responses to simultaneously and sequentially occurring abiotic stresses typical of climate change in rice and Arabidopsis
- ERC-StG (consolidator) Dolf Weijers - CELLPATTERN (2011-2016)
- NWO-VIDI Bert De Rybel - The molecular and cellular basis of vascular tissue formation (2014-2019)
- NWO-VENI Colette ten Hove - Dissecting the origin of an ancient tissue (2013-2016)

NWO-VICI Dolf Weijers - The evolutionary and structural basis for specificity in plant hormone response (2015-2020)

Outlook on Arabidopsis Research

Funding possibilities increasingly rely on comparative and evolutionary research among Arabidopsis accessions, relatives of Arabidopsis or non-relative wild plants and crops.

Road Map Related Activities

Arabidopsis Tools and Resources

- Phenovator: Flood e.a. Plant Methods 2016 12:14 (http://plantmethods.biomedcentral.com/articles/10.1186/s13007-016-0113-y). Facility for high-throughput phenotyping of Arabidopsis growth and photosynthesis.
- Angenent laboratory: ChIP-seq (both TFs and histon modifications), SELEX-seq, Immunoprecipitation-Mass Spectrometry. Pac-Bio for RNA-seq of splicing variants.
- Scheres laboratory: collaboration with physics (prof. Bela Mulder) for simulation of microtubule dynamics on realistic cell surface shapes.

Outreach Activities

The Top Sector policy of the Ministry of Economic Affairs allows funding of various collaborative projects between breeding companies and Academia. In these projects we translate knowledge and tools obtained from our Arabidopsis research to crops, e.g. brassica, lettuce and tomato. An example is a project funded by the Ministry of Economic affairs and 3 Dutch breeding companies aiming at a translation of our knowledge about ambient temperature regulation of flowering time in Arabidopsis to cauliflower. (2012-2016; 2016-2020).

Conferences and Workshops

- Experimental Plant Science Annual Meeting Lunteren
- Bi-yearly international summerschool Environmental Signaling in Plants (8th version held in 2015).
- 15th New Phytologist Workshop (Ravenstein, The Netherlands) Flooding stress: signaling through perturbations in oxygen, ethylene, nitric oxide and light

Selected Publications

- Transcriptional control of tissue formation throughout root development. Moreno-Risueno MA, Sozzani R, Yardimci GG, Petricka JJ, Vernoux T, Blilou I, Alonso J, Winter CM, Ohler U, Scheres B, Benfey PN (2015) Science 350:426-430.
- Evolution of DNA-binding sites of a floral master regulatory transcription factor. Muiño JM, de Bruijn S, Pajoro A, Geuten K, Vingron M, Angenent GC, Kaufmann K (2015) Mol Biol Evol 33(1):185-20.
- Arabidopsis BIRD zinc finger proteins jointly stabilize tissue boundaries by confining the cell fate regulator SHORT-ROOT and contributing to fate specification. Long Y, Smet W, Cruz-Ramirez A, Castelijns B, de Jonge W, Mahonen AP, Bouchet B, Sanchez-Perez G, Akhmanova A, Scheres B, Blilou I (2015) The Plant Cell 27:1185-99.
- A bHLH-based feedback loop restricts vascular cell proliferation in plants. Vera-Sirera F, De Rybel B, Úrbez C, Kouklas E, Pesquera M, Álvarez-Mahecha JC, Minguet EG, Tuominen H, Carbonell J, Borst JW, Weijers D, Blázquez MA (2015) Dev Cell. 23:432-43.
- Origin of SERKs: Bioinformatics Analysis of the Somatic Embryogenesis Receptor Kinases. Aan den Toorn M, Albrecht C, de Vries SC (2015) Mol Plant 8:762-82

New Zealand

Lynette Brownfield (lynette.brownfield@otago.ac.nz) University of Otago, Department of Biochemistry, Dunedin

General Activities

Arabidopsis Research Facilities

As agriculture plays a major role in the New Zealand economy, plant science largely focusses on forage crops such as rye, legumes and brassicas, for diary cattle and other stock, and horticultural crops such as grapes, kiwifruit, apples, stone fruits and potatoes. In this context, Arabidopsis is largely used as an easily manipulated model for the identification and testing of gene function with information translated into other species. Basic research is also conducted using Arabidopsis within the universities.

In New Zealand, research using Arabidopsis is conducted in both universities and Crown Research Institutes (CRIs), government-owned companies that carry out scientific research. Universities working with Arabidopsis include the University of Auckland (School of Biological Sciences; Plant Molecular Science), the University of Canterbury (Biological Sciences), Lincoln University (Bio-Protection Research Centre), Massey University (Institute of Fundamental Science; Institute of Agriculture & Environment) and the University of Otago (Department of Biochemistry). The major Crown Research Institutes using Arabidopsis in research programs are AgResearch and Plant and Food Research. Research in the universities and the Crown Research Institutes is often linked, with several researchers having joint appointments in two facilities.

Current Arabidopsis Projects

Major themes of research in New Zealand involving Arabidopsis:

- Flowering time. Investigating how external cues such as day length, light quality and cold regulate flowering. The University of Auckland, the University of Otago and Plant and Food Research.
- Plant pathogen interactions and stress responses. Lincoln University, Massey University and Plant and Food Research
- Plant Growth and Development. Investigating the molecular control of various aspects of plant development such as plant reproduction, organ size, regulation of branching. AgResearch, Massey University, the University of Otago and Plant and Food Research.
- Control of gene expression. Transcriptional regulation, intron-mediated transcriptional control, uORFs and translation regulation. The University of Otago and Plant and Food Research.

- Colour and nutrition. Characterization of the molecular pathways controlling the production of pigments and nutritional compounds in plants. The University of Auckland, the University of Otago and Plant and Food Research.
- Plant metabolism. Lipid biosynthesis, photosynthesis, photorespiration and nitrogen metabolism. Agresearch

Outlook on Arabidopsis Research

As agriculture and horticulture play major roles in the New Zealand economy, Arabidopsis will continue to play a key role in plant research as a model for gene discovery, the characterization of molecular pathways and the testing of the function of genes from crop species. Basic plant science at the universities will also continue using Arabidopsis.

Road Map Related Activities

Arabidopsis Tools and Resources

Methods for concurrent transmitted light and confocal imaging in plants cells developed by David Collings at the University of Canterbury: Collings DA (2015) Optimisation approaches for concurrent transmitted light imaging during confocal microscopy. Plant Methods 11:40.

Outreach Activities

The plant research environment in New Zealand strongly supports the flow of information from university to applied plant scientists and plant breeders, largely though the Crown Research Institutes that are Government-owned companies. Both Plant and Food and AgResearch have scientists with a range of skills from gene discovery and characterization to plant breeding. There are also a number of researchers that have joint appointments at both a university and a Crown Research Institute. Additionally, research funding from the Ministry of Business, Innovation and Employment (MBIE) is dependent upon collaborations between research scientists and potential end users being established early in a research program.

