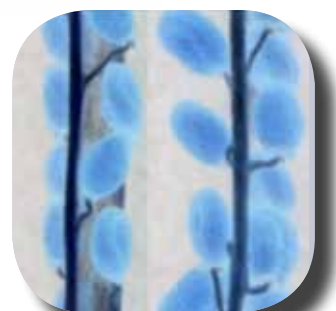
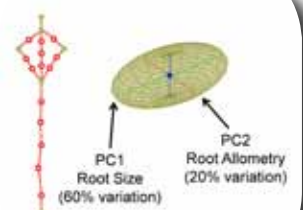
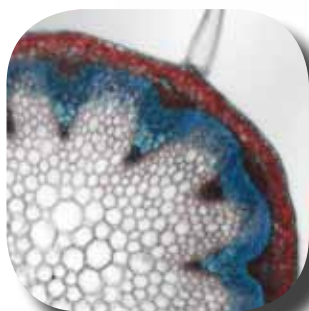


From Bench to Bountiful Harvests

Annual Report

Multinational Arabidopsis Steering Committee (MASC)

2013/2014



The Multinational Arabidopsis Steering Committee

Annual Report 2013/2014

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The Multinational Arabidopsis Steering Committee

July 2014

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Cover images

Arabidopsis plants of different size (top). Courtesy of Eleonora Paparelli (page 39).

Cross section of an Arabidopsis inflorescence stem (bottom left). Lignin, a phenolic polymer in the secondary cell wall of vessel and fiber cells, is visualized in blue by autofluorescence. Image courtesy: Lisa Sundin, Matyas Fendrych and Daniel Van Damme (page 39).

Measurement of Root System Architecture (RSA) (bottom left center). A morphometric approach to measure Root System Architecture (RSA) captures two major sources controlling the variation in both root plasticity and diversity. These quantitative traits were used to map the genes underlying RSA using genome-wide association mapping. Courtesy of Ulises Rosas and Gloria Coruzzi (page 41).

Molecular structure of interacting TIR domains involved in paired Arabidopsis R protein-mediated disease resistance (bottom right center). Loss of TIR/TIR interaction renders the plant susceptible to disease (as illustrated by dying leaf tissue (left)). Simon Williams, Kee Sohn and Daniel Ericsson are responsible for images and design. We thank Bernard Carroll and Uwe Dressel for additional raw images (page 40).

ABCA9, fatty acid transporter at the ER (bottom right). Seeds at mature stage are larger in ABCA9-overexpressing plants (right) than in wild-type plants (left). Courtesy of Dr. Sangwoo Kim (page 43).

Further information

www.arabidopsisresearch.org or www.arabidopsis.org/portals/masc/index.jsp

The MASC report 2013/14 and previous reports are available online at:

MASC, The Multinational Arabidopsis Steering Committee:

<http://arabidopsisresearch.org/index.php/publications/masc-reports>

TAIR, The Arabidopsis Information Resource:

http://www.arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp

NASC, The Nottingham Arabidopsis Stock Centre:

<http://arabidopsis.info/progreports.html>

Dr. Luise Brand and Prof. Dr. Barry Pogson wrote articles with input from Prof. Dr. Nicholas Provart if no author is stated.

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The MASC community has been coordinated by Luise Brand. MASC thanks Luise Brand for overseeing the production of the MASC annual report 2013/2014.

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Foreword to the Report

The annual report of the Multinational Arabidopsis Steering Committee (MASC) 2013/2014 truly manifests the third road map of the Arabidopsis community including presenting its title on the newly designed cover '*The Multinational Arabidopsis Steering Committee - From bench to bountiful harvests*'. Within the last 20 years two themes guided Arabidopsis research: '*The Multinational Coordinated Arabidopsis thaliana - Genome Research Project*' in the 1990s and '*The Multinational Coordinated Arabidopsis thaliana Functional Genomics Project*' in the 2000s. In this year's report you will find information on the current road map including progress made within the last 12 months since March 2014 on Arabidopsis research, which is formulated by Arabidopsis researchers from 25 countries worldwide. One of the main aims of the committee is to strengthen international collaboration and coordinations to reduce redundancy and help guiding the community to make progress on projects that can be successful only by combined international efforts. Today's major challenges we face are the handling of the massive amount of data and the translation of Arabidopsis research to the field and vice versa while maintaining hypothesis driven basic research.

MASC has its origin in the 1990s when scientists from the United States, Europe, Japan and Australia formed an ad hoc committee to promote large-scale studies in *Arabidopsis thaliana*. Since then the idea of a combined and coordinated effort accompanied by the policy of open data sharing has proven successful and led to the establishment of *Arabidopsis thaliana* as a reference plant and the Arabidopsis community to be one of the most active research communities. The Arabidopsis community can now look back on more than 20 successful years - including major achievements like the first fully sequenced plant genome, the functional annotation of many Arabidopsis genes, and the development of a plethora of techniques, tools and resources. Today one of the main aim of the Arabidopsis community 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 to be able to build a predictive model of an Arabidopsis plant, which is accompanied by the development of big data management systems. Additionally, the Arabidopsis researchers put increased efforts in outreach to other plant communities and translational approaches to allow effective exchange of information.

This year's report also holds a new page record which is due to the fact that almost all MASC members contributed including: all seven MASC subcommittees - Bioinformatics, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics, Systems and Synthetic Biology (page 13 ff.); all major Arabidopsis projects and resources including affiliated plant projects and resources (page 28 ff.); and 22 of 25 country representatives (page 50 ff.). Furthermore, this report outlines progress and activities of the MASC (page 9) as well as analysis and recommendations for the Arabidopsis community for the next year according to the current road map (Lavagi et al., 2012, *Plant Cell*, 24:2240-2247; page 11). Another way to assess progress and activity of a community is to obtain publication statistics and highlight examples of basic research published in peer-reviewed journals (page 38 ff.). This year nine publications with broad scientific impact were chosen based on recommendations by the Arabidopsis community. A way of demonstrating the increasing applicability of Arabidopsis research to industry and agriculture is to look at the number of filed patents and highlight publications on translational and applied research (page 44 ff.). It is more important than ever to generally invest more in plant research translational/applied and basic plant research to be able to meet societies demands. It should be ensured that information, tools and resources generated using Arabidopsis are not wasted and constant financial support of basic research with Arabidopsis is ensured. Whether MASC as informal body remains the best option for the Arabidopsis community or it is time to create a society, for which we can all become members and a more formal mechanism for reporting, communication, conference coordination and funding can be achieved, is up for debate.

The MASC report 2013/2014 is published at the 25th International Conference on Arabidopsis Research (ICAR) and distributed to all attendees. The ICAR is a very successful initiative of MASC members with support of the Arabidopsis community and celebrates its 25th anniversary. The next 26th ICAR will be on July 5th-9th 2015 in Paris, France. Save the date.

If you like to know more about MASC please visit our new site: www.arabidopsisresearch.org or the former site at TAIR (www.arabidopsis.org/portals/masc/index.jsp).

The Multinational Arabidopsis Steering Committee
July 2014

Executive Summary

MASC has representation from 25 countries and helps coordinate the international Arabidopsis community via three groups: MASC subcommittees, MASC country representatives and Arabidopsis community projects and resources that are informed with continuous input from the whole Arabidopsis and plant community.

In recent years the need for sustained investment in Arabidopsis research has been queried by some who view that next generation sequencing has largely negated the need for a model system and that research can now be undertaken directly in crops minimizing the risks inherent in translational biology. There is some truth in this, but it also ignores other salient facts – it is the resources, tools and techniques built for and by Arabidopsis researchers that provide much of the support for Arabidopsis. Most of us working on crops will still refer to a gene's function based on the homologue's reported function in Arabidopsis, although this is not always the case. In many instances a researcher will move backwards and forwards between a crop and a model species like Arabidopsis. The strengths of a model system, including genetic and bioinformatics resources, tools, life cycle and ease of transformation ensure its survival. To say we no longer should undertake research, be it basic, strategic or potentially applied in Arabidopsis is like saying mouse, yeast and *E. coli* hold no benefit for human researchers. Indeed, talking to mouse and human geneticists it is clear they view the Arabidopsis community and its resources with jealousy. Furthermore, 2,753 patents referring to Arabidopsis were published in 2013 (Figure 4, page 44) and more patents were published in 2009-2013 (15,003) than 2004-2008 (13,083), 1999-2003 (9,083) and 1994-1998 (1,608). With average ICAR attendance stable for over a decade (page 38) and ~16,000 labs working on Arabidopsis (http://ipg.missouri.edu/feature-stories/g_redei.cfm) the words of Mark Twain in the New York Journal, 1897 '*The report of my death was an exaggeration*' seem apt.

That said, we do face challenges and it is time for the community to evaluate what we need for the next 5-10 years. How do we position Arabidopsis research to support crop and applied research and not being seen as competing with it. This will include a better voice for plant science in the broader community and a better voice for Arabidopsis research within the plant science community. What are the challenges and how can they best be addressed by research using Arabidopsis. In this context, it is time to evaluate whether MASC remains the best option or it is time to create a society, for which we can all become members and a more formal mechanism for reporting, communication,

conference coordination and funding can be achieved. There are a number of international societies and we can pick and choose the best facets of them to make our own. Over the coming year or two hopefully there will be more discussion and consideration of the way forward for MASC.

International Conference on Arabidopsis Research (ICAR)

24th ICAR, Sydney, Australia: June 24th-28th 2013

25th ICAR, Vancouver, Canada: July 28th-August 1st 2014

Reserve dates for upcoming ICARs:

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

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

Progress and Activities of MASC

- MASC chair 2013/2014: Barry Pogson (The Australian National University Canberra, Australia)
- MASC co-chair 2013/2014: Nicholas Provart (University of Toronto, Canada)
- MASC coordinator: Luise Brand (University of Tuebingen, Germany) funded by the German Science Foundation (DFG)
- 24th International Conference on Arabidopsis Research (ICAR) 2013: June 24th-28th Sydney, Australia; 650 attendees and 351 submitted poster abstracts (www.sallyjayconferences.com.au/icar2013)
- MASC web pages: since December 2014 new URL www.arabidopsisresearch.org; information still provided by TAIR: www.arabidopsis.org/portals/masc

Analysis and Recommendations of MASC

- Better integration of websites, portals and information resources. The establishment of www.arabidopsisresearch.org provides potential for this. We would recommend links and integration with other sites and it host all ICAR meetings
- Establishment of a committee to report to MASC on the pros and cons and options for an Arabidopsis Society.
- MASC to provide synopses and links to reports for new initiatives in plant science
- Seek affiliation with the Global Plant Council (www.globalplantcouncil.org)

- Collect and collate accurate quantifiable data obtained at multiple levels of abstraction (organelle, cell, tissue, organ, organism - genomics, epigenomics, metabolomics, proteomics, phenomics, systems biology)
- Continue to develop collections of mutants and mutant lines
- Translation of quantitative data into functional network models and maps
- Develop new models across scales to build computational/mathematical models
- Survey the variation in *Arabidopsis* and related species to infer biological networks
- Analyze ecotypes and *Arabidopsis* relatives in association with their rhizosphere, endophyte and epiphyte communities in various ecological settings
- Develop a multi-scale artificial field model towards natural conditions
- Develop high-throughput methods for measuring phenotypes in the lab and in the field

MASC Subcommittees

Currently 7 MASC Subcommittees monitor progress and activities as well as point out future directions in close contact with the community on a defined field of *Arabidopsis* research and thereby promote international cooperation. Detailed information provided by all subcommittees can be found in this report (page 13 - 27)

- Bioinformatics (page 13): Many papers with big data outputs were published in 2013/14. Bioinformatics community meetings were held at 24th ICAR 2013 (Sydney, Australia) and at PAG 2014 (San Diego, U.S.). Christopher Town (J. Craig Venter Institute) and colleagues from Texas and Cambridge were awarded funding from NSF and BBSRC in September of 2013 for the development of new *Arabidopsis* Information Portal that went online in April 2014 at <http://araport.org>.
- ORFeomics (page 14): The ORF and cDNA clones table was updated again to keep track of the progress made towards clones for all annotated *Arabidopsis* protein coding genes.
- Metabolomics (page 16): The subcommittee's web page is available at www.masc-metabolomics.org. The MASCM (Multinational *Arabidopsis* Steering Committee Metabolomics) gator portal is under development (<http://gator.masc-proteomics.org/>). A workshop was held at RIKEN CSRS: Metabolomics to Better Understand Plant Specialized Metabolism (Yokohama, Japan) and *Arabidopsis* metabolomics researchers will meet at Metabolomics 2014 (Tsuruoka, Japan).
- Natural Variation and Comparative Genomics (page 17): Additional genomes were sequenced including *Capsella rubella* (Slotte et al., 2013), *Tarenaya hasslerii* (Cheng et al., 2013) *Aethionema arabicum*, *Sisymbrium*

irio, and *Levenworthia alabamica* (Haudry et al., 2013). A recently discovered phenomenon is that organellar genomic variation may be more important in the metabolome than any individual nuclear locus (Joseph et al., 2013a, 2013b). Progress was made towards agreeing on gene naming conventions across the Brassica species during many meetings including the annual meetings of the Brassicales Map Alignment Project (BMAP) and the Multinational Brassica Genome Project (MBGP).

- Phenomics (page 19): Four phenotyping facilities described their efforts in detail in this report (Belgium, Netherlands, Czech Republic and Australia) and all data bases and resources worldwide are listed including information about their recent activities. A phenomics workshop was held at 24th ICAR 2013 (Sydney, Australia). The phenomics community met at the 3rd International Plant Phenotyping Symposium (Chennai, India), organized one summer school in Europe and two other workshops.
- Proteomics (page 23): Plant proteomics tools and resources including URLs are listed. The 1001 Proteomes portal was released in 2012 and provides protein level information generated by natural variation sequencing projects. The utilization of proteomic techniques initially pioneered in *Arabidopsis* have been expanded into economically important plants in the past year, this has included work in pine, maize and rice. A workshop "Using proteomics to identify receptor complexes and signaling events" was held during 24th ICAR 2013 (Sydney, Australia).
- Systems and Synthetic Biology (page 25): Modeling approaches at a variety of scales (spatial and temporal) have become increasingly prevalent in *Arabidopsis* research as have synthetic biology approaches (see Selected Publications). A variety of *Arabidopsis*-specific tools and resources are listed, including updates on DOE Systems Biology Knowledge Base (KBase) and Bio-Analytic Resource for Plant Biology (BAR). Many Systems and Synthetic Biology sessions were held during many conferences. A workshop on Emerging Technologies and Systems Biology was held during the 24th ICAR 2013 (Sydney, Australia).

Arabidopsis Community Projects and Resources

The Arabidopsis community and the whole plant community thrive and profit from resource and stock centers, i.e. NASC, 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 (AIP) and The Arabidopsis Information Resource (TAIR). Major news from AIP is the award announcement in September 2013 by NSF and the release of preview 2 of the site www.araport.org on April 2nd 2014. TAIR implemented a new funding model with a subscription requirement for companies on October 1st 2013, followed by subscriptions for academic institutions on April 1st 2014. ABRC and MASC sites as well as data before August 1st 2013 are still available for free.

This year the MASC has decided to include and highlight major internationally collaborating research projects and resources that focus not solely on Arabidopsis but Arabidopsis researchers are heavily involved in, i.e. this year Bio-Analytic Resource for Plant Biology (BAR), BrassiBase, Epigenomics of Plants International Consortium (EPIC), European Plant Phenotyping Network (EPPN) and iPlant Collaborative.