Conferences and Workshops

- ComBio incorporating the annual meeting of the New Zealand Society of Plant Biologists and a Plant Cell Biology conference stream. September 27-October 1, 2015, Melbourne, Australia.
- QMB Plant Molecular Biology Meeting, September 1- 2, 2016. Nelson, New Zealand.

Selected Publications

- Jibran R, Sullivan KL, Crowhurst R, Erridge ZA, Chagné D, McLachlan AR, Brummell DA, Dijkwel PP, Hunter, DA. (2015). Journal of Experimental Botany 66(21):6849-6862.
- Functional and expression analyses of kiwifruit SOC1-like genes suggest that they may not have a role in the transition to flowering but may affect the duration of dormancy. Voogd C, Wang T, Varkonyi-Gasic E (2015) Journal of Experimental Botany 66:4699-710.
- Three Medicago MtFUL genes have distinct and overlapping expression patterns during vegetative and reproductive development and 35S:MtFULb accelerates flowering and causes a terminal flower phenotype in Arabidopsis. Jaudal M, Zhang L, Che C, Putterill J (2015) Frontiers in Genetics 6.
- Optimisation approaches for concurrent transmitted light imaging during confocal microscopy. Collings DA (2015) Plant Methods 11:40.
- Two linked pairs of Arabidopsis TNL resistance genes independently confer recognition of bacterial effector AvrRps4. Saucet SB, Ma Y, Sarris PF, Furzer OJ, Sohn KH, Jones DGJ (2015) Nature communications 6:6338.

Major Funding Sources

Basic research in plant sciences in New Zealand is largely supported by the Marsden Fund administered by the Royal Society of New Zealand (http://www.royalsociety.org.nz/programmes/funds/marsden/) along with funding from universities.

Translational research is funded through the Ministry for Business, Innovation and Employment (MBIE) through core funding to the Crown Research Institutes and contestable funding through the Science Investment Rounds. MBIE will also support participation by New Zealand researchers in ERA-CAPS applications (http://www.eracaps.org). Funding for translational research is also available through The Agricultural and Marketing Research and Development Trust (AGMARDT: http://agmardt.org.nz/). The Crown Research Institutes also receive funds from royalties of commercialized products.

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South Korea

Inhwan Hwang (ihhwang@postech.ac.kr) Pohang University of Science and Technology, Republic of Korea

General Activities

Arabidopsis Research Facilities

The major topics include abiotic and biotic stress, plant senescence and life history, plant hormones, photosynthesis, protein targeting and trafficking, transporters and channels, phloeme development, light signaling, and circadian clock. In addition, plant biotech-related topics are also actively studied for the purpose of developing plants as a bioreactor.

- Multi-omic approaches for systems study on plant senescence
- Phenomics center
- Mass analysis system for plant hormones and secondary metabolites
- Plant factory for GM plant growth

Current Arabidopsis Projects

- Systems & Synthetic Agrobiotech Center (~ 9 M USD/yr for 10 years by the Rural Development Administration, Korea)
- Systems understanding of plant senescence and life history (~9 M USD/yr for 10 years by Institute of Basic Research)
- Global research lab project (0.5 M$/yr for 10 years by the National Research Foundation, Korea
- Woojangchoon Project focusing on ABA signaling and synthetic biology (0.9 M USD/yr for 5 years) supported by the Rural Developmental Agency, Korea
- Woojangchoon Project focusing on chloroplast development and photosynthesis of C3 and C4 systems (0.9 M USD/yr for 5 years) supported by the Rural Developmental Agency, Korea

Outlook on Arabidopsis Research

Currently, the direction of research in plant science is more towards application using crop plants. Thus, basic research using Arabidopsis is less promising. In addition, a major funding for the basic research is given to the newly established organization, the Institute of Basic Research. In this institute, the research funding is distributed to its center with a small number of scientists. Thus, it is likely that basic research, in particular plant science using Arabidopsis, at universities will suffer in the near future.

Conferences and Workshops

- Plant Winter Conference at POSTECH
- Annual meeting of Korean Society of Plant Biologists
- A workshop for CRISPR system for application to plants, in particular Arabidopsis
- 27th International Conference on Arabidopsis research, Gyeongju, South Korea: June 29th-July 3rd 2016

Selected Publications

- DNA-free genome editing in plants with preassembled CRISPR-Cas9 ribonucleoproteins. Woo JW, Kim J, Kwon SI, Corvalán C, Cho SW, Kim H, Kim SG, Kim ST, Choe S, Kim JS (2015) Nat Biotechnol. 33(11):1162-4
- Abscisic acid transporters cooperate to control seed germination. Kang J, Yim S, Choi H, Kim A, Lee KP, Lopez-Molina L, Martinoia E, Lee Y. (2015) Nat Commun. 6:8113
- A novel thiol-reductase activity of Arabidopsis YUC6 confers drought tolerance independently of auxin biosynthesis. Cha JY, Kim WY, Kang SB, Kim JI, Baek D, Jung IJ, Kim MR, Li N, Kim HJ, Nakajima M, Asami T, Sabir JS, Park HC, Lee SY, Bohnert HJ, Bressan RA, Pardo JM, Yun DJ (2015) Nat Commun. 6:8041
- Cytosolic targeting factor AKR2A captures chloroplast outer membrane-localized client proteins at the ribosome during translation. Kim DH, Lee JE, Xu ZY, Geem KR, Kwon Y, Park JW, Hwang I. (2015) Nat Commun. 6:6843
- Fibrillin 5 is essential for plastoquinone-9 biosynthesis by binding to solanesyl diphosphate synthases in Arabidopsis. Kim EH, Lee Y, Kim HU (2015) Plant Cell 27(10):2956-71

TOC

Spain

José Luis Micol (jlmicol@umh.es) Universidad Miguel Hernández, Elche, Spain; Ana I. Caño-Delgado (ana.cano@cragenomica.es) Centre de Recerca en Agrigenòmica, Barcelona, Spain

Conferences and Workshops

- The PhD School on Environmental Regulation of Plant Development' was held on 17-19 May 2016 in Valencia (Spain), organized by M.A. Blázquez and D. Alabadí.

Selected Publications

- S-nitrosylation triggers ABI5 degradation to promote seed germination and seedling growth. Albertos P, Romero-Puertas MC, Tatematsu K, Mateos I, Sánchez-Vicente I, Nambara E, Lorenzo O (2015) Nature Communications 6, 10.
- Calcium-dependent oligomerization of CAR proteins at cell membrane modulates ABA signaling. Diaz M, Sanchez-Barrena MJ, Gonzalez-Rubio JM, Rodriguez L, Fernandez D, Antoni R, Yunta C, Belda-Palazon B, Gonzalez-Guzman M, Peirats-Llobet M, Menendez M, Boskovic J, Marquez JA, Rodriguez PL, Albert A (2016) Proceedings of the National Academy of Sciences USA 113, E396-E405.
- Red light-mediated degradation of CONSTANS by the E3 ubiquitin ligase HOS1 regulates photoperiodic flowering in Arabidopsis. Lazaro A, Mouriz A, Piñeiro M, Jarillo JA (2015) Plant Cell 27, 2437-2454.
- ELF3-PIF4 interaction regulates plant growth independently of the Evening complex. Nieto C, López-Salmerón V, Davière JM, Prat S (2015) Current Biology 25, 187-193.
- Arabidopsis MAS2, an essential gene that encodes a homolog of animal NF-kappa B Activating Protein, is involved in 45S ribosomal DNA silencing. Sánchez-García AB, Aguilera V, Micol-Ponce R, Jover-Gil S, Ponce MR (2015) Plant Cell 27, 1999-2015.
- A hierarchical multi-oscillator network orchestrates the Arabidopsis circadian system. Takahashi N, Hirata Y, Aihara K, Mas P (2015) Cell 163, 148-159.
- A bHLH-Based Feedback Loop Restricts Vascular Cell Proliferation in Plants. Vera-Sirera F, De Rybel B, Úrbez C, Kouklas E, Pesquera M, Álvarez-Mahecha JC, Minguet EG, Tuominen H, Carbonell J, Borst JW, Weijers D, Blázquez MA (2015) Developmental Cell 35, 432-443.

Major Funding Sources

About 80 grants from the Ministry of Economy and Competitiveness of Spain fund Arabidopsis research projects at individual laboratories. An European Research Council consolidator grant has been awarded to Ana I. Caño-Delgado to work on drought resistance in crops and Arabidopsis. Authors from laboratories studying Arabidopsis in Spain published about 400 papers in the last year.

Sweden

Maria E. Eriksson (maria.eriksson@umu.se) Umeå University, Umeå Plant Science Centre, Umeå

General Activities

Arabidopsis Research Facilities

There is a large community of researchers using Arabidopsis as plant model system, it is spread between more than ten Universities in Sweden. The research topics range from developmental and cell biology to ecological mechanisms. Hence, Arabidopsis is the model species of choice to address basic questions of plant growth and development, photosynthesis and stress related topics. In recent years, ecological themed work has included local adaptation of *Arabidopsis thaliana* accessions across vast latitudinal clines from Southern Europe to the North of Sweden.

Major sites of Arabidopsis research are (from South to North):

- Lund University, Department of Biology (http://www4.lu.se/molecular-plant-biology) and the plant research resource in Southern Sweden 'Plant Link' (http://www.plantlink.se/) coordinate plant research at Lund University and University of Agricultural Sciences (SUAS) in Alnarp (http://www.slu.se/en/faculties/ltv/) with a focus on bringing basic and applied work on Arabidopsis and crops together.
- Gothenburg University, Department of Biological and Environmental Sciences (http://bioenv.gu.se/english/research/physiology-and-cell-biology/plant-cell-and-molecular-biology)
- Örebro University, Life Science Centre, Molecular Biochemistry (https://www.oru.se/english/research/research-environments/ent/lsc/)
- The Linnean Centre (http://lcpu.se/), comprising Departments at Uppsala University and SUAS in Uppsala
- The Evolutionary Biology Centre (http://www.ebc.uu.se/), Uppsala University, Uppsala
- Umeå Plant Science Centre UPSC (http://www.upsc.se/) comprising Departments at Umeå University and SUAS in Umeå

Current Arabidopsis Projects

There are several ongoing, larger projects awarded in which Arabidopsis is used as the major model system. For an orientation see individual Centres as listed above.

Outlook on Arabidopsis Research

All listed major funding bodies (below), regularly advertise open calls where Arabidopsis research qualifies for funding. However, there is a trend favouring applied research, and there are an increase in specific grant calls which emphasize the need for 'products' for the stakeholders. Hence, more funding will support plant research projects in the area of Agriculture and of Forest Biotechnology with emphasis, for instance, on research aimed at crop plant disease and protection or fiber and energy related research.

Road Map Related Activities

Arabidopsis Tools and Resources

National resources used by the Arabidopsis research community:

- Max Lab hosted by Lund University (http://www.maxlab.lu.se/maxlab), a facility dedictated to high-throughput, nanovolume characterization and crystallization of biological macromolecules
- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government (http://www.scilifelab.se)
- Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis (http://www.upsc.se), found under "resources"
- The Swedish Metabolomics Centre in Umeå is a national resource (http://www.swedishmetabolomicscentre.se/)
- The Swedish National Infrastructure for Computing (SNIC, http://www.snic.vr.se/)

Outreach Activities

The major plant science centres across Sweden regularly host outreach activities such as 'Fascination of Plants Day', and other activities to increase interest in plants. On the ongoing issue on genetically modified plants, The Swedish Board of Agriculture has prompted by questions from scientists in Umeå and Uppsala in Sweden said that some plants in which the genome has been edited using the CRISPR-Cas9 technology do not fall under the European GMO definition. For information see for example http://www.upsc.se/about-upsc/news/4815-green-light-in-the-tunnel-swedish-board-of-agriculture-a-crispr-cas9-mutant-but-not-a-gmo.html.

Conferences and Workshops

- 2015, 9-13 August, Plant Biology Scandinavia, the 26th Congress of the Scandinavian Plant Physiology Society (SPPS), Stockholm, Sweden
- 2016, 24-25 February, The Umeå renewable energy meeting, UPSC, Umeå

Upcoming meetings:

- 2017, 3-6 July, Society of Experimental Biology Symposium, Gothenburg, Sweden
- 2017, 8th International Symposium on Root Development, Umeå, Sweden

Selected Publications

About 90 papers of primary work using Arabidopsis spanning from theoretical analysis, plant development and physiology to molecular ecology were published during the last year, with Swedish scientists as lead or co-authors. Highlights are listed below.

- Chromatin assembly factor CAF-1 represses priming of plant defence response genes. Mozgová I, Wildhaber T, Liu Q, Abou-Mansour E, L'Haridon F, Métraux J-P, Gruissem W, Hofius D, Hennig L (2015) Nature Plants 1:15127
- Intercellular communication in *Arabidopsis thaliana* pollen via AHG3 transcript movement from the vegetative cell to sperm. Jiang H, Yi J, Boavida LC, Chen Y, Becker JD, Köhler C, McCormick S (2015) Proc Natl Acad Sci U S A 112(43):13378-83
- The Multi-allelic genetic architecture of a variance-heterogeneity locus for molybdenum concentration in leaves acts as a source of unexplained additive genetic variance. Forsberg SK, Andreatta ME, Huang XY, Danku J, Salt DE, Carlborg Ö (2015) PLoS Genet 11(11):e1005648
- Cell-type-specific cytokinin distribution within the Arabidopsis primary root apex. Anatoniadi I, Plačková L, Simonovik B, Doležal K, Turnbull C, Ljung K, Novák O (2015) Plant Cell 27(7):1955-67
- Gibberellic acid signaling is required for ambient temperature-mediated induction of flowering in *Arabidopsis thaliana*. Galvão VC, Collani S, Horrer D, Schmid M (2015) Plant J 84(5):949-62

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)
- The Royal Academy of Agriculture and Forestry (http://www.ksla.se)
- The Swedish Research Council Formas (http://www.formas.se) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.