Arabidopsis Basic Research and its Impact on Applied Research

Scientific Highlights in 2013/2014

The past year continued to be strong for Arabidopsis publications. 4,271 Arabidopsis peer-reviewed research papers were published in 2013, almost 200 publications more than in 2012, 2-fold increase within last decade and more than 10-fold increase in previous 20 years (Figure 3, page 38). This report includes summaries of only a few research highlights published in 2013 and early 2014 with contributions from at least three different countries including:

- New enzyme relevant for lignin biosynthesis (Science 341(6150):1103-6)
- Sweet dreams make plants larger – Carbohydrate metabolism influences plant growth via GA-mediated signal (Plant Cell 25(10):3760-9)
- How do plants make jigsaws? (Science. 343(6174):1025-8)
- Structural requirements for a pathogen effector detector (Science 18;344(6181):299-303)
- Plasticity constraints and developmental evolution in root architecture (PNAS USA10;110(37):15133-8)
- Change direction - The mechanisms behind microtubule reorientation (Science 6;342(6163):1245533)
- New hints why plants don't flower under salt stress conditions (Nat Commun 4:1352)
- Get it inside - New complex necessary for endocytosis identified (Cell 156(4):691-704)
- Fatty acid transport to the ER (PNAS USA 110(2):773-8)

Impact of Arabidopsis Research on Applied Research and Industry in 2013/2014

To measure the impact and evaluate 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 minimum 10 years elapse between the discovery and the subsequent successful application. A way of demonstrating the increasing applicability of Arabidopsis research to industry and agriculture is to look at the number of filed patents (Figure 4, page 44). In 2013 2,753 international patent applications were published referring to Arabidopsis. More and more applications consider Arabidopsis, which is reflected by the 19-fold increase within the last 20 years. Another way to point out the interdependency of basic and applied research is to highlight examples published in peer-reviewed journals. This report includes summaries of some applied studies vitally dependent on Arabidopsis data and resources published in 2013 and early 2014 including:

- Transporters as toolkits for improved plant growth under nutrient limiting conditions (Front Plant Sci 5:125)
- Conserved function of Nod factors in legumes and nonlegumes (Science 341(6152):1384-7)
- Don't shatter your pods - Lignified fibre cap cells make the difference in soybean (Nat Commun 5:3352)
- Single gene hybrid vigor in oil palm (Nature 500(7462):340-4)
- The global "flowering" of the potato tuber crop (Nature 495(7440):246-50)
- Blue light switch - Interfering transcription in mammalian cells (Nature 500(7463):472-6)
- Winter beet - A new way of cultivating sugar beet
- Stable targeted genome modifications in plants (PNAS USA 111(12):4632-7)

Country Highlights

The wider Arabidopsis and plant community supports MASC by appointing individual country representatives, whom are nationally and internationally well connected Arabidopsis researchers. In 2013/2014 three additional countries joined the MASC network: Denmark represented by Michael Palmgren, Greece represented by Polydefkis Hatzopoulos and South Korea represented by Inhwon Hwang. To date 25 countries support MASC and the international Arabidopsis community, out of these 22 countries are represented in this MASC annual report 2013/2014.

Researcher 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.

Progress and Activities of MASC

In 2013, Barry Pogson succeeded Wolfram Weckwerth to become MASC chair and Nicholas Provart became co-chair (Figure 1). Nicholas Provart will become the new MASC chair when Barry Pogson steps down following the 25th International Conference on Arabidopsis Research (ICAR) July, 2013 in Vancouver, Canada. Currently, the MASC coordinator is Luise Brand. The 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). The coordinator position was established in 2002 and has been previously supported by NSF (U.S.) for six years, by DFG (Germany) for one year and BBSRC (U.K.) 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. Organize annual MASC meeting during ICAR.

MASC helps coordinate the international Arabidopsis community via three groups that receive continuous input from the whole Arabidopsis and plant community: MASC subcommittees, Arabidopsis community projects and resources and MASC country representatives (Figure 1). MASC subcommittees, proposed in 2002, were established to help track the progress and advances made by the international Arabidopsis community. This year reports by all seven current subcommittees chairs/co-chairs are included: Bioinformatics, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics and Systems and Synthetic Biology (page 13 ff.). The subcommittee Systems Biology was renamed Systems and Synthetic Biology. 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.

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 28 ff.). The three

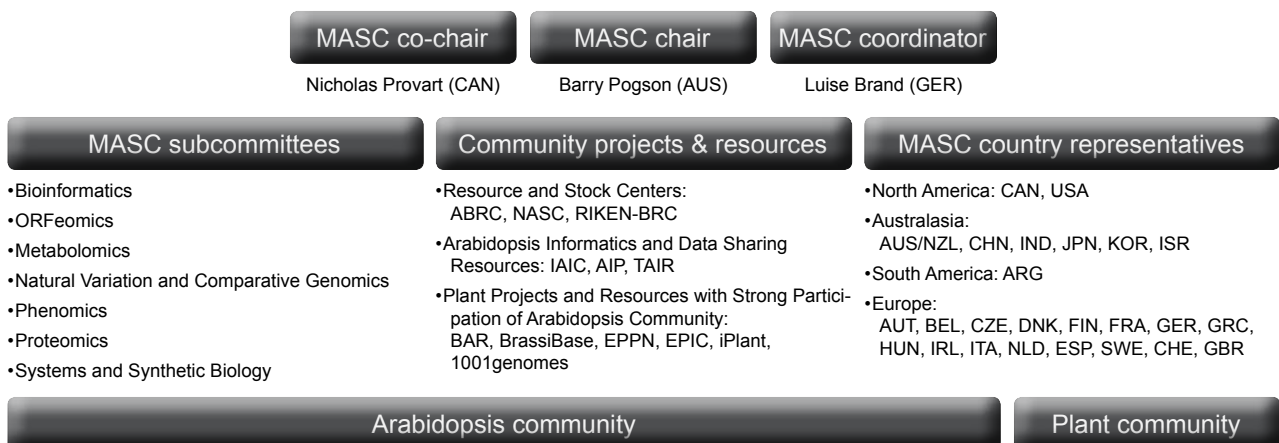


Figure 1. Multinational Arabidopsis Steering Committee (MASC). For explanation of abbreviations see MASC subcommittee (page 13 ff.), Arabidopsis community projects and resources (page 28 ff.) and MASC country reports (page 50 ff.)

resource and stock centers, Arabidopsis Biological Resource Center (ABRC, U.S.), the Nottingham Arabidopsis Stock Centre (NASC, U.K.) and the RIKEN BioResource Center (RIKEN BRC, Japan), expanded their repertoire last year and continued to deliver stocks to researchers worldwide. Arabidopsis informatics and data sharing resources are also included in this year's report, the International Arabidopsis Informatics Consortium (IAIC), the Arabidopsis Information Portal (AIP) and The Arabidopsis Information Resource (TAIR). The Preview 2 of the AIP site was released on April 2nd 2014 and in its opening days seems to be running without problems (www.araport.org). TAIR funding ended in August 2013 and led to the implementation of a subscription requirement for companies on October 1st 2013, followed by subscriptions for academic institutions on April 1st 2014. New to this report is a section outlining the efforts of community projects and resources with strong participation of the Arabidopsis community (page 34). Five internationally coordinated projects with a strong involvement of Arabidopsis researchers give information on their aims and progress.

Country representatives attend the annual MASC meeting held during ICARs and contribute to the annual MASC report by submitting country reports. In 2013/2014 25 countries have been involved in MASC and 22 contributed to this year's report. Three additional countries recently joined MASC: Denmark represented by Michael Palmgren, Greece represented by Polydefkis Hatzopoulos and South Korea represented by Inhwang Hwang. In 2013 José Luis Micol and Ana I. Caño-Delgado succeeded the Spanish country representative Javier Paz-Ares. Catherine Perrot-Rechenmann and Loïc Lepiniec succeeded the French country representative Heribert Hirt. MASC thanks the former country representatives for their valuable contributions and highly encourages researchers working on Arabidopsis to get involved in MASC activities by e.g. in subcommittees, projects and resources or as country representatives.

Since December 2013 the MASC sites are hosted at www.arabidopsisresearch.org. The coordinator began to transfer the data from the MASC pages hosted by TAIR to the new server and the process will be finished within the next months. 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. It is planned to provide a news feed and a forum or email discussion list like U.S. BIOSCI/Bionet (arab-gen@net.bio.net) or U.K. JISMAIL (ARABUK@JISMAIL.AC.UK) for MASC members and the international Arabidopsis community. It is also planned to host the sites for ICAR at www.arabidopsisresearch.org. There will be discussions with TAIR about the possibility to implement the abstract submission system established in 2007 by TAIR in order to guarantee a smooth implementation of ICAR abstracts into the TAIR data base.

The 24th International Conference on Arabidopsis Research (ICAR) was held in Sydney, Australia from June 24th-28th 2013. Members of the subcommittees, projects and resources were involved in the program of the 24th ICAR. e.g. ABRC and NASC booth, RIKEN booth and workshops on the topics: 'IAIC-The transition from TAIR to the AIP', 'Emerging technologies and systems biology', 'Genetic traits from phenomics data', 'Using proteomics to identify receptor complexes and signaling events' and two workshops on 'Natural variation evolution and phenomics'. Additionally, there were sessions on 'Plant nutrition in the face of impending global resource limitation opportunities for model plant research', 'Translational biology' and 'Teaching workshop for early career scientists'. 650 people attended the 24th ICAR in Sydney and 351 poster abstracts were submitted (Figure 2). In 2012 and 2013 the upload of the abstracts to the TAIR servers was not possible but will be followed up next year. Within the last 9 years on average 60% of the attendees presented a poster during the ICAR and since 10 years the number of attendees is high proofing its success.

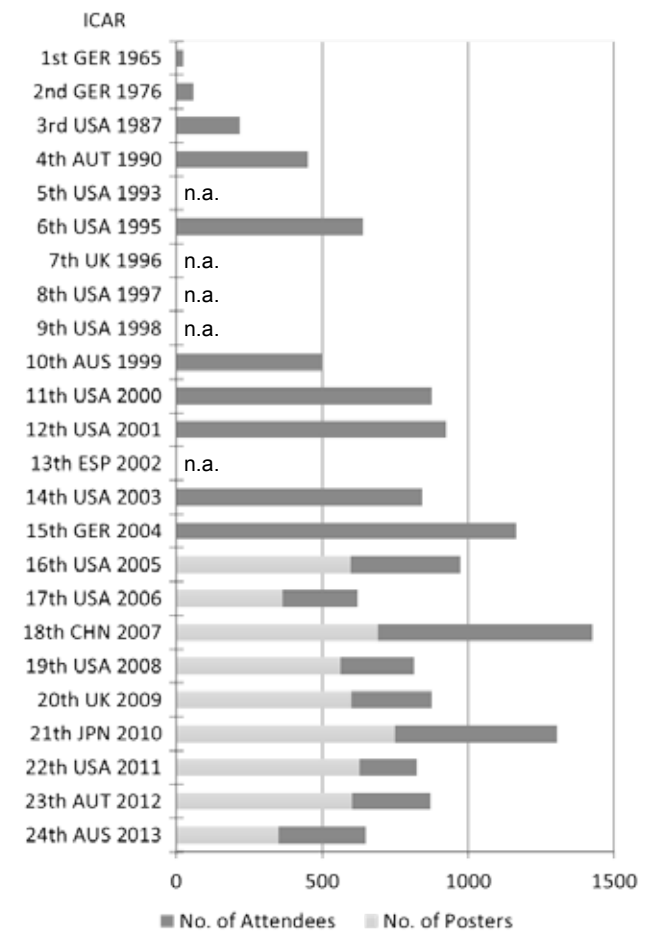


Figure 2. Number of attendees (dark grey) and number of posters presented at the International Conference on Arabidopsis Research since 1965 (n.a - no data available and 1965-2004 no number of posters available).

Analysis and Recommendations by MASC

The demand of society for secure food and energy supply in the prospect of climate change, decreasing fossil fuels and environmental friendly solutions brings plants more and more into public attention. Therefore the necessary investments in applied plant research have been increased in recent years. It seems however that these investments in applied and translational research are on the expense of basic research i.e. the research with the reference plant *Arabidopsis thaliana*. But the past has proven that applied research is inevitably connected to and dependent on basic research and an increased fundamental understanding is highly desirable. It is important that basic research is constantly funded and not reduced as that would be a negative outcome for basic and applied projects. The fact that companies support basic research i.e. with the reference plant *Arabidopsis thaliana* more and more can be considered as one of the strongest arguments for funding bodies to continue constant funding of basic research with *Arabidopsis thaliana*. However, the country reports (page 50 ff.) clearly state that funding bodies of many countries require translational approaches although it is more important than ever to generally invest more in plant research to meet societies demands.

The MASC report again highlights basic as well as applied research using *Arabidopsis thaliana* directly or indirectly by translating knowledge gained from this reference plant. A major advantage of basic research is the aim to understand basic biological processes in detail which in the end leads more often than expected to useful applications. The Arabidopsis community is still diverse and many laboratories have taken on the challenges of the new era of plant basic research - data management to extract relevant information in order to model and eventually predict plant behavior. The Arabidopsis community faces the bioinformatics challenge in a coordinated fashion by the National Science Foundation (NSF, U.S.) funded project International Arabidopsis Informatics Consortium (IAIC). The major aims stated in the MASC 2021 road map 'From Bench to bountiful harvests' (Lavagi et. al, 2012) were met by IAIC like the approval of NSF funded Arabidopsis Information Portal (AIP) and the development of data standards is in progress. Besides the NSF the German Science Foundation (DFG) and the British Biotechnology and Biological Sciences Research Council (BBSRC) fund the module development for AIP. The development of standards for the community and the AIP (www.araport.org) and its modules, which both allow for translational applications, will be the main focus of IAIC in the coming years.

Another major aim of the 2021 road map is to deepen international cooperation and coordination. This is possible due to constant funding of the International Conference on Arabidopsis Research (ICAR) and the funding of the MASC coordinator. The fact that today researchers representing 25 countries are involved in MASC proofs that the Arabidopsis community is still growing as well as the fact that every year more articles are published referring to Arabidopsis (page 50 ff., page 38). In the previous year three additional country representative joined the MASC, i.e. Denmark, Greece and South Korea and its recommended to include more countries from Africa, South America, Europe and Australasia. Its highly recommended to foster international coordination in order to increase output by reducing redundancy and increasing synergistic effects through combined efforts. The basic research highlights section includes ten examples of collaborating laboratories by authors from of at least three countries. The outreach activities of MASC were also strengthened in the previous year e.g. eight examples of the impact on applied research and industry are highlighted in this report (page 44 ff.), a session on translational biology during the 24th ICAR 2013 and the extension of the community projects and resources in this year's annual report (page 34 ff.) as well as including outreach activities into the country reports (page 50 ff.). The Arabidopsis community should strengthen and continue these outreach efforts to translational, applied as well as other plant and research communities

The Arabidopsis community including Arabidopsis projects and resources and individual research laboratories as well as bigger research consortia made it possible to announce major progress on the MASC 2021 road map. Most of the progress is monitored by the MASC subcommittees (page 13 ff.), can be also found in the Arabidopsis projects and resources section (page 28 ff.) and in the country reports (page 50 ff.). In the next years the Arabidopsis community should focus on the goals outlines in the 2021 road map (Lavagi et al. 2012, MASC report 2012).

Special recommendations for 2014/2015 are:

- Better integration of websites, portals and information resources. The establishment of www.arabidopsisresearch.org provides potential for this. We would recommend links and integration with other sites and it host all ICAR meetings
- Establishment of a committee to report to MASC on the pros and cons and options for an Arabidopsis Society
- MASC to provide synopses and links to reports for new initiatives in plant science
- Seek affiliation with the Global Plant Council (www.globalplantcouncil.org)
- Collect and collate accurate quantifiable data obtained at multiple levels of abstraction (organelle, cell, tissue, organ, organism - genomics, epigenomics, metabolomics, proteomics, phenomics, systems biology)
- Continue to develop collections of mutants and mutant lines (ongoing)
- Translation of quantitative data into functional network models and maps
- Develop new models across scales to build computational/mathematical models
- Survey the variation in Arabidopsis and related species to infer biological networks (already ongoing, see especially Natural Variation and Comparative Genomics Subcommittee, page 17 ff.)
- Analyze ecotypes and Arabidopsis relatives in association with their rhizosphere, endophyte and epiphyte communities in various ecological settings
- Develop a multi-scale artificial field model towards natural conditions (already ongoing, see especially Phenomics Subcommittee, page 19 ff.)
- Develop high-throughput methods for measuring phenotypes in the lab and in the field (already ongoing, see especially Phenomics Subcommittee, page 19 ff.).

Reports of the MASC Subcommittees

Bioinformatics

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

By Nicholas Provart with input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community. 7 April 2014.

Tools and Resources

Several new Arabidopsis bioinformatics tools and large data sets were published or released in 2013 or early in 2014.

Big data - transcriptomics

Ken Birnbaum's group at New York University published a map of cell type-specific auxin responses (Bargmann et al., 2013). The transcriptional response to auxin was analyzed in four root cell types. These data were cross-referenced with spatial expression maps to help understand auxin's role in regulating gene expression in the root meristem. Atle Bones' group at the Norwegian University of Science and Technology published a transcriptome study of ten ecotypes of *Arabidopsis thaliana* in response to heat stress, measured using ATH6 Nimblegen arrays (Barah et al., 2013). Yves Chupeau's group at INRA in France performed transcriptional profiling of events leading to totipotency in an Arabidopsis protoplast culture system (Chupeau et al., 2013).

Big data - methylation patterns

Alan Jones' group at the University of North Carolina - Chapel Hill reported a genome-wide study of differential DNA methylation sites in Arabidopsis grown at different water potentials (Colaneri et al., 2013). There are over 700 epigenomic, 300 RNA-seq, and 300 resequenced ecotype experiments loaded the EPIC (Epigenomics of Plants International Consortium)-CoGE Browser, built by Eric Lyons (U. Arizona) and Brian Gregory (U. Pennsylvania). Try it at http://genomevolution.org/wiki/index.php/EPIC-CoGe#Try_EPIC-CoGe!

Other big data

The EVEX database provides access to a large effort by Yves van de Peer and colleagues (Landeghem et al., 2013) to mine abstracts and PubMed full-text articles to retrieve information about molecular events between Arabidopsis proteins. See <http://www.evexdb.org/>. Haudry et al., (2013) published an atlas of over 90,000 conserved non-coding regions in the Brassicaceae, which will be useful in elucidating potential regulatory regions in Arabidopsis

and other cruciferous species. Richard Vierstra's group (Kima et al., 2013) published a comprehensive proteomic analysis documenting ubiquitylation targets in Arabidopsis. Christine Queitsch at University of Washington in Seattle has generated genome-wide DNase I hypersensitive site data for a number of different Arabidopsis tissues and conditions, which can be used to elucidate which parts of the genome are occupied by DNA binding proteins in those tissues and under the examined conditions. The data are available at <http://plantregulome.org> (Sullivan et al., 2014). A data set of approximately 800 Arabidopsis transcription factor binding specificities should be available by the summer of 2014, from Matthew Weirauch, Tim Hughes, Joe Ecker and collaborators. Peter McCourt's group in Toronto published a "meso-scale" abscisic acid hormone interactome (Lumba et al., 2014).

Other tools

Harvey Millar's group at the University of Western Australia has developed a protein proteotypic predictor resource, called APP, to allow researchers to select the best peptides from given an AGI ID for targeted mass spectrometry for Arabidopsis. See <http://www.plantenergy.uwa.edu.au/APP/> (Taylor et al., 2014).

Work towards creating a new Arabidopsis Information Portal by the International Arabidopsis Informatics Consortium proceeded (International Arabidopsis Informatics Consortium, 2012), with community meetings at ICAR in Sydney last summer, and at the PAG Conference in San Diego in January 2014. Christopher Town of the J. Craig Venter Institute and colleagues from Texas and Cambridge were awarded funding from the NSF and BBSRC in September of 2013 for the development of the framework and certain key modules for this new portal. The new portal went online in April 2014 at <http://araport.org>. Three groups internationally were funded to contribute towards building modules for the AIP: Nicholas Provart & Stephen Wright at the University of Toronto were awarded funds by Genome Canada to share Bio-Analytic Resource data sets and BAR applications; Sean May at the University of Nottingham was awarded funds by the BBSRC in the UK to develop a Stock Centres module; and Bjoern Usadel of the Rheinisch-Westfaelische Technische Hochschule (RWTH, Aachen) was awarded funds from the DFG in Germany to contribute MapMan annotations and other tools.

Eva Huala and colleagues at TAIR meanwhile worked with iPlant to keep TAIR data accessible after the end of the funding period in August 2013. TAIR itself is in the process of moving to a subscription-based model. See the IAIC section of this report for further updates.

Arabidopsis Bioinformatics in Teaching: Several Arabidopsis bioinformatic tools and databases, such as the BAR's eFP Browser, ATTED-II's coexpression tool, and the ATHENA tool made appearances in the Bioinformatic Methods I and II MOOCs, which ran on Coursera.org in the winter and spring of 2014.

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Clone-Based Functional Genomics Resources (ORFeomics)

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

By Motoaki Seki (Chair) and Joe Ecker (Co-Chair) with contributions from subcommittee members, Masatomo Kobayashi (RIKEN BRC) and Eric Grotewold (ABRC)

The goal of the subcommittee ORFeomics is to keep track of the progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes. 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 bold. New clones include 400 transcription factor Gateway entry clones from RIKEN group.

In Japan, IBBP (Interuniversity Bio-Backup Project for Basic Biology) has started to back up the bioresources, such as RIKEN Arabidopsis Full-Length (RAFL) cDNA clones, to evade damage and disappearance by a glitch or the disaster, in IBBP Center (National Institute for Basic Biology, NIBB) and 7 Universities (Hokkaido Univ., Tohoku Univ., Univ. of Tokyo, Nagoya Univ., Kyoto Univ., Osaka Univ. and Kyushu Univ.).

Conferences and Workshops

Training Course for Wheat Germ Cell-Free Protein Synthesis System using Arabidopsis ORF clones (RIKEN Yokohama, Japan; July 23-24, 2013)

Selected Publications

- Hanada, K., Higuchi, M., Okamoto, M., Yoshizumi, T., Shimizu, M., Nakaminami, K., Nishi, R., Ohashi, C., Iida, K., Tanaka, M., Horii, Y., Kawashima, M., Matsui, K., Toyoda, T., Shinozaki, K., Seki, M. and Minami, M. (2013) *Small open reading frames associated with morphogenesis are hidden in plant genomes*. *Proc. Natl. Acad. Sci. USA* 110: 2395-2400.

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/abrhome.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/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12.114	signal.salk.edu/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18.258	http://interactome.dfc.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3.041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1.282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15.543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7.300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6.448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/sheenweb/category_genes.html	ABRC
Steve Clouse	Gateway expression	N-terminal Flag tagged kinases		782	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, Y1/2H, AD vector	Transcription factor	Full sequence	1.600		BRC
RIKEN	Gateway entry, no stop, Y1/2H, AD vector	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
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

Metabolomics

<http://arabidopsisresearch.org/index.php/subcommittees/metabolomics> and www.masc-metabolomics.org

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 recently 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/>
Arabidopsis metabolome expression databases AtMetExpress development, AtMetExpress 20 ecotypes and ReSpect for Phytochemicals.
- 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

- 2013/9/17-18: RIKEN CSRS Workshop: Metabolomics to Better Understand Plant Specialized Metabolism, Yokohama, Japan
- 2014/6/23-26: Metabolomics 2014, Tsuruoka, Japan

Selected Publications

- Haug K, Salek RM, Conesa P, Hastings J, de Matos P, Rijnbeek M, Mahendrakar T, Williams M, Neumann S, Rocca-Serra P, Maguire E, González-Beltrán A, Sansone SA, Griffin JL, Steinbeck C (2013) MetaboLights - an open-access general-purpose repository for metabolomics studies and associated meta-data. *Nucl. Acids Res.*, 41, D781-D786.
- Sakurai T, Yamada Y, Sawada Y, Matsuda F, Akiyama K, Shinozaki K, Hirai MY, Saito K (2013) PRIME Update: Innovative Content for Plant Metabolomics and Integration of Gene Expression and Metabolite Accumulation. *Plant Cell Physiol.*, 54 (2): e5. doi: 10.1093/pcp/pcs184.

Natural Variation and Comparative Genomics

<http://arabidopsisresearch.org/index.php/subcommittees/natural-variation-comparative-genomics>

By J. Chris Pires (Chair) and Brian Dilkes (Co-chair) with contributions from subcommittee members and the wider community

Progress Towards Road Map Goals

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

- Progress was made in expanding the genome by including organellar genomic variation. Organellar genomic variation has been found to be more important in the metabolome than any individual nuclear locus (Joseph et al., 2013a, 2013b). Most mapping populations were not made to study variation in the organelle so this is an area ripe for investigation.

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

- Progress in comparative genomics was made in sequencing additional genomes including *Capsella rubella* (Slotte et al., 2013), *Tarenaya hasslerii* (Cheng et al., 2013) *Aethionema arabicum*, *Sisymbrium irio*, and *Leavenworthia alabamica* (Haudry et al., 2013). These studies in comparative genomics and natural variation illuminated several aspects of Arabidopsis biology, including the discovery on numerous conserved noncoding sequences in the Brassicaceae.
- Progress in the natural variation of Arabidopsis was made at both the genetic and epigenetic level (Long et al., 2013, Schmitz et al., 2013).

(E) Deepen international cooperation and coordination

- Progress was made toward international cooperation and coordination at various meetings, including the annual meetings of the Brassicales Map Alignment Project (BMAP) and the Multinational Brassica Genome Project (MBGP).

(F) Subcommittee specific goals

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

Future Goals

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

Future goals include building predictive models with insights from:

- Studying natural variation within Arabidopsis and comparisons to other related species of plants. One recently discovered phenomenon is that organellar genomic variation may be more important in the metabolome than any individual nuclear locus (Joseph et al., 2013a, 2013b). Thus, new mapping populations should be created to study variation in the organelle.

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

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

- Exploring the variation in Arabidopsis and related species at numerous levels of biological organization to infer biological networks from various -omics datasets, including genomic, epigenomic, proteomic, metabolomic, ionic, interactomic, and phenomic.
- Analyzing Arabidopsis ecotypes and related plant species in association with their rhizosphere, endophyte and epiphyte communities in various ecological and agricultural settings.
- Integrating studies across species and environments by analyzing and classifying natural diversity in the Brassicaceae, dissecting the genomic basis of diversified traits, and developing the infrastructure to maximize common benefits from genetic, genomic, ecological and systematics tools.
- Generating a multi-locus nuclear phylogeny of all the genera and species of the Brassicales for comparative biology, and to quickly identify transcriptome variation, life history traits, and genome size for future candidates of species for genome sequencing.
- Developing computational resources to understand and utilize the natural variation of Arabidopsis and related species. This will include interactions among the all the MASC subcommittees with the 1001 Arabidopsis Genomes project, Multinational Brassica Genome Project (MBGP), and Brassicales Map Alignment Project (BMAP) to consider natural variation and comparative -omics in the roadmap. Ensure that the Arabidopsis Information Portal (AIP) be built to work for Brassica and other plant species.

- Creating germplasm resources that are publicly available (e.g., Brassica diversity sets) and create a database for managing diversity (e.g., Brassibase, brassica.info)
- (C) Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa
- Pursuing systems biology research programs and analyze -omics datasets in other plant systems using key knowledge gained through the analysis of Arabidopsis, starting with the crop Brassicas (vegetables and oilseeds), biofuel crops (e.g., Camelina), and other economically important species (e.g., horseradish, wasabi, etc.).
 - Establishing data standards and ontologies to provide uniform data on growth conditions and experimental metadata to enable modeling from controlled environments to the field.
 - Developing high-throughput methods in the lab and the field for measuring phenotypes and identifying QTLs that have subtle effects. Develop appropriate open access informatics and data infrastructure for storage, retrieval and analysis of natural variation and QTL. Establish accessible statistical and computational methods for the analysis of natural variation and QTL data.
- (D) Build the IAIC and develop efficient informatics tools and repositories further
- Integrating -omics data and informatics infrastructure in Arabidopsis with other species.
 - Developing international standards for population genomics (Arabidopsis 1001 genomes, Brassica 100 genomes) and comparative genomics (BMAP 100 genomes) to maintain high-quality reference genomes and re-sequenced genomes.
 - Developing open access ontology-driven database tools and promote the adoption of uniform vocabularies and machine-readable formats for describing experimental data and metadata. Data from Haudry et al. (2013) are being made viewable in an Arabidopsis-centric way on the Bio-Analytic Resource (BAR) via a tool called GeneSlider)
- (E) Deepen international cooperation and coordination
- Undertaking a coordinated analysis of natural variation and comparative -omics with the international Brassicales Map Alignment Project (BMAP), Multinational Brassica Genome Project (MBGP), International Arabidopsis Informatics Consortium (IAIC), and Brassibase.
 - Continuing BMAP workshops at international conferences to coordinate efforts, share expertise, and develop -omics standards and comparative ontologies.
- (F) Subcommittee specific goals
- Studying natural variation within Arabidopsis and comparative -omic and systems biology investigations in related species is central to understanding plant biology and plant environment interactions.
 - Coordinating gene naming conventions across the Brassica species, with planned discussions among the Arabidopsis and Brassica communities to coordinate various standards and ontologies, as well as conventions for annotation, pan-genomes, ancestral genomes, and other -omics efforts within and across species in the Brassicales.

Conferences and Workshops

In addition to regular annual meetings, the following conferences are also noteworthy:

- Plant Genome Evolution took place in Amsterdam, Netherlands in September 2013, and will meet again in Fall 2015.
- Brassica 2014 met in Wuhan China in Spring 2014
- The next Crucifer Genetics Workshop will be in September 2016 in Melbourne, Australia
- Brassica 2018 will meet in St. Malo, France
- Two joint workshops “Natural Variation, Evolution and Phenomis” were held during the International Conference on Arabidopsis Research (24th ICAR) 2013, Sydney, Australia

Selected Publications

- Cheng S, van den Bergh E, Zeng P, Zhong X, Xu J, Liu X, Hofberger J, de Bruijn S, Bhide AS, Kuelahoglu C, Bian C, Chen J, Fan G, Kaufmann K, Hall JC, Becker A, Bräutigam A, Weber AP, Shi C, Zheng Z, Li W, Lv M, Tao Y, Wang J, Zou H, Quan Z, Hibberd JM, Zhang G, Zhu XG, Xu X, Schranz ME (2013) The *Tarenaya hassleriana* genome provides insight into reproductive trait and genome evolution of crucifers. *Plant Cell* 25(8):2813-30.
- Haudry A, Platts AE, Vello E, Hoen D, Leclercq M, Williamson RJ, Forczek E, Joly-Lopez Z, Steffen JG, Hazzouri KM, Dewar K, Stinchcombe JR, Schoen DJ, Wang X, Schmutz J, Town CD, Edger PP, Pires JC, Schumaker KS, Jarvis DE, Mandáková T, Lysak MA, van den Bergh E, Schranz ME, Harrison PM, Moses AM, Bureau TE, Wright SI, Blanchette M. (2013) An atlas of over 90,000 conserved non-coding sequences yields detailed insight into crucifer regulatory regions. *Nature Genetics* 45: 891-900.
- Joseph B, Corwin JA, Li B, Atwell S, Kliebenstein DJ (2013a) Cytosolic genetic variation and extensive cyto-nuclear interactions influence natural variation in the metabolome. *eLife* 2:e00776.
- Long Q, Rabanal FA, Meng D, Huber CD, Farlow A, Platzer A, Zhang Q, Vilhjálmsson BJ, Korte A, Nizhynska V, Voronin V, Korte P, Sedman L, Mandáková T, Lysak MA, Seren Ü, Hellmann I, Nordborg M (2013) Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden. *Nature Genetics* 45: 884-890.

- Schmitz RJ, Schultz MD, Urich MA, Nery JR, Pelizzola M, Libiger O, Alix A, McCosh RB, Chen H, Schork NJ, Ecker JR (2013) Patterns of population epigenomic diversity. *Nature* 495: 193-8.

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- Haudry A, Platts AE, Vello E, Hoen D et al. (2013) An atlas of over 90,000 conserved non-coding sequences yields detailed insight into crucifer regulatory regions. *Nature Genetics* 45: 891-900.
- Joseph B, Corwin JA, Li B, Atwell S et al. (2013a) Cytosolic genetic variation and extensive cytonuclear interactions influence natural variation in the metabolome. *eLife* 2:e00776.
- Joseph B, Corwin JA, Züst T, Li B et al. (2013b) Hierarchical nuclear and cytoplasmic genetic architectures for plant growth and defense within *Arabidopsis*. *Plant Cell* 25(6):1929-45.
- Long Q, Rabanal FA, Meng D, Huber CD et al. (2013) Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden. *Nature Genetics* 45: 884-890.
- Slotte T, Hazzouri KM, Agren JA, Koenig D et al. (2013) The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution. *Nature Genetics* 45: 831-5.
- Schmitz RJ, Schultz MD, Urich MA, Nery JR et al. (2013) Patterns of population epigenomic diversity. *Nature* 495: 193-8.
- Cheng S, van den Bergh E, Zeng P, Zhong X et al. (2013) The *Tarenaya hassleriana* genome provides insight into reproductive trait and genome evolution of crucifers. *Plant Cell* 25(8):2813-30.