- The Wallenberg Foundations (http://www.wallenberg.com) 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

Switzerland

Kentaro K. Shimizu (kentaro.shimizu@ieu.uzh.ch) and Misako Yamazaki (misako.yamazaki@ieu.uzh.ch), University of Zurich
Zurich-Basel Plant Science Center (info-plantscience@ethz.ch)

General Activities

Arabidopsis Research Facilities

- Swiss Plant Science Web (Swiss-wide network of plant science, https://swissplantscienceweb.ch/)

It is composed of Zurich-Basel Plant Science Center (competence center linking and supporting the plant science research community of the University of Zurich, ETH Zurich and the University of Basel, http://www.plantsciences.uzh.ch/index.html), Arc lémanique plant science (http://www.unil.ch/alps/home.html), and BeNeFri network.

- Functional Genomics Center Zurich (e.g. genome sequencing of *Arabidopsis halleri*)
- Genetic Diversity Center (e.g. genome-wide polymorphisms of *Arabidopsis halleri*)

Current Arabidopsis Projects

Plant research projects and researchers are listed at the website of Swiss Plant Science Web: https://swissplantscienceweb.ch/research/research-portfolios/, https://swissplantscienceweb.ch/research/researchers/

There are a large number of projects supported by Swiss National Science Foundation.

PLANT FELLOWS is an international post doc fellowship programme in the field of plant sciences co-funded by the SEVENTH FRAMEWORK PROGRAMME (FP7) Marie Curie Actions – People, Co-funding of Regional, National and International Programmes (COFUND). It is chaired by Prof. Ueli Grossniklaus and run by the Zurich-Basel Plant Science Center. PLANT FELLOWS offers capacity for +49 new post-doctoral fellowships of average 24 – 36 months each spread between three different schemes (incoming, outgoing and reintegration), between 2012 until February 2016 on Arabidopsis and other plants. The EU will contribute 40% (EUR 4,994,000) to the fellowship program while 60% is co-funded by the host organization, i.e. the hosting principal investigators. The program is accompanied by a structured training program, including workshops, dedicated training in complementary skills and industrial placements. PLANT FELLOWS has established a qualification framework in the area of life-long learning/continuous education, which complements the present postdoctoral training in plant sciences with an international competitive dimension.

IDP BRIDGES is an Innovative Doctoral Program supporting 14 PhD students for working in the most challenging areas of plant sciences. In IDP BRIDGES, a cohort of 14 PhD fellowships - funded by 7th Framework Programme of the European Union for 36 months - is linked to the training program Science & Policy.

SystemsX.ch

PlantGrowth2 In a Changing Environment, Apr. 2013 – Mar. 2017 (http://www.systemsx.ch/projects/research-technology-and-development-projects/plantgrowth2/)

MecanX Understanding Physics of Plant Growth, Apr. 2013 – Mar. 2017 (http://www.systemsx.ch/projects/research-technology-and-development-projects/mecanx/)

Outlook on Arabidopsis Research

The National Centre of Competence in Research (NCCR) “Plant Survival – Plant Survival in Natural and Agricultural Ecosystems” finished in 2013. It would be valuable for proposing Arabidopsis related researches in the next calls.

Road Map Related Activities

Arabidopsis Tools and Resources

- Further development of Genevestigator database (Zimmerman et al. 2014)
- Swiss-Prot database contributes to TAIR database
- Schmid, M.W. and Grossniklaus, U. (2015) Rcount: simple and flexible RNA-Seq read counting. Bioinformatics 31, 436-437.
- Geiser C, Mandakova T, Arrigo N, Lysak MA & Parisod C. (2016) Repeated whole-genome duplication, karyotype reshuffling and biased retention of stress-responding genes in Buckler Mustard. Plant Cell 28: 17-27.

Outreach Activities

- Plant Science Center Discovery Program for Youth (Supported by AGORA of Swiss National Science Foundation) (2015-)
- Gen Suisse program (http://www.gensuisse.ch/) for high school students in French, “Agriculture from the Garden of Eden to GMOs” by Prof. Christian Fankhauser
- Continuing Education Program in Plant Sciences for Secondary School Teachers

http://www.plantsciences.uzh.ch/outreach/atschool.html

Plant research was a missing element in continuing education and is, therefore, very well received by the teachers and collaborators in the regional learning centers. At the interface we now offer several workshops with an innovative format, topics at the forefront of current plant science research but well linked to the curricula of secondary schools, exchange with active researchers in interactive discussion, robust teaching material that can be transferred easily to classroom teaching, and guidance and support through our flying trainer during and after the workshop. Topics have been discussed with teachers before setting up the training to make sure that they are meeting the requirements of teachers and school classes. Participation in our workshops is fully accredited as continuing education in the teacher’s portfolio.

- Plant Molecular Biology II: Angewandte evolutionsforschung mit Gemüse aus dem Supermarkt (2), Evolution du Broccoli (Development in 2014 / first time offered in Dec 2014) (WS V)

Conferences and Workshops

- SwissPlant Symposium 2016, LesDiablerets, Switzerland, 25-27 Jan 2016
- Plant lectures at the latest Lausanne Genomics Days http://www.genomyx.ch/thu-feb-18-fri-feb-19-2016-lausanne-genomics-days-2016/
- PSC Summer school, Tackling Wicked Problems, Zurich-Basel Plant Science Center, 21-25 Sept 2015
- Frontiers in Plant Sciences Courses Series

Selected Publications

- Adaptation of Root Function by Nutrient-Induced Plasticity of Endodermal Differentiation. Barberon M, Vermeer JE, De Bellis D, Wang P, Naseer S, Andersen TG, Humbel BM, Nawrath C, Takano J, Salt DE, Geldner N (2016) Cell 28;164(3):447-59
- Functional overlap of the Arabidopsis leaf and root microbiota. Bai Y, Müller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, Dombrowski N, Münch PC, Spaepen S, Remus-Emsermann M, Hüttel B, McHardy AC, Vorholt JA, Schulze-Lefert P (2015) Nature. 17;528(7582):364-9
- Abscisic acid transporters cooperate to control seed germination. Kang J, Yim S, Choi H, Kim A, Lee KP, Lopez-Molina L, Martinoia E, Lee Y (2015) Nat Commun. 3;6:8113
- Evolution of selfing: recurrent patterns in molecular adaptation. Shimizu, K.K., Tsuchimatsu, T (2015) Annu. Rev. Ecol. Evol. Syst. 46, 593-622
- Balancing of B6 vitamers is essential for plant development and metabolism in Arabidopsis. Colinas M, Eisenhut M, Tohge T, Pesquera M, Fernie AR, Weber AP, Fitzpatrick TB (2016) Plant Cell. 28(2):439-53

Major Funding Sources

Swiss National Science Foundation

European Research Council (ERC)

SystemsX.ch

EU Cofund "Plant Fellows" run by the Zurich-Basel Plant Science Center (see above)

Syngenta (Plant Science Center - Syngenta Fellowship)

Human Frontier Science Project

Research and Innovation Staff Exchange (RISE) of European Commission

State Secretariat for Education, Research, and Innovation (SERI)

United Kingdom

Geraint Parry (geraint@garnetcommunity.org.uk), Cardiff University, UK; Ruth Bastow (ruth@garnetcommunity.org.uk) GARNet, Cardiff University, UK

General Activities

Arabidopsis Research Facilities

The UK has active Arabidopsis research occurring at over 40 academic departments and research institutes. The major funder of this research is the Biotechnology and Biological Science Research Council (BBSRC) who shows continued support of Arabidopsis research as a model for discovery and as a pathway to translation. The BBSRC supports the Nottingham Arabidopsis Stock Centre (uNASC) that, as one of two global stock centres hold over 1 million genotypes and annually supply over 100,000 tubes of seed.