Phenomics

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

Fabio Fiorani (co-chair) and Robert Furbank (co-chair) with contribution from subcommittee members and the wider Arabidopsis community

Progress Towards Road Map Goals

- In 2013 there has been a continued development of automated platforms 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.
- The requirement to exploit statistical and structural functional models to predict traits in *Arabidopsis* and facilitate applicability diverse crops remains high. During this reporting period there were significant examples of comprehensive pipeline approaches to link genome to phenome and enable multi-trait analysis towards this goal.
- Efforts to deepen national and international collaborations towards plant phenomics programs have continued and have become increasingly visible through the activities of the International Plant Phenotyping Network, the European Plant Phenotyping Network (2011-2015), providing access to external users and enabling about 40 projects including *Arabidopsis* ones since its beginning, and the implementation of national phenotyping networks in Germany (DPPN), France (Phenome), UK (UKPPN), and Australia (APPF) in particular.
- It is recommended that a new census of current programs and capacities would be valuable to enable novel flagship projects to link genome to phenome in *Arabidopsis* and in other crops.
- Options for dynamic and integrated analyses of shoot and root and resource allocation should be considered.

Future Goals

- Coordination of experimentation across phenotyping centers regarding germplasm used for sequencing within the 1001 genome project and mutant collections would be desirable.
- Towards a definition of a minimum information regarding protocols used in phenotyping experiments: promote best practices in phenotyping experimentation including such as the need for optical and environmental sensor calibration and for simplified but precise schemas for reporting experimental meta-data.
- Promote ontology driven approaches to databases towards interoperability, data reuse and meta-analytical approaches for virtual laboratory environments and genome to phenome linkages.

- Continue the development of methods and studies for phenotyping across environments from lab to field.

Tools and Resources

Updates contributed by Stijn Dhondt, Nathalie Wuyts, Dirk Inzé (VIB, Gent, Belgium), Minami Matsui (RIKEN, Japan), Jan Humplík, Dusan Lazar and Lukás Spíchal (Olomouc, Czech Republic), Jeremy Harbinson (Wageningen University), Xavier Sirault (CSIRO Australia), Justin Borevitz (Australian National University)

Development of Novel Phenotyping Infrastructure and Phenotyping Pipelines

VIB, Plant Systems Biology, Gent, Belgium,

At VIB, Plant Systems Biology, Gent, Belgium, the Systems Biology of Yield group has been investing in the development of plant phenotyping systems for several years to support its activities in *Arabidopsis* research on growth regulatory networks and mild drought stress (<http://www.yieldbooster.org/research/87-plant-phenotyping-system-and-tool-development>). RGB top-view imaging robots, located in growth chambers for controlled environmental conditions, include the IGIS system for *in vitro* *Arabidopsis* rosette growth analysis and the MIRGIS system for plants grown in soil-filled trays. The IGIS is equipped with infrared light emitting diodes to allow for the hourly image acquisition in the dark. Wild-type *Arabidopsis* plants, under mild osmotic, salt and oxidative stress conditions, and transgenic lines enhancing leaf growth have been analyzed in a time resolved manner at high resolution (Dhondt et al., submitted). The WIWAM weighing, irrigation and imaging system for *Arabidopsis* grown in individual pots (Skirycz et al., 2011) has been upgraded (motion and user interface) in 2013 in a second generation robot, including an enlargement of its capacity from 216 to 396 pots. The two *Arabidopsis* WIWAMs are used for rosette growth analysis and reproducible leaf growth under mild drought stress conditions. A second major pillar in current activities is translational research towards crop species, with a focus on maize. Therefore, the WIWAM system was reproduced in an adapted version for maize shoot and leaf growth analysis under growth chamber conditions. RGB image acquisition in a multiple viewing angle setup allows for 3D reconstruction of shoots and the extraction of quantitative growth traits. Finally, in 2013, a conveyor belt system dedicated to crops was developed and installed in a 150 m² greenhouse compartment. PHENOVISION enables the daily weighing, irrigation and imaging of 392 plants. It contains three types of imaging systems: RGB cameras in a multi-view imaging setup, a thermal infrared camera, and a hyperspectral imaging system, consisting of a visible to near-infrared camera (VNIR, 400-1000 nm) and a short-wave infrared camera (SWIR, 1000-2500 nm). Both WIWAMs and PHENOVISION operate as stand-alone machines with a database and intuitive user interface installed locally on the respective control computers, but are connected to a group managed database and interface

dedicated to plant phenotyping. Significant efforts towards centrally organized and ontology-driven data management and proper meta-data collection have thus been realized through the development of the web application PIPPA (the PSB Interface for Plant Phenotype Analysis). PIPPA consists of the central database and user interface, and modules for image analysis by means of scripts that run on a computer cluster. The interface provides the tools for setting up platform-specific experiments, linked with meta-data, the visualization of data retrieved from the platform, including irrigation results, environmental data and images, the visualization and curation of measurements originating from image analysis tasks, and the export of annotated data for further analysis. Future developments within PIPPA include its extension towards full support for all of the current and planned plant phenotyping robots within the group, the provision of modules for data analysis, including meta-analyses, and the inclusion of plant phenotyping data originating from measurements obtained at higher resolution and other levels of organization, such as the individual leaf, tissues and cells (Dhondt et al., 2013).

The Laboratory of Genetics and Horticulture and Product Physiology group, Wageningen University, The Netherlands

In the previous report the focus was largely on the design and functionality of the phenotyping system, which is basically a moving chlorophyll fluorescence imaging camera built into a growth room. This phenotyper has been intensively used since it became functional, with a typical experimental cycle for *Arabidopsis thaliana* lasting 4 weeks. This limit is due to plant overlap which begins after 3-4 weeks of growth and prevents automated analysis of the chlorophyll fluorescence (and other) images made by the phenotyping system. While *A. thaliana* is the target species for the system, small plants of other species can also be easily accommodated. Our phenotyping system was designed to allow us to obtain data of sufficient quantity and quality to allow the localization of genetic factors that affect photosynthetic traits. As the system can accommodate 1440 plants, 360 genotypes can be measured with 4 replicates multiple times per day. This is enough genotypes for effective Genome Wide Association Studies (GWAS) and enough measurements per day to characterize daily fluctuations in photosynthesis. Using a GWAS approach upon various mapping populations we have begun to map and identify the genes that contribute to natural variation in important photosynthetic traits, such as P_{max}, cold tolerance, and photosynthetic acclimation to a changing irradiance. The initial GWAS investigations are often backed up by screens using RILs; the genetically diverse mapping populations used in GWAS offer high genomic mapping resolution, but the statistical power can be low, while the reverse is true for RILs, so a combination of both seems to us to be an effective strategy for getting the best of both options. The analysis of the data obtained from the phenotyper and the curation of this data is still a bottleneck for us,

as for many other phenotyping groups. It is clear we need a closer symbiosis between the data collection and analysis tasks, requiring that the software for collection and analysis are mutually flexible. We are therefore continually evolving both the software for the data collection and that for data analysis together with colleagues in WUR Glastuinbouw and Biometris, the mathematics group of Wageningen University. For the GWAS the main system for data analysis is based on efficient mixed model analysis, while for data collection we use a custom-written package that controls the phenotyping system. At this point, the genetic analysis of photosynthetic traits is progressing well. Using both GWAS and RILs, candidate genes have been identified for the traits that we are interested in. This is work in progress and it would be premature to be specific about the candidates, but over the course of the coming year we hope to confirm that these genes play a role in determining the traits with which they are associated. Our approach to identifying the genetic basis of naturally occurring variation is based upon correlating variation in the nuclear genome with phenotypic variation. The extent to which diversity in the organellar genomes (mitochondrial and chloroplast) contributes to this phenotypic variation is unanswered by this approach, yet both the mitochondrial and chloroplast genomes contain genes that contribute directly or indirectly to photosynthesis. To explore the extent that variation in these organelle genomes contributes to photosynthetic variation we created a population of 49 genotypes in which the nuclear and cytoplasmic genomes of 7 photosynthetically diverse accessions have been reciprocally swapped. We are using this population to explore the contribution of the cytoplasmic genome to photosynthetic variability and the co-evolution of the nuclear and cytoplasmic genomes.

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

The Centre of the Region Haná for Biotechnological and Agricultural Research, Palacky University Olomouc, Czech Republic has installed in 2013 two PlantScreen phenotyping systems and a hydroponic growing unit (Photons Systems Instruments, Brno, Czech Republic; <http://www.psi.cz>). These systems for high throughput phenotyping are located in climate chambers with with LED illumination (max. 1000 μ E) and controlled environment (10-40°C, 30-99% Relative Humidity).

The first fully automated system with a capacity for 1200 Arabidopsis pots or 480 culture multiwell plates in fixed positions employs robotic arm for XYZ positioning. The arm is equipped with chlorophyll fluorescence imaging to measure photosynthetic parameters, visual imaging to analyze leaf area and growth rate, and with VIS-NIR hyperspectral imaging to evaluate different optical indexes and parameters. The system is now validated for use in either high throughput phenotyping of Arabidopsis plants, or high throughput screenings of compound libraries in various

plate-based bioassays (e.g. seed germination, vigour enhancement, abiotic stress tolerance, antifungal activity and herbicidal activity). The other system, with roller conveyer, has a capacity for high throughput phenotyping of up to 640 Arabidopsis, cereals and other crops grown in standardized pots. The measuring cabinet contains acclimation chamber for dark adaptation of plants coupled with an automated weighting and watering area. The cabinet is equipped with chlorophyll fluorescence imaging and visual imaging (top and 2 side views), thermal imaging and SWIR hyperspectral imaging to determine water content. The platforms can be controlled either from the place or via Internet. The operating software enables automatic data evaluation. The hydroponic growing unit allows parallel growing of in total 1200 standardized Arabidopsis pots in eight different hydroponic solutions. The solution can be applied automatically from eight individual tanks with on-line monitored pH and EC stability of the solution by ebb and flow or drip irrigation. During the cultivation the samples of “flow-through” solutions can be collected by auto-sampler and subsequently analyzed using ICP-MS system.

High Resolution Plant Phenomics Centre, Australian National University / CSIRO

ANU has been developing the SpectralPhenoClimatron (SPC), a high throughput system that enables visual growth phenotyping of up to 320 plants per chamber in 7 Conviron climate chambers with multi-spectral LED lighting and dynamic environmental conditions. SolarCalc software controls light intensity and spectrum and chamber temperature and humidity at 1-minute intervals. This allows the creation of more realistic, dynamic growth conditions with diurnal and seasonal cycles and simulated climate shifts for any growing region. 18MP RGB Images are taken at 10 min. intervals and processed into quantitative measures of plant color, size, and growth rate. Quantified developmental phenotypes are tested for genetic association through our GWAS pipeline to yield the genetic loci by which plants sense the environment to control growth.

To generalize and integrate next generation genomics with high throughput phenomics, an open-source software pipeline called 'TraitCapture' is under development (Brown et al, 2014). TraitCapture is a “seeds to traits” pipeline which allows users to track seed/genotype selection, set growth conditions, and analyze phenotypic variation for heritable components through to mapping causative loci via GWAS and QTL analysis. Web-based visualization tools will allow real-time graphing of environment data with associated plant growth in time-lapse. Cloud-enabled GWAS on plant growth variation can be performed during an experiment allowing for real time capturing of heritable traits and trait loci across environments. This feedback allows a user to tune the environments, phenotyping protocols and image analysis to improve QTL detection. When QTL are identified, a user can resort plants based on alternative genotype classes to look for pleiotropic effects on growth, development, and

physiology. Finally, published results should include links to the datasets and analysis protocols expanding on projects like the Phenomics Ontology Driven Data repository. This will allow new and previously cryptic traits to be identified. Importantly, standardized seed sets, growth protocols, phenotyping and analysis tools, will allow replication of experiments between different labs.

A brief list of experiments enabled by TraitCapture includes:

- Iterative QTL identification and tests of pleiotropy.
- Heritability of potential spectral indices using hyperspectral cameras.
- Spatial and temporal distribution of fluorescent pigments under environmental stress.
- Light and temperature interactions on transpiration using Infrared (IR) cameras.
- Genetic basis of photosynthetic activity and efficiency using chlorophyll fluorescence cameras.
- Integration of 2.5D and 3D quantification of plant growth with stereo imaging.

Databases and Other Resources

- CSIRO and the Australian National University are working to develop an open-source software pipeline ('TraitCapture') that will integrate the approaches non-invasive imaging, environmental sensing and modeling to facilitate wider application of phenotyping techniques (Brown et al, 2014).
- IBG2 at Forschungszentrum Jülich is completing the implementation of a fully automated pipeline for Arabidopsis shoot growth and photosynthesis analysis capturing plant histories in the newly developed Phenomis database (Schmidt et al. 2013).
- The PHENOPSIS platform data are publicly available via a web portal interfacing with the database (Fabre et al., 2011; <http://bioweb.supagro.inra.fr/phenopsis/>).
- The Chloroplast Function Database II: The phenotype and segregation data of Arabidopsis Ds/Spm and T-DNA-tagged mutants of nuclear genes encoding chloroplast proteins is available through the Chloroplast Function Database II (<http://rarge.psc.riken.jp/chloroplast>), which includes more than 300 morphological mutants and 48 transmission electron microscopic images of mutant plastid (Fumiyoshi Myouga and Kazuo Shinozaki).
- RIKEN Arabidopsis Genome Encyclopedia (RARGE) has been newly developed as RARGE II. <http://rarge-v2.psc.riken.jp/>. RARGE II includes an integrated phenotype database with RIKEN RAPID and CSHL Trapper DB both for Ac/Ds transposon tagged lines in Arabidopsis, based on using a controlled vocabulary (Akiyama et al., 2014; Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki).

- A Database SciNetS (<https://database.riken.jp>) has been developed to provide an integrated access point for RIKEN data (Tetsuro Toyoda). In this database phenotype information of Activation tagging lines, Ac/Ds transposon lines and FOX lines are available.
- For Genome to Phenome, information of location of T-DNA in the genome is available for RIKEN Arabidopsis Activation Tagging lines (<http://amber/gsc.riken.jp/act/top.php>) (Minami Matsui collaboration with NEC Soft co ltd.) and around 10,000 Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA over-eXpressing) lines is available (Contact Minami Matsui).
- At the National Institute of Agrobiological Sciences (NIAS, Japan) conducted Phenome research on Japonica and Indica rice funded by Genomics for Agricultural Innovation Project (2008-2012). In this project Phenome research is focused on rice root development using root image analysis system (NIAS Agrogenomics Research Center, Dr. Habu, Y).
- At the University of Tokyo, Phenotype analysis program has been developed to characterize the pattern of epidermal cells and guard cells of Arabidopsis leaves and seedlings. This research is funded by JST Project (<http://www.jst.go.jp/pr/announce/20120829-2/index.html>) for evaluation of morphological measurement and named by the software CARTA (clustering-aided rapid training agent) that was developed for autolearning system (Dr. Kutsuna, N. and Hasezawa, S. Univ. Tokyo).

Conferences and Workshops

- Phenomics workshop and two joint workshops "Natural Variation, Evolution and Phenomis" were held during the International Conference on Arabidopsis Research (24th ICAR) 2013, Sydney, Australia
- The 3rd International Plant Phenotyping Symposium "Phenotyping for agriculture sustainability" took place in Feb, 2014 in Chennai, India, by the M. S. Swaminathan Research Foundation, and the International Plant Phenotyping Network, IPPN (http://www.plant-phenotyping.org/chennai_2014). There were about 200 participants, six thematic session and three workshops dedicated to imaging approaches in plant phenotyping, phenotyping protocols for drought stress, and spectral analysis for plant phenotyping.
- The European Plant Phenotyping Network organized a summer school July 2013 on phenotyping methods in Szeged, Hungary and the 2nd Information Workshop (access to EPPN phenotyping facilities) in September at EPSO 2013 meeting held in Porto Heli, Greece.
- NIAS held a Phenome Workshop consisting of 6 talks and 3 training courses on phenome analysis (organized by Dr. Habu, Y).