The BBSRC research institutes of the John Innes Centre, Rothamsted Research, the Institute of Biological Environmental and Rural Science (IBERS) and The Genome Analysis Centre (TGAC) have a plant science focus that includes Arabidopsis research. The National Plant Phenomics Centre, NPPC is located at IBERS Aberystwyth. BBSRC also supports CyVerseUK and the Centre for Integrative Biology, CPIB in Nottingham.

The Gatsby Charitable Foundation supports two plant science research institutions. The Sainsbury Laboratory, Norwich) and the Sainsbury Laboratory Cambridge University both have significant Arabidopsis research programmes.

Current Arabidopsis Projects

The majority of UK Arabidopsis grants are awarded to individual research groups, although the BBSRC also funds a number of 'Networks in Industrial Biotechnology and Bioenergy' (NIBB) that have the aim of encouraging the translation of fundamental research, most of which is occurring in Arabidopsis. These NIBBs include the 'High Value in Chemicals Network (http://hvcfp.net/)' and the 'Lignocellulosic Biorefinery Network (http://lb-net.net/)'

By mid-2016 the BBSRC funds almost 100 active individual research grants that include most aspects of Arabidopsis research, awarded to over 75 different academics. This amounts to over £39million of support.

Since the start of 2015 there have been 35 grants awarded to a value of £15.3million. Amongst these recent grants, highlights include:

- £540K: EpiSpiX - Unlocking plant genetic diversity via epimodification & targeted recombination. Ian Henderson (University of Cambridge). http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN007557%2f1

- £778K: Diversifying Transcription Termination Function. Gordon Simpson (James Hutton Institute at University of Dundee). http://gtr.rcuk.ac.uk/project/B3D5249E-D3F9-4641-9A64-3798E7F39DB4
- £320K: Mechanisms involved in plant resistance to the green peach aphid *Myzus persicae*. Saskia Hogenhout (John Innes Centre). http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB%2fN009169%2f1
- £440K: Bilateral NSF/BIO-BBSRC: Modelling Light Control of Development. Karen Halliday (University of Edinburgh) http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB/M025551/1
- £583K: Bilateral NSF/BIO-BBSRC - Translational landscape to link cell growth with proliferation in the root meristem. Laszlo Bogre (Royal Holloway, University of London). http://www.bbsrc.ac.uk/research/grants-search/AwardDetails/?FundingReference=BB/M025047/1

UK-based Arabidopsis researchers have also benefited from individual grants from the EU, Levi Yant (John Innes Centre), Yiliang Ding (John Innes Centre) and Steven Spoel (University of Edinburgh) gained ERC Starting Grants whilst Kirsten Bomblies (John Innes Centre) and Ian Henderson (University of Cambridge) were successful in their applications for ERC Consolidator grants.

The BBSRC has provided significant support for UK Synthetic Biology, in which a number of Arabidopsis researchers have generated tools to aid discovery and translation. Notably BBSRC funded the OpenPlant Synthetic Biology Centre (www.openplant.org/) as well as the recently established Synthetic Biology Centres that include Arabidopsis researchers in their research membership (SynthSysEd, BrisSynBio).

PhD Studentships to support Arabidopsis research are largely provided through 'Doctoral Training Programs (DTP)' that offer grants on a competitive basis within consortium of usually geographically similar areas. Therefore this provides excellent opportunities to train the next generation of plant scientists.

Outlook on Arabidopsis Research

Over the past four years the BBSRC funding provided to Arabidopsis-focused grants has been maintained (£10M, 2015; £21M, 2014; £10M, 2013; £11.5M, 2012) indicating that fundamental research remains an important part of BBSRC research funding. Researchers have adapted well to a changing funding requirement that requires greater translation of fundamental research. The involvement of Arabidopsis researchers with BBSRC NIBBs and Synthetic Biology programs indicates that they are embracing the new areas of research.

In late 2016 the UK Plant Science Federation intend to publish a 'Roadmap for UK Plant Science', which will aim to influence government policy and funding priorities in this area. It will recommend that aspects of the UK bioeconomy dependent on plant science require the maintainance of close links between basic academic research and potential industrial partners. The report will state that erosion of this basic research base will have a significant detrimental effect on UK productivity in this area.

Road Map Related Activities

Arabidopsis Tools and Resources

- Release of the new Arabidopsis Genome Annotation, ARAPORT11. Gos Micklem (University of Cambridge) is part of the Arabidopsis Information Portal team that has developed this improved annotation along with a host of other analysis tools (https://www.araport.org/)
- BioDare (Biological Data Repository) is an online resource for the sharing, processing and analysis, with the main focus on timeseries data produced in circadian experiments. This resource was developed by a consortium of researchers from Edinburgh SynthSys (https://www.biodare.ed.ac.uk/robust/)
- CPIB continues to add to their portfolio of supplying publicly-available software, hardware and database resources that are useful for a wide range of plant scientists (https://www.cpib.ac.uk/tools-resources/)
- Paul Knox (University of Leeds) continues to develop antibodies targeted against components of the plant cell wall and are available at the not-for profit PlantProbes (http://www.plantprobes.net)
- Nicola Patron (The Sainsbury Lab, Norwich) led a broad selection of researchers, including those from ENSA, RIPE and C4 Gates-funded projects who recommended 'Standard Plant Synthetic Biology: a common syntax for exchange of DNA parts' (http://onlinelibrary.wiley.com/doi/10.1111/nph.13532/full)
- Gordon Simpson (James Hutton Institute, Dundee) was involved in setting up the PolyAdb database that provides access to information that has been generated by Direct RNA sequencing about polyadenylation sites in Arabidopsis genes. (https://www.compbio.dundee.ac.uk/polyADB/)

Outreach Activities

- The BBSRC-funded GARNet community network continues to support UK plant science by providing regular updates regarding new developments that involve Arabidopsis research. This is provided via the @GARNetweets feed, the 'Weeding the Gems' blog (http://blog.garnetcommunity.org.uk/), the GARNet website (http://www.garnetcommunity.org.uk/) and through the ArabUK email group. The dissemination of a weekly Arabidopsis Research Roundup provides an update on newly published papers and includes occasional audio-descriptions by leading academics. The bi-annual GARNish newsletter continues to inform the worldwide community about recent events and technical developments (http://www.garnetcommunity.org.uk/newsletters). GARNet has collaborated with the Gatsby Foundation to provide £500 travel grants for UK-based PhD students to attend the ICAR2016

- In May 2015, many UK research groups participated in worldwide Fascination of Plants day, which connected plant scientists with 1000s of members of the public: http://goo.gl/NlUWKf
- The BBSRC engaged a media company to create videos focusing on excellence in UK Plant Science, including descriptions of research that began in Arabidopsis: https://goo.gl/L2Uknr
- CPIB continued to encourage interaction between different research areas with their organisation of the '7th Mathematics in the Plant Sciences Study Group (MPSSG)'.