Selected Publications

- Dhondt S, Wuyts N, Inzé D (2013) Cell to whole-plant phenotyping: the best is yet to come. *Trends in Plant Science*. 18(8):428 -39.
- Fiorani F, Schurr U (2013) Future scenarios for plant phenotyping. *Annual Review of Plant Biology*, 64: 267-291.
- Brown TB, Cheng R, Sirault X, Rungrat T, Murray KD, Trtilek M, Furbank RT, Badger M, Pogson BJ, Borevitz JO (2014) TraitCapture: genomic and environment modelling of plant phenomic data. *Current Opinion Plant Biology*, 18C:73-79.
- Moore CR, Johnson LS, Kwak IY, Livny M, Broman KW, Spalding EP (2013) High-throughput computer vision introduces the time axis to a quantitative trait map of a plant growth response. *Genetics*, 195: 1077 -1086.
- Granier C, Vile D (2014) Phenotyping and beyond: modelling the relationships between traits. *Current Opinion Plant Biology*, 18C:96-102.

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- Akiyama K, Kurotani A, Iida K, Kuromori T et al. (2014) RARGE II: An Integrated Phenotype Database of Arabidopsis Mutant Traits Using a Controlled Vocabulary. *Plant Cell Physiology*, 55(1): e4 doi:10.1093/pcp/pct165P.
- Dhondt S, Gonzalez N, Blomme J, De Milde L et al. High resolution time-resolved imaging of in vitro Arabidopsis rosette growth. (submitted).
- Dhondt S, Wuyts N, Inzé D (2013) Cell to whole-plant phenotyping: the best is yet to come. *Trends in Plant Science*. 18(8):428 -39.
- Fabre J, Dauzat M, Nègre V, Wuyts N et al. (2011) PHENOPSIS DB: an information system for Arabidopsis thaliana phenotypic data in an environmental context. *BMC Plant Biology* (11): 77.
- Schmidt F, Bruns B, Bode T, Scharr H et al. (2013) A Distributed Information System for Managing Phenotyping Mass Data, 33. *Lecture Notes in Informatics*, pp. 299-302.
- Skirycz A, Vandenbroucke K, Clauw P, Maleux K et al. (2011) Survival and growth of Arabidopsis plants given limited water are not equal. *Nat Biotech*. 29(3):212 -4.

Proteomics

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

By Joshua Heazlewood (Co-chair) and Alexandra Jones (Co-chair) with contributions from subcommittee members.

Progress Towards Road Map Goals

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

- Members of the proteomics subcommittee (MASCP) maintain and continually update extensive Arabidopsis proteomic repositories that provide extensive information on protein expression, annotation and function. Much of this information has also been made readily available through an aggregation tool, the MASCP Gator, which enables a simple overview of these data.
- The targeted and accurate quantitation of Arabidopsis proteins by mass spectrometry (MRM) is a fast developing field. A number of subcommittee members have created resources to support these types of analyses. In the past years, the Arabidopsis Proteotypic Predictor was developed to further assist in the selection of protein specific peptides for these types of analyses.

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

- The 1001 Proteomes portal was released in 2012 and provides protein level information generated from the natural variation sequencing projects. These data were updated to the latest TAIR model in the past year.

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

- Members of the proteomics subcommittee also serve as members of International Plant Proteomics Organization (INPPO) which aims to employ proteomic approaches to assist in the development of crops. An INPPO meeting will be held in 2014, with a number of MASCP members in attendance.
- The utilization of proteomic techniques initially pioneered in Arabidopsis have been expanded into economically important plants in the past year, this has included work in pine, maize and rice.

(D) Build the International Arabidopsis Informatics Consortium (IAIC), an international informatics and data infrastructure

- Many of the resources developed by subcommittee members have been constructed to enable integration with the resources being developed by the IAIC. The subcommittee intends to encourage new resources to be compatible with the emerging informatics infrastructure for Arabidopsis.

(E) Deepen International Cooperation and Coordination

- The subcommittee has an active involvement with the Model Organism Proteomes program (iMOP) as part of the Human Proteome Organization (HUPO).
 - The subcommittee has an active involvement with the International Plant Proteomics Organization (INPPO)
 - The subcommittee continues to run proteomic workshops. A workshop was held at ICAR 2013 (Sydney, Australia).
- (F) Subcommittee specific goals
- Maintain an active Arabidopsis proteomics subcommittee (<http://www.masc-proteomics.org/>)

Future Goals

- (A) Build a predictive model of an Arabidopsis plant from its molecular parts
- Maintain a network of proteomic data repositories and tools to support the development of a predictive model of Arabidopsis. Key to this is the ongoing interoperability of these resources to readily enable the data to be captured and utilized. The subcommittee is continually adding and updating connections between these resources through the MASCP Gator.
- (B) Exploit the wealth of natural variation that exists in Arabidopsis to further our understanding of adaptation and evolution
- With the development of targeted proteomic resources and the 1001 Proteomes, MASCP has provided substantial infrastructure for the community to explore Arabidopsis natural variant collections using proteomic approaches. These tools and utilities will be maintained by relevant subcommittee members.
- (C) Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa
- Many of the proteomic techniques initially pioneered in Arabidopsis are now being applied to other plant systems. We will continue to support this process by making the online infrastructure and workflows available to the community e.g. the MASCP Gator code is available through GitHub
- (D) Build the IAIC and develop efficient informatics tools and repositories further
- By integrating new resources and upgrading current repositories, the Arabidopsis proteomics subcommittee is well placed to support the development of the AIP.
- (E) Deepen international cooperation and coordination
- We will continue our involvement with Model Organism Proteomes program (iMOP) as part of the Human Proteome Organization (HUPO) and the International Plant Proteomics Organization (INPPO).

Tools and Resources

- Pep2Pro - proteo-genomic resource (<http://fgcz-pep2pro.uzh.ch/>) by Baerenfaller
- ProMEX - mass spectral resource (<http://www.promexdb.org/>) 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 va Wijk
- AT_CHLORO - plastid proteomic resource (http://www.grenoble.prabi.fr/at_chloro/) by Rolland
- AraPeroX - peroxisome proteomic database (<http://www3.uis.no/AraPeroXV1/>) by Reumann
- PhosPhAt - phosphoproteome database (<http://phosphat.mpimp-golm.mpg.de/>) by Schulze
- P3DB - plant phosphoproteome database (<http://digbio.missouri.edu/p3db/>) by Thelen
- RIPP-DB - phosphoproteome database (<http://phosphoproteome.psc.database.riken.jp/>) by Nakagami
- MASCP Gator - proteomics aggregation portal (<http://gator.masc-proteomics.org/>) by MASCP
- 1001 Proteomes - non-synonymous SNPs from natural variants (<http://1001proteomes.masc-proteomics.org/>) by Heazlewood
- MRMAid - MRM design tool (<http://elvis.misc.cranfield.ac.uk/mrmaid/>) by Jones

Conferences and Workshops

Workshop "Using proteomics to identify receptor complexes and signaling events" 24th International Conference on Arabidopsis Research 2013

Workshop organizers: Joshua Heazlewood (Lawrence Berkeley National Laboratory, USA), Alexandra Jones (The Sainsbury Laboratory, UK), Harvey Millar (The University of Western Australia, Australia)

Selected Publications

New Proteomic Approaches:

- Li L, Nelson CJ, Carrie C, Gawryluk RM, Solheim C, Gray MW, Whelan J, Millar AH (2013) Subcomplexes of ancestral respiratory complex I subunits rapidly turn over *in vivo* as productive assembly intermediates in Arabidopsis. *J Biol Chem* 288(8):5707-5717.

New Proteomic Tools:

- Behrens C, Blume C, Senkler M, Eubel H, Peterhansel C, Braun HP (2013) The 'protein complex proteome' of chloroplasts in *Arabidopsis thaliana*. *J Proteomics* 91:73-83.

- Taylor NL, Fenske R, Castleden I, Tomaz T, Nelson CJ, Millar AH (2014) Selected reaction monitoring to determine protein abundance in *Arabidopsis* using the *Arabidopsis* proteotypic predictor. *Plant Physiol* 164(2):525-536.

Cross-species proteomic approaches:

- Parsons HT, Weinberg CS, Macdonald LJ, Adams PD, Petzold CJ, Strabala TJ, Wagner A, Heazlewood JL (2013) Golgi enrichment and proteomic analysis of developing *Pinus radiata* xylem by free-flow electrophoresis. *PLOS ONE* 8(12):e84669.
- Facette MR, Shen Z, Bjornsdottir FR, Briggs SP, Smith LG (2013) Parallel proteomic and phosphoproteomic analyses of successive stages of maize leaf development. *Plant Cell* 25(8):2798-2812.

Systems and Synthetic Biology

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

Siobhan Brady (Chair), Malcolm Bennett (Co-chair), Susannah Lydon

Progress Towards Road Map Goals

Key aims of the MASC subcommittee members will be to

- Promote systems biology research in *Arabidopsis* research. Systems approaches involving computational and mathematical modeling are becoming much more important as our knowledge of the regulatory signals and pathways controlling plant growth and development become increasingly detailed and their network behavior and outputs less intuitive.
- Help bridge the 'genotype to phenotype gap', by encouraging researchers to move beyond the network and cellular scales, and use multiscale modelling to predict emergent dynamics at the tissue, organ and organismal levels through the use of virtual organ models and digital organisms.
- Underpin synthetic biology applications in crops by facilitating translation of knowledge generated using systems approaches in *Arabidopsis* and other plant species.

Considerable progress has been made towards the goals outlined in the MASC road map and for our subcommittee. Of particular note, modeling approaches at a variety of scales (spatial and temporal) have become increasingly prevalent in *Arabidopsis* research as have synthetic biology approaches. Several of these studies are highlighted in the Selected Publications section. Also – many different training programs and workshops took place in the past year across the world. There is an increasing number of *Arabidopsis* scientists that are being trained in both computational and experimental biology and who are able to intersect these fields more seamlessly.

Future Goals

The US National Science Foundation Directorate for Biological Sciences (NSF/BIO) and the United Kingdom Biotechnology and Biological Sciences Research Council (BBSRC) have announced a pilot program to allow for reciprocal acceptance of peer review through unsolicited mechanisms. This pilot program will allow for submission of a single collaborative research proposal with particular priorities for data driven biology and for systems approaches to biosciences. In the Fall of 2015 funding proposals will also be accepted for synthetic biology. This funding effort will be an important mechanism by which multinational collaborations in systems and synthetic biology using *Arabidopsis thaliana* as a model organism can be realized.

Incorporating the vast variety of modeling in Arabidopsis that has been described in the literature and translating these to central databases like that of the Arabidopsis Information Portal will be a much needed data resource for systems and synthetic biology.

Tools and Resources

A variety of Arabidopsis-specific tools and resources have been generated that visualize the connections between co-expression and gene regulation in Arabidopsis as well as with projections to other species. Other highlights include profiling experiments which link cell type-expression profiles to secondary metabolite abundance and cis-regulatory motif enrichment to gene expression networks. Finally – the DOE Systems Biology Knowledge Base (KBase) has implemented tools for modeling metabolism and co-expression networks, while the Bio-Analytic Resource for Plant Biology has updated their molecular interaction set and is making strides towards making these interaction data available in a standardized format for the systems biology community.

- The ATTED-II database contains co-expression data for Arabidopsis genes and has now been updated with RNAseq data for Arabidopsis as well as coexpression for four dicots (soybean, poplar, grape and alfalfa) and one monocot, maize (<http://atted.jp/>).
- Secondary metabolite data has now been profiled at cell type resolution in the Arabidopsis root (Moussaief et al., 2013, PNAS).
- The Bio-Analytic Resource for Plant Biology (www.bar.utoronto.ca) now contains approximately 100,000 interactions in PSISCQUIC format which standardizes molecular interaction databases programmatically. In addition, from the regulatory network perspective, 355 Arabidopsis-bacterial protein interactions have now been included in the Arabidopsis Interactions Viewer. These advances will likely be included in “apps” for the new Arabidopsis Information Portal via funding through Genome Canada.
- The DOE Systems Biology Knowledge Base (KBase) has tools developed for building genome scale metabolic model reconstruction as well as tools for the construction of co-expression networks (www.kbase.us).

Conferences and Workshops

- GARNet Plant Synthetic Biology meeting, Nottingham (21-22 May 2013)
- International Conference on Arabidopsis Research, Sydney, Australia (24-28 June 2013)
A session on Emerging Technologies and Systems Biology was chaired by Brian Gregory and Motaki Seki (UPenn and RIKEN respectively) where research highlighting chromatin dynamics and gene expression at spatiotemporal resolution as well as for gene regulatory networks and membrane protein interactomes were discussed.

- Society of Experimental Biology Main Meeting, Valencia Spain (3-6 July 2013)
A session – “Root biology: modeling across the scales into the rhizosphere” was organized by Stefan Kepinski and Malcolm Bennett.
- ASPB Plant Biology 2013, Providence Rhode Island (20-24 July 2013)
A minisymposium on phenomics and on metabolic flux detailed how high spatial and temporal resolution phenomic data can be linked with gene regulatory and metabolic networks.
- Data Mining with iPlant, Warwick (17-20 September 2013)
An introduction to iPlant, followed by tutorials and advanced workshops on using the iPlant cyberinfrastructure. Organised by GARNet.
- Open meeting of the Synthetic Biology Leadership Council, London (16 October 2013)
- Panamerican Association for Biochemistry and Molecular Biology, Puerto Varas, Chile (9-14 November 2013)
A symposium on Genomics and Systems Biology was organized by Rodrigo Gutierrez.
- Second International Symposium on the Nitrogen Nutrition of Plants (18-22 November 2013)
A Systems Biology session was chaired by Rodrigo Gutierrez.
- Applications for Synthetic Biology in Industrial Biotechnology (29 November 2013)
- Plant Genomes and Biotechnology – From Genes To Networks, Cold Spring Harbor Laboratory, New York (4-7 December, 2013)
A session on Synthetic Biology and Networks was held.
- SEB special symposium on Synthetic Biology, Charles Darwin House, London (8-10 January 2014)
- EMBO Practical Course on Metabolomics Bioinformatics for Life Scientists, European Bioinformatics Institute (17-21 March 2014)
- Agri-innovation 2014: Emerging science and technologies in crop research, Imperial College London (25 March 2014)

This conference provided an update on several areas of crop research, with focus on innovation in agriscience and technology, including synthetic biology

Selected Publications

- Peret B, Middleton A, French A, Larrieu A, Bishopp A, Njo M, Wells D, Porco S, Mellor N, Band L, Casimiro I, Kleine-Vehn J, Vanneste S, Sairanen I, Mallet R, Sandberg G, Ljung K, Beeckman T, Benkova E, Friml J, Kramer E, King J, De Smet I, Pridmore T, Owen M, Bennett M (2013) Sequential induction of auxin efflux and influx carriers regulates lateral root emergence. *Molecular Systems Biology*, 9:699
- Chang KN, Zhong S, Weirauch MT, Hon G, Pelizzola M, Li H, Huang SS, Schmitz RJ, Urich MA, Kuo D, Nery JR, Qiao H, Yang A, Jamali A, Chen H, Ideker T, Ren B, Bar-Joseph Z, Hughes TR, Ecker JR. (2013) Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in *Arabidopsis*. *Elife*. 2:e00675
- Umezawa T, Sugiyama N, Takahashi F, Anderson JC, Ishihama Y, Peck SC, Shinozaki K. (2013) Genetics and phosphoproteomics reveal a protein phosphorylation network in the abscisic acid signaling pathway in *Arabidopsis thaliana*. *Science Signaling*. 6(270):rs8
- Geng Y, Wu R, Wee CW, Xie F, Wei X, Chan PMY, Tham C, Duan L, Dinneny JR. A Spatiotemporal Understanding of Growth Regulation during the salt stress response in *Arabidopsis*. *Plant Cell*. 25(6):2132-2154.
- Krouk G, Lingeman J, Colon M, Coruzzi G, Shasha S. (2013) Gene regulatory networks in plants: Learning causality from time and perturbation. *Genome Biology*. 13(6):124. (There was a special issue of *Genome Biology* in June 2013 on Plant Genomics: Plant Genomics: Sowing the Seeds of Success.)