Conferences and Workshops

- In September 2015 GARNet and OpenPlant collaborated to organise a workshop on CRISPR/Cas that brought together many Arabidopsis researchers to learn hands-on approaches to this important technology. A commentary piece resulting from the meeting was recently published: Parry et al. Plant Methods (2016) 12:6 DOI 10.1186/s13007-016-0104-z
- The OpenPlant consortium organised an inaugural OpenPlantForum that presented exciting aspects of plant SynBio including examples of use of Arabidopsis as a chassis for synthetic biology approaches
- In 2016 GARNet will organise three workshops that will bring together Arabidopsis researchers from the UK and beyond:

  - April: Integrating Large Data into Plant Science: From Big Data to Discovery, Exeter: http://goo.gl/eHBZOM

  - September: GARNet2016- Innovation in the Plant Sciences, Cardiff: http://garnet2016.weebly.com/

  - December: Natural Variation as a tool for gene discovery and crop improvement, Cambridge: http://garnetnatvar2016.weebly.com/
- In April 2016 both 'The Sainsbury Lab, Cambridge University ' and the UK Plant Science Federation (UKPSF) organised meetings that brought together Arabidopsis researchers under the more general topics of 'Induced Plant Development' and 'Plants in a changing world: molecule to ecosystem' respectively.
- The Society for Experimental Biology's annual conference will be held in Brighton in the UK in July 2016.

Selected Publications

During 2015 UK researchers published over 150 papers that involved work on Arabidopsis, 70% of which were Open Access. These are some selected highlights:

- A Plant Immune Receptor Detects Pathogen Effectors that Target WRKY Transcription Factors. Sarris PF, Duxbury Z, Huh SU, Ma Y, Segonzac C, Sklenar J, Derbyshire P, Cevik V, Rallapalli G, Saucet SB, Wirthmueller L, Menke FL, Sohn KH, Jones JD (2015) Cell 161:1089-1100 http://dx.doi.org/10.1016/j.cell.2015.04.024
- The circadian clock rephases during lateral root organ initiation in *Arabidopsis thaliana*. Voß U, Wilson MH, Kenobi K, Gould PD, Robertson FC, Peer WA, Lucas M, Swarup K, Casimiro I, Holman TJ, Wells DM, Péret B, Goh T, Fukaki H, Hodgman TC, Laplaze L, Halliday KJ, Ljung K, Murphy AS, Hall AJ, Webb AA, Bennett MJ (2015) Nature Communication 6:7641. http://dx.doi.org/10.1038/ncomms8641
- Monodehydroascorbate reductase mediates TNT toxicity in plants. Johnston EJ, Rylott EL, Beynon E, Lorenz A, Chechik V, Bruce NC (2015) Science 349:1072-1075. http://dx.doi.org/10.1126/science.aab3472
- Lin Z, Eaves DJ, Sanchez-Moran E, Franklin FC, Franklin-Tong VE (2015) The *Papaver rhoeas* S determinants confer self-incompatibility to *Arabidopsis thaliana* in planta Science 350(6261):684-7 http://dx.doi.org/10.1126/science.aad2983
- The MYB36 transcription factor orchestrates Casparian strip formation. Kamiya T, Borghi M, Wang P, Danku JM, Kalmbach L, Hosmani PS, Naseer S, Fujiwara T, Geldner N, Salt DE (2015) Proc Natl Acad Sci USA. 112 (39):12099-12104. http://dx.doi.org/10.1073/pnas.1507691112

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

Engineering and Physical Sciences Research Council
http://www.epsrc.ac.uk

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

The Gates Foundation

http://www.gatesfoundation.org/

TOC

United States

Joanna Friesner (jdfriesner@ucdavis.edu), University of California, Davis, NAASC Coordinator, with input by Keiko Torii, NAASC President, University of Washington (ktorii@u.washington.edu), Siobhan Brady, Sarah Assmann, Erich Grotewold, Doris Wagner, Rick Vierstra, Elizabeth Haswell and Jose Dinneny.

General Activities

Arabidopsis Research Facilities

There are a large number of US institutions, companies, and facilities that conduct Arabidopsis research and it would be impossible to list them all within the report's space restrictions. Therefore we list ABRC, the US stock center which, in partnership with NASC, the European Stock Centre (UK) and RIKEN BioResourceCenter (Japan), provide valuable Arabidopsis seed (and other) resources to the global community:

The Arabidopsis Biological Resource Center (ABRC) collects, preserves, reproduces and distributes diverse seed and other stocks of *Arabidopsis 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.

Current Arabidopsis Projects

There are a large number of US Arabidopsis projects that include many partners and encompass a vast array of topics. It would be impossible to parse out the 'major projects' within the report's space restrictions; therefore we list four NAASC-initiated and/or led community consortium proposals that focus on: (1) Research and training for plant biology in the 21st Century; (2) the Arabidopsis reference genome and related resources (3) International collaboration and cooperation for informatics efforts and resources and (4) US and international collaboration to prioritize goals and research needs aimed at efficiently deciphering how chromatin and epigenetic regulation at the genome level controls plant form and function.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; http://1.usa.gov/25ys7ao

(2) NSF Award #1262414 (PI C. Town, Co-PIs G. Micklem, M. Vaughn, A. Chan, J. Miller, K. Krampos) ABI Development: The Arabidopsis Information Portal; Sept. 2013- Aug. 2018; http://1.usa.gov/1P5IB09

(3) NSF Award #1062348 (PI B. Meyers, CoPIs E. Grotewold, V. Brendel D. Ware) RCN: An International Arabidopsis Informatics Consortium; June 2011-May 2016; http://1.usa.gov/1Pked7H

(4) NSF Award #0925071 (PI D. Wagner, Co-PIs C. Pikaard, R. Martienssen) RCN: Establishment of an Epigenomics of Plants International Consortium (EPIC); April 2010-March 2016; http://1.usa.gov/25B55D4

Outlook on Arabidopsis Research

NAASC recently recommended a comprehensive reassessment of training needs for 21st century plant biology to meet the evolving demands of careers in the life sciences. NAASC member Siobhan Brady submitted a 5-year funding proposal to the US National Science Foundation (1) which was awarded in June 2015. The Research Collaboration Network (RCN) focuses on convening US plant biologists with experts from computational, quantitative, and diverse education-oriented fields in the US to consider and evaluate the changing training needs for 21st century plant biology; activities will include participation of international collaborators. The challenge for Arabidopsis researchers, and all biologists, is to study and understand the complexity of biological systems, new datatypes and the myriad large datasets that are increasingly available; this will require a larger focus on quantitative, systems and computational approaches in combination with biological experimentation. Furthermore, with global climate instability and worldwide agricultural crises, an important mission of plant biologists is to carry out plant research in economically important crop species to ensure agricultural sustainability. Concurrently, non-academic 21st century biology careers will continue to grow and outnumber those in academia while the US student population will continue to increase in diversity, mirroring larger national trends. Therefore new training and educational approaches are necessary. The NAASC-led series of collaborative activities in the RCN focuses on three key aspects of training and research approaches: (1) identification of emerging technologies using Arabidopsis, including strong integration of wet-lab, computational, quantitative, and bioinformatic approaches; (2) enhancement of interdisciplinary training of biologists for academic and non-academic careers; and (3) increasing the diversity of US plant biology researchers using targeted mechanisms.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; http://1.usa.gov/25ys7ao

Road Map Related Activities

Outreach Activities

- ICAR 2016 (Korea): (1) NAASC will fund participation of 11 US scientists in the 27th ICAR being held this June in South Korea. As in past years, NAASC will provide funding and travel scholarships to enable ICAR participation by 7 early-career US scientists and groups under-represented in US science (2 additional NAASC members will attend). These 'ambassadors' from the US will interact with the international community and further goals for diversity and excellence in US science and international collaboration and cooperation. (2) NAASC members will organize or participate in two community workshops at ICAR 2016: (A) NAASC member Siobhan Brady will co-lead (with Cranos Williams) an RCN (1) workshop entitled "Emerging Genomics Techniques and the Future of Research using *Arabidopsis thaliana*". Scheduled presentations include: Doris Wagner, University of Pennsylvania, "Speeding up discovery: from genomic data to mechanism and traits"; Bob Schmitz, University of Georgia, "Methods for mapping epigenomes from samples with limited starting material"; Nicola J. Patron, The Sainsbury Lab, "Expanding and improving the plant genome engineering toolbox"; Cranos Williams, North Carolina State University, "Engineering Computational and Analytical Solutions for Plant Systems Research". (B) NAASC member Doris Wagner is a presenter in the "Epigenetics and Environmental Stress" workshop co-organized by June Kwak and Yun Ju Kim. Doris will also give a presentation in the NAASC workshop.
- January 2016: Joanna Friesner, NAASC Coordinator, presented an outreach seminar entitled 'Community collaborations: Advancing Arabidopsis Research and Training (ART-21) and the International Arabidopsis Informatics Consortium' during the Plant and Animal Genomes Conference in San Diego, USA. A pdf of the presentation is publicly available for viewing or downloading at http://bit.ly/1QfMh4V
- July 2015: NAASC members Siobhan Brady and Joanna Friesner held an interactive RCN (1) workshop at ICAR 2015 (Paris) entitled 'Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology". The workshop included presentations and an interactive panel discussion on the bioinformatics and computational skills needed by plant scientists in the 21st century, and the bottlenecks or barriers to providing these skills to students, postdoctoral scholars and faculty. The workshop was attended by approximately 150 participants and a survey was distributed at the end of the workshop asking attendees to list the key skills and barriers. The results from the approximately 50 students and postdocs that responded are: Key bioinformatic, quantitative, or computational skills they wanted to learn (in order from most to least desired): (1) Computer programming, (2) statistical analysis, (3) modeling, (4) data analysis, and (5) fundamental mathematics. Biggest obstacles to obtaining these skills (in order from biggest to smallest obstacle): (1) Lack of time since their work is primarily wet-lab, (2) lack of fundamental knowledge (their education did not include programming, modeling, advanced math or statistical analysis), (3) a rapidly changing field makes it challenging to keep up, (4) lack of access to relevant training or coursework, and (5) their PI doesn't prioritize them to do non-wet-lab work.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; http://1.usa.gov/25ys7ao

Conferences and Workshops

May 2016 (Arizona, USA): NAASC RCN - (1) Steering Committee members Siobhan Brady, Joanna Friesner, Blake Meyers, and Nick Provart convened the first NAASC RCN focus group with 35 participants entitled "Computational training of plant biologists for academia and industry in the 21st Century". The over-arching questions for the focus group to consider were: (A) What are the bioinformatics and computational skills needed by plant scientists of the 21st century to deal with more complex datasets (predictive, quantitative and theory-driven)? (B) What are the bottlenecks to providing students with the needed skills? (C) What do employers (of various types) need/want from employees; what are marketable skills in this area? The key topics were:

(i) **Training and Education**: Skills needed for positions: Industry Positions; Faculty Positions; Undergraduate, Graduate and Postdoc Education (ii) **Collaborations**: Working with a biologist: a quantitative expert's perspective; Working with a quantitative expert: a biologist's perspective; Retraining: Yourself; From a funding perspective (iii) **Training Arabidopsis Biologists for High-Throughput Phenotyping**; and (iv) **Translating from Arabidopsis to Crop Species, and Vice Versa**. A workshop white paper with recommendations and analysis will be forthcoming.

June 2016: NAASC community workshop scheduled for ICAR 2016 (Korea) - "Emerging Genomics Techniques and the Future of Research using *Arabidopsis thaliana*"; see 'Outreach' section.

July 2015: NAASC community workshop held at ICAR 2015 (Paris) - "Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology" see 'Outreach' section.

(1) NSF Award #1518280 (PI S. Brady, Co-PI J. Friesner) RCN: Arabidopsis Research and Training for the 21st century (ART-21); June 2015-May 2020; http://1.usa.gov/25ys7ao

Selected Publications

50 years of Arabidopsis research: highlights and future directions. Provart NJ, Alonso J, Assmann SM, Bergmann D, Brady SM, Brkljacic J, Browse J, Chapple C, Colot V, Cutler S, Dangl J, Ehrhardt D, Friesner JD, Frommer WB, Grotewold E, Meyerowitz E, Nemhauser J, Nordborg M, Pikaard C, Shanklin J, Somerville C, Stitt M, Torii KU, Waese J, Wagner D, McCourt P (2016) New Phytol. 209(3):921-44.

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HHMI-GBMF: http://news.sciencemag.org/2011/06/biomedical-institute-adds-15-plant-biologists-its-roster; https://www.hhmi.org/scientists
Bill and Melinda Gates Foundation: http://www.gatesfoundation.org/

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@jcvi.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)

Ian Small
The University of Western Australia, Australia
ian.small@uwa.edu.au

Christopher Town
J. Craig Venter Institute, US
cdtown@jcvi.org

Epigenenetics and Epigenomics

Doris Wagner
University of Pennsylvania, US
(chair)
wagnerdo@sas.upenn.edu

Craig Pikaard
Indiana University, US
(co-chair)
cpikaard@indiana.edu

Rob Martienssen
Cold Spring Harbor Laboratory, US
(co-chair)
martiens@cshl.edu

Metabolomics

Kazuki Saito
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

Robert Furbank
CSIRO Plant Industry Canberra, Australia
Robert.Furbank@csiro.au
(Co-chair until 2015)

Fabio Fiorani
Forschungszentrum Jülich, Germany
f.fiorani@fz-juelich.de
(Co-Chair)

Christine Granier
INRA-SUPAGRO, France
granier@supagro.inra.fr
(Co-Chair)

Justin Borevitz
Australian National University, Australia
justin.borevitz@anu.edu.au