References

Moussaief A, Rogachev I, Brodsky L, Malitsky S et al. (2013) High-resolution metabolic mapping of cell types in plant roots. *PNAS*. 110(13):E1232-41.

Arabidopsis Community Projects and Resources

One of the major goals of the Multinational Arabidopsis Steering Committee (MASC) is to coordinate and strengthen international collaboration. The Arabidopsis community is and has always been very open and researchers and funding bodies look back now on more than 20 years of strong international collaboration and data sharing. Since 1991 the Arabidopsis community has announced three decadal plans outlining major goals. Each of the last decades was flagged by one major unifying aim.

In the early days of the Arabidopsis genome research project (1991-2001) the protruding aim was the completion of the Arabidopsis genome. This efforts included the founding of the two stock and resource centers ABRC (Arabidopsis Biological Resource Center, U.S.) and NASC (Nottingham Arabidopsis Stock Center, U.K.). The next decade also brought a great new initiative that met the needs of the growing Arabidopsis research community: TAIR (The Arabidopsis Information Resource) was founded in 2001. At this time one of the major unifying aims of the Arabidopsis community was to functionally annotate the *Arabidopsis thaliana* genes. Today one major goals the Arabidopsis community wants to focus on together is to obtaining 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 (Weckwerth, 2008; Lavagi, 2012). To achieve this goal new ways and platforms have to be developed, to enable open sharing of the vast amount of data generated by today's omics approaches. In order to provide a flexible platform the IAIC (International Arabidopsis Informatics Consortium) founded the AIP (Arabidopsis Information Portal) in 2013 that is funded by NSF (National Science Foundation, U.S.) and BBSRC (Biotechnology and Biological Science Research Council, U.K.).

The Arabidopsis community and the whole plant community thrive and profit from the resource and stock centers (page 29) as well as from informatics and data sharing resources (page 31). TAIR and the resource and stock centers contribute since 2007 to the annual MASC report. This year the MASC has decided to include and highlight major internationally collaborating research projects and resources that are strongly supported by Arabidopsis researchers and focus on outreach to other plant species (page 34). It is important to highlight these international efforts besides the national efforts of individual research labs that can be found e.g. in the country reports section (page 50). The projects and resources listed here also showcase the big network of the Arabidopsis with other plant communities.

This year the following projects and resources contributed to the MASC report:

Resource and Stock Centers

- Arabidopsis Biological Resource Center (ABRC) (page 29)
- Nottingham Arabidopsis Stock Center (NASC) (page 30)
- RIKEN-Biological Resource Center (BRC) (page 30)

Arabidopsis Informatics and Data Sharing Resources

- International Arabidopsis Informatics Consortium (IAIC) (page 31)
- Arabidopsis Information Portal (AIP) (page 32)
- The Arabidopsis Information Resource (TAIR) (page 32)

Plant Projects and Resources with Strong Participation of Arabidopsis Community

- Bio-Analytic Resource for Plant Biology (BAR) (page 34)
- BrassiBase (page 34)
- Epigenomics of Plants International Consortium (EPIC) (page 35)
- European Plant Phenotyping Network (EPPN) (page 36)
- iPlant Collaborative (page 36)

Besides these many other international initiatives with major contributions from Arabidopsis researchers exist, e.g. The 1001 genomes Project (www.1001genomes.org), The Plant and Microbial Metabolomics Resource (<http://metnetdb.org/PMR/>) and the International Plant Phenotyping Network (<http://www.plant-phenotyping.org/>).

Your Arabidopsis related project/consortium/network/initiative was not listed here? Please contact MASC coordinator: luise.brand@uni-tuebingen.de.

References

- Lavagi I, Estelle M, Weckwerth W, Beynon J, Bastow RM (2012) *From Bench to Bountiful Harvests: A Road Map for the Next Decade of Arabidopsis Research. The Plant Cell, Vol. 24: 2240-2247*
- Weckwerth W, Baginsky S, van Wijk K, Heazlewood JL, Millar H (2008). *The multinational Arabidopsis steering subcommittee for proteomics assembles the largest proteome database resource for plant systems biology. J. Proteome Res. 7: 4209-4210.*

Resource and Stock Centers

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

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

The ABRC collects, preserves, reproduces and distributes diverse seed and other stocks of *Arabidopsis thaliana* and related species for research and education. Seed stock holdings include insertion lines covering 28,929 genes (24,894 protein-coding), out of which 48,830 lines (covering 27,159 loci) represent the SALK Homozygote T-DNA Collection; the 11,000+ TILLING lines; 2,925 distinct natural accessions, a number of which has been sequenced by the 1001 Genomes Project; 31 recombinant inbred populations; a set of near-isogenic lines; a set of AMPRIL lines (Arabidopsis Multiparent Recombinant Inbred Lines); RNAi lines; transgenic lines; 50+ accessions of the genus Brassica; and approximately 70 accessions of other closely related species. DNA resources at ABRC include full-length ORF and cDNA clones for almost 17,000 genes, BACs covering the entire genome, BACs of nine related species, the AGRIKOLA GST entry clones, various sets of expression clones, 12,466 amiRNA clones, and over 500 vectors.

Within the reporting period, the Center sent over 93,000 samples for all resources combined, excluding the education kits. A total of 3,411 stocks in this category has been distributed to 16 countries and 36 US states since their release three years ago. The education website (<http://abrcoutreach.osu.edu>) continues to provide news and information related to Arabidopsis education resources, as well as ordering to teachers, parents and other educators.

ABRC worked closely with The Arabidopsis Information Resource (TAIR) to complete the transition of their servers to iPlant. TAIR has since moved to a subscription-based model. Subscription is now required for companies and will be required for academic users after April 2014. Subscription will provide access to TAIR pages, except for the ABRC stock detail and ordering pages which will remain free of charge. ABRC will continue to collaborate with the Nottingham Arabidopsis Stock Centre (NASC) on the development of a database independent of TAIR that can seamlessly interact with the Arabidopsis Stock Module database and with the Arabidopsis Information Portal (AIP).

Quality control at ABRC is performed on newly donated stocks, on stocks being reproduced and on stocks in preservation on a regular basis. In addition, user complaints are recorded in our local database and the issues are being addressed when presented to the ABRC. Our current error rates, defined as the number of complaints/number of stocks ordered, are between 800 per million and 2,000 per million for seed stocks. DNA stocks have a slightly higher error rate, and ABRC is starting to sequence and analyze DNA stocks in a more routine basis to decrease errors. In addition to

continuing to enforce community-driven quality control, ABRC started checking and removing from distribution all T-DNA insertion lines for which we confirm an original report that a researcher was not able to identify an insertion. Based on the recommendations of the Advisory Board, we made available online (<http://abrc.osu.edu/quality-control>) the metrics of T-DNA insertion analysis and germination tests, thus making the quality control process more transparent to users.

Retirement of certain types of DNA stocks, in agreement with our Advisory Board, is planned for the next year. Cost-saving measures (e.g. re-plating DNA stocks from 96- to 384-well plates to save space) have been applied.

News

We have created a Tweeter account @ABRC_News which we use in addition to the TAIR Breaking News and ABRC News feature to communicate new events or donations to our users. Based on the suggestion of the Advisory Board, we have also made available online a set of slides talking about the ethics of sharing resources, with a goal to educate the public and young researchers about the importance of donating stocks and hoping that in this way we can improve the culture of donating stocks.

Significant number of T-DNA lines received last year was represented by the GABI-Kat collection donated by Bernd Weisshaar through the European Arabidopsis Stock Center (NASC). Many confirmed T-DNA-insertion lines have been donated by researchers in the community. As an example, we received 128 confirmed lines from Rob Last's lab and 122 from Jeff Dangl's lab in this period. 326 amiRNA lines from Julian Schroeder's lab represent a novel type of seed resource that we anticipate will get a lot of interest in the near future. New DNA stocks received this year include a number of vectors and clones and 20 amiRNA libraries donated by Julian Schroeder's lab.

More specifically, new DNA donations are highlighted by:

- 20 amiRNA libraries for large-scale genetic screens addressing the functional redundancy of genes in gene families
- 800+ amiRNA clones
- 81 vectors (including 44 biovectors: cloning system for functional genomics studies and 32 aequorin expression vectors that target the calcium sensor aequorin to specified subcompartments of the plant cell)
- 2 seed phage display cDNA libraries

New seed donations are represented by:

- 500+ SALK_C lines
- 8 INTACT lines - enables the isolation of nuclei from
- natural accessions
- 362 amiRNA lines
- 404 RIL population for genetic mapping studies

Two Education Kits have also been released in this period.

The Nottingham Arabidopsis Stock Centre (NASC) www.arabidopsis.info

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

For regular updates on releases of stocks and array data from NASC please see the news section of our website or visit/subscribe to @NascArabidopsis (<http://twitter.com/#!/NASCArabidopsis>).

We have one major item of very positive news about NASC Stock Centre longevity and stability: Thanks to the BBSRC (UK funding agency) who have re-funded NASC germplasm bioinformatics until 2018. This new grant will maintain and extend our capabilities and is also specifically aimed at integrating our informatics services with AIP (please also see their report in this MASC document). We already offer many formalized Web Services (SOAP2) and for the module we will also be offering REST.

As part of the new grant we have inaugurated a new strategic advisory panel and are fortunate to have this headed by a long time supporter: Prof. Don Grierson (FRS, OBE) - familiar to many of you for his work on tomato. The committee includes various community representatives including specialists in distributed computing.

Although you, our community, are always welcome to send us queries, suggestions and comments directly (please do also drop in at our booth at the ICAR - shared with ABRC and toting various goodies and smiling faces) - we really do appreciate and encourage long-term strategic ideas and yes, even complaints! So if you are too shy to suggest things directly - the emails of the panel are all on our site, please do make use of them.

Ordering statistics at NASC continue to be healthy and high for the seed service (over 160,000 stocks sent in the 2013/14 NASC year: Apr-Mar); and we have released several new stocks, collections and lines this year. Please see our site for a comprehensive list as always.

See you in Canada!

RIKEN BRC

www.brc.riken.jp/lab/epd/Eng/

By Masatomo Kobayashi (coordinator)

RIKEN BioResource Center (RIKEN BRC) is the core center for Arabidopsis as well as mice, microbes, cells and DNA materials in the National BioResource Project (NBRP) funded by the Japanese government. Experimental Plant Division (plant@brc.riken.jp) collects, preserves and distributes seed stocks of Arabidopsis that include transposon-tagged lines (RATM line, 17,671 lines; insertion site information available; 3,119 homozygous lines also available), activation-tagged (T-DNA) lines (for phenotype screening; 36,650), FOX lines (Arabidopsis plants that over-express Arabidopsis or rice full-length cDNA; for phenotype screening; 20,739), natural accessions (SASSC stock) and individual mutants and transgenic lines generated in Japan. In

addition, the Division distributes DNA resources such as full-length cDNA clones of Arabidopsis (RAFL clone; 251,382), *Physcomitrella patens* (149,363), poplar (23,100), cassava (19,968), tobacco (3,068), *Thellungiella halophila* (19,429), *Brassica rapa* (9,903) and *Striga hermonthica* (35,198). In 2013, RIKEN BRC started distributing 39,746 full-length cDNA clones of *Brachypodium distachyon*, a monocot plant suitable for laboratory works. We also preserve and distribute plant cultured cell lines which include Tobacco BY-2 and Arabidopsis T87 cells. We shipped cell lines both domestic and overseas institutions and universities. Total number of plant materials in the Division is 829,252, and 1,746 laboratories around the world have received our materials.

RIKEN BRC has joined in Asian Network of Research Resource Centers (ANRRC). Last year, 5th ANRRC meeting was held in Japan during October 30 - November 1, 2013. The 6th meeting will be held in China in this autumn.

News

The SABRE (Systematic consolidation of Arabidopsis and other Botanical REsource) database enables users to cross-search plant cDNA resources, using TAIR gene models as a skewer. The cDNA clones of six species in NBRP (wheat, barley, morning glory, lotus, Glycine, tomato) were newly added to the SABRE under the support by the Grant-in-Aid for the Life Science Database Integration Project "Integration of plant genome databases in Japan based on genomic information". Now users can search cDNA clones of 14 plant species including Arabidopsis using various types of key words. In addition, its interface has been reformed to create a user-friendly environment. (<http://sabre.epd.brc.riken.jp/SABRE2.html>)

Fukami-Kobayashi K, Nakamura Y, Tamura T, Kobayashi M. SABRE2: a database connecting plant EST/full-length cDNA clones with Arabidopsis information. *Plant Cell Physiol.* 2014 Jan;55(1):e5. doi: 10.1093/pcp/pct177. PMID: 24323624.

Conferences

The 38th Naito Conference "Molecule-based biological systems" will be held in Sapporo, Japan from Oct.7 to 10, 2014. In oral sessions, 27 eminent scientists invited from the world will give lectures. Young scientists will join the conference and present posters. The Naito Foundation supports this conference.

Japanese government starts a new project in 2014

- A new project, "Cross-Ministerial Strategic Innovation Promotion Program (SIP) will launch in 2014. Total amount of the budget is expected to be \$500M. One of the subjects in SIP is "Technologies for creating next-generation agriculture, forestry and fisheries", in which both basic and applied plant scientists will join and collaborate to improve knowledge and technologies useful for agriculture.

Arabidopsis Informatics and Data Sharing Resources

International Arabidopsis Informatics Consortium (IAIC)

<http://www.arabidopsisinformatics.org/>

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

The purpose of the International Arabidopsis Informatics Consortium (IAIC), initiated in 2009 and formally established in 2011, based on funding awarded by the US National Science Foundation, is to better coordinate global Arabidopsis informatics efforts, advance plant biology, create novel opportunities for research and education, and strengthen international collaborations. The impetus for the development of the consortium was to determine how best to maintain the continuity of key Arabidopsis bioinformatics resources while simultaneously expanding the breadth and depth of available resources. The overarching aim is to include new technologies, resources, and participants on a global scale.

A key request by the IAIC to the community is to participate in the IAIC through workshops and meetings, and through the development of your own resources (modules) that can integrate into the AIP for use by the community.

Project goals include

1. Bringing together groups to identify and address key informatics needs and challenges of the Arabidopsis community, in both the near term and longer term.
2. Establish an IAIC website to coordinate activities and serve as a resource for the community to stay abreast of progress, learn of IAIC events, and participate in activities, including providing feedback.
3. Facilitate a collaborative, international effort to establish an Arabidopsis Information Portal (AIP) that will serve the current and future needs of the global plant biology community and replace TAIR, the previous community resource.
4. Facilitate community governance via election of a Scientific Advisory Board (SAB).
5. Maintain a dialog with the Arabidopsis community via scientific publications, presentations, and workshops at key plant biology conferences, seeking opportunities to present project updates and solicit input in conference platform sessions.
6. Engage with PIs of AIP-funding proposals and facilitate communication with the IAIC SAB to ensure community engagement and participation in development of the AIP.
7. Advocate for community interests, e.g. maintenance and curation of the 'gold-standard genome', and convey information for community involvement via the modules it produces.

8. Liaise with leaders of the major global Arabidopsis stock centers to ensure continued collaborations with the AIP.
9. Develop a plan for the IAIC to communicate with funding agencies and effectively convey relevant funding opportunities to the community.

Key goals accomplished recently

1. Collaborative development of a paper entitled 'Developing the Arabidopsis Information Portal', published as an Open Access article in the journal *The Plant Cell* (June, 2012). The publication focused on outcomes of a previously-held Design Workshop, a discussion of the steps needed to move from the concept of the AIP to implementation, lessons learned from the Design Workshop, and the importance of a community governance and guidance mechanism.
2. The project's Steering Committee (SC) and the Scientific Advisory Board (SAB) worked collaboratively with a team of community members interested in submitting a proposal to secure funding to establish the new Arabidopsis Information Portal. A proposal was submitted by Chris Town and colleagues to the U.S. National Science Foundation and funding was awarded in September, 2013.
3. Three AIP modules were funded by international IAIC collaborators in 2013: Nick Provart (Canada), Bjorn Usadel (Germany) and Sean May (UK).
4. An electronic newsletter was developed and distributed to the community.

Future IAIC goals

1. Hold a satellite workshop at the summer Arabidopsis Conference, including a public preview release of the AIP, to provide an overview of the requirements/APIs for developers to provide tools or data sets to the portal and to provide a guided tour of the portal and show how the typical user can access the various data sets available.
2. Facilitate inclusion into the AIP of new resources, or those under development by community members.
3. Plan for a 'module hackathon' potentially for the fall of 2014.

Conferences

The IAIC's Interim Director, members of the IAIC Steering Committee, the AIP PIs, and other collaborators gave presentations on aspects of AIP and IAIC efforts including (1) progress on AIP development, (2) various modules under development, (3) linking the AIP internationally, and (4) TAIR and its new sustainability model including:

2013: Plant and Animal Genome Meeting (San Diego, USA); 24th International Conference on Arabidopsis Research (Sydney, Australia)

2014: Plant and Animal Genome Meeting (San Diego, USA); Upcoming: workshops at the 25th International Conference on Arabidopsis Research (Vancouver, Canada), including a training opportunity for Arabidopsis researchers and computational users.

Funding Acknowledgement

IAIC activities are supported by an award from the US National Science Foundation to Interim Director Blake Meyers; Award #1062348.

Governance

The Scientific Advisory Board is composed of: Mark Estelle, Chair (USA), Xuemei Chen (USA), Gloria Coruzzi (USA), Mark Forster (UK), Paul Kersey (UK), Magnus Nordborg (Austria) and Kazuki Saito (Japan).

Community Stewardship

The Steering Committee is composed of: Blake Meyers, Interim IAIC Director (USA), Ruth Bastow (UK), Jim Beynon (UK), Volker Brendel (USA), Rion Dooley (USA), Erich Grotewold (USA), Nick Provart (Canada), Dan Stanzione (USA) and Doreen Ware (USA).

The Arabidopsis Information Portal (AIP)

www.araport.org

By Chris Town (Principal Investigator)

The concept of the Arabidopsis Information Portal (AIP) as a second generation center for the aggregation, integration and dissemination of information was developed through a series of workshops organized by the IAIC that culminated in the design workshop in Atlanta in December 2011. Proposal development, led by Chris Town, began early in 2012, ultimately involving the Texas Advanced Computing Center (TACC), the University of Cambridge, UK and TAIR as collaborating institutions. The proposal was submitted to NSF in September 2012. A series of discussions, the development of a detailed Project Execution Plan and a reverse site visit culminated in an award announcement in September 2013. The 5-year project is initially funded for 2 years with further funding contingent upon a successful reverse site visit early in 2015.

After a kick-off meeting at J. Craig Venter Institute (JCVI) last October, work on portal development began. This included acquiring computational resources, installing software etc. prior to actual data assimilation. The long term goal of the AIP is to achieve integration via federation where data are retrieved on demand from diverse distributed resources that independently managed and funded. However, until sufficient web services are available we are adopting a hybrid model in which diverse data types are retrieved in bulk and loaded into a project-specific instance on InterMine, a database design that has been adopted by many of the non-plant model organisms.

After a fleeting glimpse of Araport (www.araport.org) at the IAIC Workshop at PAG in January, much effort was invested in improving the usability and stability of the user interface and data infrastructure and adding new data types. Preview 2 of the site was released on April 2, 2014 and in its opening days seems to be running without problems, although the load has not so far been very heavy. This first release provided various views of the *Arabidopsis thaliana* Col-0 genome using TAIR10 data with two genome browsers, JBrowse and GBrowse, and an instance of InterMine called ThaleMine that has been customized to present many of the data types familiar to users of TAIR "Locus Detail" pages as well as other information such as protein interaction and Affymetrix-derived expression data provided by BAR. Over the coming months we will continue to improve the site usability and plan to add various data types that may include epigenomics, RNA-seq, 1001 genomes' SNPs and co-expression data as well as other data types or new features suggested by our Scientific Advisory Board or the user community. A full site release is scheduled ahead of the Vancouver ICAR meeting.

Looking ahead, the AIP will present in the "Bioinformatics Resources for Plant Biology Research" minisymposium at the ASPB meeting in Portland Oregon in July 2014 and will host a developer and user workshop immediately prior to the formal opening of ICAR 2014 in Vancouver. One part of this workshop will provide guidance to potential developers of apps for the AIP; the second will be a demonstration of how to navigate and make best use of the AIP functionalities. A hands-on workshop for developers is planned for the fall 2014 in Austin, Texas.

The AIP project receives funding from the NSF (USA) and BBSRC (UK).

The Arabidopsis Information Resource (TAIR)

www.arabidopsis.org

By Eva Huala (Director)

Over the past year, TAIR has focused efforts on two main areas where we see the greatest need and greatest potential for a positive impact on plant research. These are development of a sustainable funding model capable of providing stable support for research infrastructure and datasets over the long term, and capture of experimentally validated results on plant gene function from the research literature. These efforts are complementary to those described elsewhere in the MASC report such as development of the AIP portal and other informatics resources. Taken together, these infrastructure components will provide plant researchers with a rich and diverse set of data and tools for the long term.

Sustainable Funding Model

As a popular and highly used database, TAIR is in a good position to pioneer a new approach to funding scientific resources that relies on contributions by its many users. This approach has several advantages over the traditional grant funding model, including potentially greater stability

and longevity for fundamentally important datasets, close alignment of project goals with the needs of the research community, and the ability to scale up funding support in proportion to the demand for a resource. A subscription model also provides a way to fund valuable activities that are difficult to support via traditional grant funding, including manual curation of research literature and software maintenance and improvements. To realize the goal of sustainable long-term funding, the TAIR staff have founded a new nonprofit entity, Phoenix Bioinformatics, to serve as TAIR's new institutional home. Moving the TAIR project from its previous home at the Carnegie Institution for Science to Phoenix Bioinformatics has allowed us to make the transition to support from subscriptions at the country, consortium, university library, laboratory and individual levels. It also provides the freedom to explore additional future funding possibilities such as advertising revenue and open access fees for data deposition or curation to support TAIR's work of capturing and integrating data.

Progress on Subscriptions

TAIR implemented a subscription requirement for companies on Oct. 1 2013, followed by subscriptions for academic institutions on April 1 2014. We have had an excellent response from both companies and academic institutions, and with this support we will be able to continue our work for the research community. A list of academic and research institutions that have subscribed to date is available at <http://bit.ly/1mve2UN>.

Data sharing

TAIR's new subscription funding model requires that we maintain a delay in releasing the data it has captured from research literature to other public databases in order to preserve an incentive for researchers to subscribe. To minimize any negative impact this might have on the research community we are keeping this period as short as possible. The delay is currently set at one year, but in future we plan to reduce it to 6 months if this is possible without significantly undercutting subscription support. Datasets resulting from our grant-funded data curation and collection work will be released with no delay.

Access for all researchers

To ensure the widest possible access to TAIR data we have provided a diverse set of subscription options, ranging from multi-year country-level subscriptions covering all academic and nonprofit researchers and students to individual monthly subscriptions affordable to students and postdocs. Free subscriptions are available to all students enrolled in a course in which TAIR is used as a part of the course materials. We also provide an option for casual users (e.g. researchers working on other organisms who need TAIR only occasionally) by providing free access to a small number of pages each month.

Plant Gene Function

During the development of the new funding model and supporting software and methods, we have continued to add plant gene function data to TAIR from research literature and community submissions. In the coming months we will ramp up our efforts in this area to achieve more extensive and efficient capture from literature, with the goal of covering all literature for Arabidopsis and expanding our curation efforts to additional plant genomes.

Plant Projects and Resources with Strong Participation of Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR) www.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) researcher in mind. Data sets include:

- 128,000 Single Nucleotide Polymorphisms
- 90.2 million gene expression measurements (75 million from *A. thaliana*), plus "expressologs" (homologs showing similar patterns of expression in equivalent tissues) for many genes across 8 species. View expression patterns with our popular eFP Browser.
- Documented subcellular localizations for 6.5k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.
- 70,944 predicted protein-protein interactions plus 29,777 documented PPIs (rice interologs also available!).
- 67,275 predicted protein tertiary structures and 495 experimentally-determined structures.

News

PSICQUIC webservice are now available for around 100k protein-protein interactions in the BAR's Arabidopsis Interaction Viewer database. See the PSICQUIC registry (<http://www.ebi.ac.uk/Tools/webservices/psicquic/registry/registry?action=STATUS>) for more information, under the BAR entry. We've also enabled queries of three other protein-protein interaction databases which use PSICQUIC: IntAct, STRING and the BioGRID, which contain interactions not found in the AIV database. We've added 355 Arabidopsis-bacterial protein interactions from Pascal Braun's AI-1 PPI data set to the AIV database, and made these viewable in the AIV.

It is now possible to explore cis-elements in the promoter of a given gene via one-click-link icon from the eFP Browser.

A new eFP 2.0 Browser made its debut for exploring the expression patterns of 40 genes at once in a pictographic manner.

The BAR will contribute towards building a new Arabidopsis Information Portal through a Genome Canada Bioinformatics and Computational Biology grant. The AIP framework is being funded by a recently announced NSF grant.

For non-Arabidopsis researchers, we have developed Triticale (Tran et al., 2013) and *Eutrema saulsugineum* (Champigny et al., 2013) eFP Browsers.

Note that we've renamed ourselves to the "Bio-Analytic Resource" to better reflect the diversity of data types the BAR encompasses.

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

www.brassibase.cos.uni-heidelberg.de

By Marcus A. Koch (director)

The Brassicaceae family (mustards or crucifers) includes *Arabidopsis thaliana* as one of the most important model species in plant biology and a number of important crop plants such as the various Brassica species (e.g. cabbage, canola and mustard). Moreover, the family comprises an increasing number of species that serve as study systems in many fields of plant science and evolutionary research. However, the systematics and taxonomy of the family are very complex and access to scientifically valuable and reliable information linked to species and genus names and its interpretation are often difficult. BrassiBase is a continuously developing and growing knowledge database (<http://brassibase.cos.uni-heidelberg.de>) that aims at providing direct access to many different types of information ranging from taxonomy and systematics to phylo- and cytogenetics. Providing critically revised key information, the database intends to optimize comparative evolutionary research in this family and supports the introduction of the Brassicaceae as the model family for evolutionary biology and plant sciences. Some features that should help to accomplish these goals within a comprehensive taxonomic framework have now been implemented in the new version 1.1.9. A 'Phylogenetic Placement Tool' should help to identify critical accessions and germplasm and provide a first visualization of phylogenetic relationships. However, this tool does not replace any carefully conducted phylogenetic analysis since we are actually lacking a reliable and fully-resolving family-wide phylogeny. This work is in progress and might need another 2-3 years until presented with the scientific community and incorporated with BrassiBase.

The 'Cytogenetics Tool' provides in-depth information on genome sizes, chromosome numbers and polyploidy, and sets this information into a Brassicaceae-wide context. The taxonomy tool provides some first information on the most actual taxonomic treatments on genus level.

The next important step to be accomplished by the end of 2014/beginning of 2015 will be the incorporation of a family-wide species checklist that will replace the genus-based backbone of the database. This will enable us to start incorporating characters and traits of the various species that can later be explored by the user.

The "BrassiBase" project is supported by the German Research Foundation (DFG) and within the Priority Research Programme "Adaptomics": Evolutionary plant solutions to ecological challenges - Molecular mechanisms underlying adaptive traits in the Brassicaceae s.l. (<http://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html>).

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

By Doris Wagner (PI), Craig Pikaard (coPI) and Rob Martienssen (coPI)

EPIC is an initiative with the goal of "Reading the second code: mapping plant epigenomes to understand plant growth and adaptation to the environment". The initiative is helping to define the intellectual questions, transformative methodologies and infrastructure requirements necessary for advancing plant epigenomics, some of which have been detailed in a White Paper published in 2012 (<http://www.plantcell.org/content/24/6/2257.full>). In the last year, EPIC has focused on the accomplishment of two aims: establishment of (1) an international plant epigenomics research network to communicate and coordinate research activities internationally and of (2) a user-friendly epigenome browser platform that allows easy upload and display of user-generated epigenomic datasets and published datasets. Development of standards for plant epigenomics data collection, deposition and display has been an important part of the latter aim.

Three main activities were undertaken. First, a series of workshops were held, including workshops at the International Conference on Arabidopsis Research in July in 2013 in Australia (organized by Liz Dennis and Doris Wagner) and at the Plant and Animal Genome Conference in San Diego in 2014 (organized by Rob Martienssen). These workshops served as community information sessions, EPIC membership recruitment events, and forums for scientific exchange. Attendance was high and response was excellent.

Second, members of the international EPIC Planning committee convened in October 2013 at the John Innes Centre in Norwich England (organized by Caroline Dean and Jose Gutierrez-Marcos) to address how EPIC should advance international coordination of plant epigenomics research. Two main models were discussed. One model for the future of EPIC would have EPIC take an active role in facilitating plant epigenomic research, for example by seeking funding from funding agencies and industry for a group effort to elucidate cell-type specific, environmentally induced, and/or developmental stage-specific plant epigenomes. A funded initiative of this type was viewed as having the potential to serve as an important catalyst for the field. However, it was feared that such large initiatives can be static and constraining, and that the approaches used and goals stated can become obsolete or outdated during the lifespan of the initiative. It was also debated whether the emphasis of such an initiative should be on cataloging of epigenetic marks and chromatin

states or on biology driven questions. No final decisions have been reached, and further discussions with industry and government funding agencies will be helpful, and are being planned. A second model for EPIC's future is to have EPIC focus on its role as a facilitator of information flow, via its website, yearly conferences and organizational meetings, and by maintenance and further development of the unified plant Epigenome browser (below). All current stakeholders in EPIC agree that these are useful and important activities that should be continued. It was decided that future EPIC organizational meetings will be held in conjunction with scientific symposia, with each yearly venue placed alternatively in the Americas, Asia or Europe. The scientific symposia topics will include epigenetics and noncoding RNAs. The first such EPIC meeting will be held on May 20, 2014 in Philadelphia (organized by Doris Wagner). At this meeting the role of EPIC in advancing international coordination of plant epigenomics research will be discussed further.

News

The International Conference on Arabidopsis Research, held in Sydney Australia in July 2013, the first unified plant Epigenome browser was announced and made available for public use. This is a major step forward for the Plant Epigenetics community and will enhance comparative analyses investigating the relationships between the epigenome and the physiology, growth and development of plants, as well as the inheritance of traits, in a given environment. The Comparative Genomics (CoGe) browser was developed in collaboration between EPIC, the Gordon and Betty Moore Foundation (<http://www.moore.org/>) and iPlant (<http://www.iplantcollaborative.org/>). The CoGe browser aims to be a one-stop entry point for all plant epigenomics data. A first version, developed jointly by Eric Lyons and Brian Gregory, centers on Arabidopsis epigenomics data. Features of the browser include ability for users to compare their data to existing plant epigenomics datasets, and broad scalability. The browser also provides new tools for data visualization and analysis. Most existing Arabidopsis epigenomics datasets were uploaded by the end of 2013. A grant proposal requesting funding for further development of the CoGe Browser is being submitted to the NSF. It is envisioned that the EPIC CoGe will be linked as a module to the Arabidopsis Information Portal (AIP). EPIC will continue to oversee/coordinate the browser development in collaboration with iPlant. The standing Planning Committee will continue to be involved in this activity and will hold yearly meetings to discuss the browser(s) and current and future needs of the plant epigenetics and epigenomics communities. The CoGe platform has already been adopted by many large epigenomics data generators.

Conferences

In addition to the workshops mentioned above, EPIC will hold a workshop at the International Conference of Arabidopsis Research in Vancouver in 2014 that will serve both as an informational session about EPIC activities and as a scientific exchange, highlighting Arabidopsis epigenetics research.

Goals

Goals of the EPIC initiative in 2014 include formation of an International Consortium Board that will represent the epigenetics/epigenomics community and help continue to oversee EPIC's current and future efforts. Further expansion, development and maintenance of the EPIC database and browser is a high priority, as it will be of key importance to streamline and accelerate plant epigenomics research in the future.