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

Gloria Coruzzi
New York University, US
gc2@nyu.edu

Pascal Falter-Braun
Technische Universität München, Germany
pbraun@wzw.tum.de

Rodrigo A. Gutiérrez
Pontificia Universidad Católica de Chile, Chile
rgutierrez@bio.puc.cl

Gabriel Krouk
Centre National de la Recherche Scientifique, CNRS, France
krouk@supagro.inra.fr

Susannah Lydon
University of Nottingham, UK
susannah.lydon@nottingham.ac.uk

TOC

Members of the Multinational Arabidopsis Steering Committee

Loïc Lepiniec
INRA, France
Loic.Lepiniec@versailles.inra.fr
(MASC Chair, Representing France)

Inhwan Hwang
Pohang University of Science and Technology, South Korea
ihhwang@postech.ac.kr
(MASC Co-chair, Representing South Korea)

Marília K. F. de Campos
University of Tübingen, Germany
marilia.campos@zmbp.uni-tuebingen.de
(MASC coordinator, Representing Germany)

Wagner Araújo
Universidade Federal de Viçosa, Brazil
wlaraujo@ufv.br
(Representing Brazil)

Ruth Bastow
GARNet, Cardiff University, UK
ruth@garnetcommunity.org.uk
(Representing UK)

María Francisca Blanco
Universidad Andrés Bello
mblanco@unab.cl
(Representing Chile)

Dario Bonetta
University of Toronto, Canada
dario.bonetta@uoit.ca
(Representing Canada)

Lynette Brownfield
University of Otago, New Zealand
lynette.brownfield@otago.ac.nz
(Representing New Zealand)

Ana I. Caño-Delgado
Centre for Research in Agricultural Genomics, Spain
ana.cano@cragenomica.es
(Representing Spain)

Maura Cardarelli
IBPM-CNR c/o Sapienza Università di Roma, Italy
maura.cardarelli@uniroma1.it
(Representing Italy)

Sacco De Vries
Wageningen University, Netherlands
sacco.devries@wur.nl
(Representing Netherlands)

Maria E. Eriksson
Umeå University, Sweden
maria.eriksson@umu.se
(Representing Sweden)

Joanna D. Friesner
University of California, US
jdfriesner@ucdavis.edu
(Representing US/NAASC, IAIC coordinator)

Rodrigo A. Gutiérrez
P. Universidad Católica de Chile
rgutierrez@bio.puc.cl
(Representing Chile)

Klaus Harter
University of Tübingen, Germany
klaus.harter@zmbp.uni-tuebingen.de
(Representing Germany)

Polydefkia Hatzopoulos
Agricultural University of Athens, Greece
phat@aua.gr
(Representing Greece)

Marie-Theres Hauser
University of Natural Resources and Applied Life Sciences BOKU, Austria
marie-theres.hauser@boku.ac.at
(Representing Austria)

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

Minami Matsui
Center for Sustainable Resource Science, Japan
minami@riken.jp
(Representing Japan)

José Luis Micol
Universidad Miguel Hernández, Elche, Spain
jlmicol@umh.es
(Representing Spain)

Moritz K. Nowack
VIB-Ghent University, Belgium
moritz.nowack@vib.be
(Representing Belgium)

Adriano Nunes-Nesi
Universidade Federal de Viçosa, Brazil
nunesnesi@ufv.br
(Representing Brazil)

Michael Palmgren
University of Copenhagen, Denmark
palmgren@plen.ku.dk
(Representing Denmark)

Geraint Parry
GARNet, Cardiff University, UK
geraint@garnetcommunity.org.uk
(Representing UK)

Catherine Perrot-Rechenmann
CNRS, France
catherine.rechenmann@cnrs-dir.fr
(Representing France)

Barry Pogson
The Australian National University Canberra, Australia
barry.pogson@anu.edu.au
(Representing Australia)

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

Ben Scheres
Wageningen University, Netherlands
ben.scheres@wur.nl
(Representing Netherlands)

Kentaro K. Shimizu
University of Zurich, Switzerland
kentaro.shimizu@ieu.uzh.ch
(Representing Switzerland)

Charles Spillane
National University of Ireland Galway, Ireland
charles.spillane@nuigalway.ie
(Representing Ireland)

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

Keiko Sugimoto
RIKEN Center for Sustainable Resource Science, Yokohama, Japan
keiko.sugimoto@riken.jp
(Representing Japan)

László Szabados
Biological Research Center Szeged, Hungary
szabados@brc.hu
(Representing Hungary)

Michael Wrzaczek
University of Helsinki, Finland
michael.wrzaczek@helsinki.fi
(Representing Finland)

Weicai Yang
Chinese Academy of Sciences, Bejing, China
wcyang@genetics.ac.cn
(Representing China)

Marcelo J. Yanovsky
Instituto Leloir, Argentina
mjyanovsky@gmail.com
(Representing Argentina)

Viktor Žárský
Charles University, Czech Republic
viktor@natur.cuni.cz
(Representing Czech Republic)

Parker Antin
University of Arizona, US
pba@email.arizona.edu
(CyVerse principal investigator)

Tanya Berardini
Phoenix Bioinformatics, US
tberardi@arabidopsis.org
(TAIR scientific curator)

Jelena Brkljacic
The Ohio State University, US
brkljacic.1@osu.edu
(ABRC associate director)

Marcos Castellanos-Uribe
uNASC, Loughborough, UK
marcos.castellanos@nottingham.ac.uk
(uNASC Operations Manager)

Joanna D. Friesner
University of California, US
jdfriesner@ucdavis.edu
(Representing US, IAIC Coordinator)

Erich Grotewold
The Ohio State University, US
grotewold.1@osu.edu
(ABRC director, CAPS director)

Eva Huala
Phoenix Bioinformatics, US
huala@phoenixbioinformatics.org
(TAIR Executive Director)

Masatomo Kobayashi
RIKEN BRC, Japan
kobayasi@rtc.riken.jp
(RIKEN BRC coordinator)

Marcus A. Koch
University of Heidelberg, Germany
marcus.koch@cos.uni-heidelberg.de
(BrassiBase director)

Sean May
uNASC, Loughborough, UK
sean@arabidopsis.info
(Representing U.K., uNASC director)

Blake C. Meyers
University of Missouri, US
bmeyers@danforthcenter.org
(Representing US, Interim IAIC Director)

Roland Pieruschka
Forschungszentrum Jülich, Germany
r.pieruschka@fz-juelich.de
(EPPN/EMPHASIS Project Manager)

Nicholas Provart
University of Toronto, Canada
nicholas.provart@utoronto.ca
(BAR director, Bioinformatics SC chair)

Marcela K. Tello-Ruiz
Cold Spring Harbor Laboratory, US
telloruiz@cshl.edu (Gramene Project Manager)

Chris Town
J. Craig Venter Institute, US
cdtown@jcvi.org
(Araport Project PI)

Doreen Ware
Cold Spring Harbor Laboratory, & USDA-ARS, US
ware@cshl.edu
(Gramene PI)

MASC

www.arabidopsisresearch.org