European Plant Phenotyping Network (EPPN) www.plant-phenotyping-network.eu

By Roland Pieruschka (Project Manager), Ulrich Schurr (Coordinator)

Plant phenotypic analysis has become the major limiting factor in genetic and physiological analyses, in plant sciences as well as in plant breeding. During the past ten years molecular plant biology and molecular-based breeding techniques have developed rapidly. In contrast, the understanding of the link between genotype and phenotype has progressed more slowly. Faster progress is currently hampered by insufficient capacity (both technical and conceptual) of the plant science community to analyse the phenotypes of existing genetic resources for their interaction with the environment. Improvement in phenotyping is therefore a key factor for success in modern breeding, as well as for basic plant research.

The European Plant Phenotyping Network (EPPN) is an integrating activity, research infrastructure project funded by the European Union under FP7 Capacities Programme (Grant Agreement No. 284443). The four year project started on 01.01.2012. The aim of EPPN is to create structural and functional synergies between the leading plant phenotyping institutions in Europe as the core for the developing European Plant Phenotyping Network. The project includes three major components:

1. Joint Research Activities with the aim to develop and adapt novel sensors and establish experimental as well as IT standards for application in plant phenotyping.
2. Networking activities provide a link between phenotyping experts, user communities and technology developers. This effort will provide the basis for novel scientific approaches in the utilisation of the existing facilities.

3. Transnational Access is one of the key elements of EPPN. Within the framework of the Transnational Access users can obtain access to 23 plant phenotyping facilities across Europe. The call for Transnational Access is permanently open. The access is based on a simple application procedure and includes scientific and logistic support needed to complete the proposed experiment. Within the first project period (01.2012-06.2013) of the project 28 experiments were initiated within the Transnational Access scheme and 16 experiments were completed. Currently the number of experiments supported by EPPN increased to over 45. Approximately 1/3 of the user applications were related to phenotyping of Arabidopsis under a range of different environmental conditions such as water or nutrient limitation. Over 600 Arabidopsis lines have been screened in all EPPN experiments so far. A short summary of the completed experiments is available online: http://www.plant-phenotyping-network.eu/eppn/selected_projects.

News

EPPN facilities are open for Transnational Access (<http://www.plant-phenotyping-network.eu/eppn/access>)

Conferences

- European Field Phenotyping in Copenhagen, September 2014
- CropSense Symposium in Bonn, Germany, September 2014
- Summer School at the Aberystwyth University, UK, September 2014

Detailed information will be available at: <http://www.plant-phenotyping-network.eu/eppn/events>

The iPlant Collaborative www.iplantcollaborative.org

By Stephen A. Goff (director), Eric Lyons (Co-PI), Nirav Merchant (Co-PI), Matthew Vaughn (Co-PI), and Doreen Ware (Co-PI)

In 2008, the National Science Foundation created the iPlant Collaborative (iPlant) to facilitate significant advances in the understanding of plant biology by fostering the development of a diverse, multi-disciplinary community of scientists, teachers, and students applying computational thinking and approaches to Grand Challenge problems in plant biology. The original proposal included five deliverables from which three main strategies were developed and revised as the project matured. The three strategies included:

1. Create an extensible cyberinfrastructure (CI) platform for plant biologists
2. Establish mechanisms to engage the plant science research community to solve Grand Challenges
3. Promote computational thinking across the community.

Creating the Cyberinfrastructure

A principal deliverable of iPlant is a community-extensible generic CI platform to support solutions to major problems in plant biology, and ultimately be useful across all of the life sciences. The CI effort can be thought of in two distinct parts. The first is the components of the core CI, identified and implemented through requirements analysis and community feedback. These components continue to evolve, incorporating input from ongoing activities. The second part is composed of specific tools and science capabilities incorporated into the core CI.

The foundational elements of the core CI include the web accessible Discovery Environment, the iPlant Data Store, Application Programming Interfaces, the cloud computing platform Atmosphere, the image analysis platform Bisque, and the application stack that enables access to large-scale computing resources. Underlying these elements is the computational infrastructure (hardware and networking), as well as the organization to efficiently operate and support them. Each of these elements continues to evolve with new resources and technologies, as the base of tools, workflows, and datasets incorporated into the infrastructure grows.

Engaging the Plant Science Research Community

A major strategy of iPlant is to federate cyberinfrastructure development activities with other major cyberinfrastructure projects, and support smaller projects by enabling them with iPlant's CI. For example, the DOE is investing in a similar cyberinfrastructure project to support efforts at national laboratories focused on sustainable biofuel production. iPlant's CI leverages early breakthrough technologies developed by other NSF-funded research groups in the fields of computer science, CI, and biological informatics. iPlant's efforts unify and extend these technologies under an easy-to-use platform and brings high performance computing (HPC) and big data management to scientists. Previously biologists relied on computationally savvy collaborators to perform their analysis for them, but with iPlant, they are now empowered to execute the analysis independently. This allows researchers to analyze their growing datasets more efficiently, with greater flexibility, and to address questions that were difficult or impossible before.

Two important outcomes of the CI development effort include the Powered by iPlant program and Computational Scaling. Powered by iPlant provides computational support for external scientific computing platforms, enabling both academic and industrial groups to scale their resources as demands grow and focus on delivering scientific discoveries rather than maintaining infrastructure. A prime example of such a project is the Comparative Genomics portal, CoGe (www.genomevolution.org/CoGe). For Computational Scaling, iPlant works with scientists to restructure or rewrite their software algorithms to scale on larger computational systems. In one example, iPlant scaled a problem that previously would have taken centuries to run to complete in

just a few hours (see Figure XY for additional metrics). In addition to establishing and enhancing the CI platform, more than 450 tools and workflows are now integrated into the web-based iPlant Discovery Environment.

Promoting Computational Thinking

iPlant 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. iPlant's Education, Outreach, and Training efforts address the human component of cyberinfrastructure by creating training resources and by providing participant feedback into the development of the CI. Ultimately, a comprehensive understanding of how to leverage CI empowers scientists to generate knowledge from large-scale datasets; by enabling their access to distributed analysis tools and high performance computing from their own desktop computers, iPlant is empowering new generations of scientists.

iPlant has created a robust, widely used, and evolving CI that is having an impact on plant science, bioinformatics, and the way biologists do research. iPlant has achieved considerable success, helping scientists solve problems that once took years in a matter of hours or days, in genome analysis, phylogenetics, and other data-driven areas of inquiry. The iPlant CI or various components of the CI, driven by community needs, has been adopted by numerous large-scale informatics projects and thousands of individual users. Through partnerships and direct engagement, iPlant has helped accelerate the pace of science for many labs and individual researchers by offering computational and data management solutions that meet the demands created by modern scientific technologies.

Arabidopsis Basic Research and its Impact on Applied Research

Scientific Highlights in 2013/14

Sufficient food supply is one of basic human needs and ensures stability and progress of human societies. Agriculture plays an essential role these days as we are facing an ever increasing world population and the effects of climate change. In order to secure food supply governments began to place greater emphasis on plant research in recent years. A better understanding of plant processes from the biggest to the smallest parts will help to ensure food supply.

Basic research with *Arabidopsis thaliana* serves the plant community since more than 40 years as great resource. Studies in Arabidopsis have greatly benefited from strong international collaborations and these were strengthened in the last two decades during the Arabidopsis genome project and the Arabidopsis functional genomics project both spanning across several countries and continents. The great success of Arabidopsis research led to the establishment of Arabidopsis as reference plant to study many aspects of plant research today. The plant community has enjoyed the ease of manipulating Arabidopsis to better understand plant biology and the underlying molecular processes and its well-known features include its small size, short generation time, high fertility, small genome, ease of genetic manipulation and transformation, and its diverse natural populations.

With the release of the Arabidopsis genome sequence in 2000, the genomic era of Arabidopsis research truly began, allowing a rapid increase in discoveries and publications (Figure 3). In total 37,832 articles referring to Arabidopsis were published since 2000. Considering classic model organisms such as corn, the Arabidopsis publication record remains impressive, reflecting its ease of use as a genetic system, the advanced resources and data sets, and the collegiality of the worldwide community, each of which contributed to its success as reference plant. Alongside Arabidopsis rice became another reference plant especially for monocotyledonous species. This is reflected by a comparable number of publications on rice and Arabidopsis indicating that rice research leveraged from studies in Arabidopsis. The success of Arabidopsis research based on peer-reviewed publication record is massive having increased 10.6-fold between 1994 and 2013, while rice and corn publications increased about 6.2-fold and 3.2-fold, respectively. Last year 4,271 peer-reviewed Arabidopsis publications were released many of which contain exciting new breakthroughs that will no doubt have impacts on studies in plants and other species.

With the emergence of the omics era plant biology faces new challenges like storage and free availability of large data sets comprising genomics, epigenomics, transcriptomics, proteomics, metabolomics and systems biology data in general. Browsers and online data bases provided by Arabidopsis researchers are increasing in number reflecting the efforts to share data to facilitate the extraction of meaningful data. Besides online tools and resources a wide range of other tools and resources were developed by the Arabidopsis community ranging from shared Arabidopsis lines and natural accessions to large open reading frame libraries, just to name a few. The constant development of tools and resources that adapt to the evolving needs of the community have greatly facilitated a large body of cutting-edge research that allows for rapid advances in plant biology. However, the time lapse between an original scientific discovery and its biotechnological application is often quite long and studying an organism that is easier to manipulate may be beneficial in the long term.

Arabidopsis research is broad ranging from ecology, biotic interactions, abiotic stress, development, cell biology and molecular biology to translational research and biotechnology. The following section provides summaries of just a

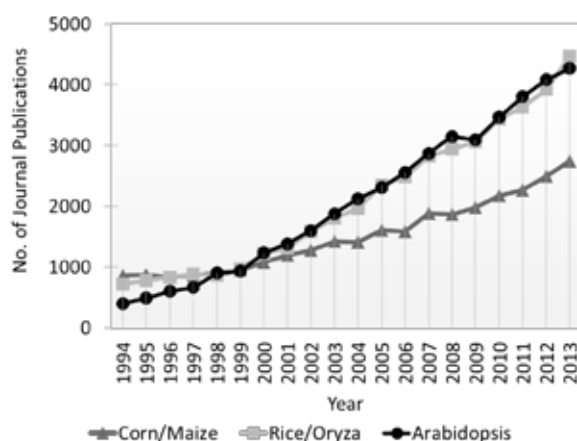


Figure 3. Number of Journal Publications from 1994 until 2013 citing the model organisms Arabidopsis, rice or corn,

Source (2014-05-14): <http://www.ncbi.nlm.nih.gov/pubmed> query e.g.: Arabidopsis[Title/Abstract] AND ("journal article"[Publication Type] OR "review"[Publication Type]) AND ("2013"[PDAT] : "2013"[PDAT]).

few significant advances; notably, the authors of these publications are from three or more countries, reflecting the collegiality and truly international nature of the Arabidopsis community.

New enzyme relevant for lignin biosynthesis

By Igor Cesarino (VIB Gent, Belgium), Wout Boerjan (VIB Gent, Belgium), Claire Halpin (University of Dundee, U.K.)

The complexity, rigidity, and hydrophobic nature of lignin is crucial to plant water transport and upright growth but presents a major barrier to enzymatic hydrolysis of cellulose and hemicellulose for biorefining. Plants with less lignin or with more-degradable lignin would reduce the costs and carbon footprint of processing biomass to paper, biofuels, and chemicals.

The lignin biosynthetic pathway was thought to be fully resolved over a decade ago, but in 2013, based on co-expression analyses, Vanholme and colleagues (Belgium, UK, USA) identified a new enzyme, caffeoyl shikimate esterase (CSE) that is central to the biosynthesis of lignin in Arabidopsis. In dicots, lignin is made from two monolignols, coniferyl and sinapyl alcohol, giving rise to guaiacyl (G) and syringyl (S) lignin units. Additional p-hydroxyphenyl (H) lignin units are found in grasses but are not usually prominent in dicots. *Arabidopsis thaliana cse* mutants deposit 36% less lignin than wild-type plants, and the relative proportion of H units in the remaining lignin is increased over 30-fold. The increase in H units suggested that CSE is active in the biosynthetic pathway after the branch leading to H units but before the pathway branches again to G and S units. The change in lignin composition in *cse* mutants indicated a shift in phenolic metabolism and phenolic metabolite profiling revealed the accumulation of the lignin pathway intermediate caffeoyl shikimate in *cse* mutants, suggesting it as the substrate for CSE. Accordingly, recombinant CSE was able to hydrolyze caffeoyl shikimate into caffeate and shikimate, further supporting its role in lignification. Because lignin limits the processing of plant biomass to fermentable sugars, the cellulose-to-glucose conversion of senesced stems from *cse* mutants and wild-type plants was compared. On saccharification without pretreatment, *cse* mutants released 75% more glucose per plant than the wild type.

Collectively, this work suggests that currently accepted models of the lignin pathway should be revised. Although CSE orthologues exist in many plant species, it remains to be determined how broadly this revision should apply. The presence of CSE orthologues in industrial biomass crops such as switchgrass, poplar and eucalyptus may present opportunities for improving these for bioprocessing.

Vanholme R, Cesarino I, Rataj K, Xiao Y, Sundin L, Goeminne G, Kim H, Cross J, Morreel K, Araujo P, Welsh L, Haustraete J, McClellan C, Vanholme B, Ralph J, Simpson GG, Halpin C, Boerjan W. (2013) Caffeoyl shikimate esterase (CSE) is an enzyme in the lignin biosynthetic pathway in Arabidopsis. *Science* 341(6150):1103-6.

Sweet dreams make plants larger – Carbohydrate metabolism influences plant growth via GA-mediated signal

By Corinna Speth (University of Tuebingen, Germany)

Plant growth is modulated by many external and internal cues, among them nutrients, light, plant hormones and sugars. Two well studied signals, which affect the size of a plant, are the plant hormone gibberellin (GA) and carbohydrates produced by photosynthesis. Despite the fact that both signals promote plant growth, little is known about the interplay between GAs and carbohydrates to ensure optimal plant growth.

The study of Parparelli and colleagues (Italy, Germany, Switzerland) provides insights how the efficiency of the photosynthesis influences GA biosynthesis and thereby affects plant growth. Mutants defective in GA biosynthesis and signaling share some phenotypic characteristics, like dwarfism and late flowering, with mutants defective in starch biosynthesis (e.g. *pgm*) or degradation (e.g. *sex1-1*). Astonishingly, the dwarf phenotype of starch mutants can be reverted by exogenously applied GA leading the authors to the suggestion that GA biosynthesis is affected in starch mutants. GAs are produced from the C20 terpenoid geranylgeranyl diphosphate by a multistep process. The diurnal expression of *ent*-kaurene synthase (KS), an enzyme of early GA biosynthesis, peaks in the afternoon leading to increased accumulation of GAs at the end of the day. In contrast starch mutants, which suffer from sugar starvation at night, lack the KS peak in the afternoon and therefore accumulate lower amounts of GAs at the end of the day. Exogenously applied sucrose at night restores the afternoon peak of KS in starch mutants, suggesting that sugar starvation at night triggers the reduction of KS at daytime. In wild-type plants sugar starvation at night can be induced by exposing plants to low light intensities. Interestingly, the starvation-induced decrease of KS expression is only visible at the following day after exposure to low light intensities. Subsequently, the decreased expression of KS correlates with reduced expression of GA-induced genes and a reduced growth rate of the plant.

In summary, Parparelli and colleagues could show, that the sugar status of a plant at night time serves as a signal, which affects GA biosynthesis the following day, thereby determining the growth rate of the plant.

Paparelli E, Parlanti S, Gonzali S, Novi G, Mariotti L, Ceccarelli N, van Dongen JT, Kölling K, Zeeman SC, Perata P (2013) Nighttime sugar starvation orchestrates gibberellin biosynthesis and plant growth in Arabidopsis. *Plant Cell* 25(10):3760-9.

How do plants make jigsaws?

By Irene Lavagi (University of California, Riverside, U.S.)

The small phytohormone auxin was discovered almost 100 years ago by Charles Darwin and has since been the object of numerous studies leading to our current understanding that hold it responsible for nearly all aspects of plant growth and development. Major breakthroughs in auxin biology came with the discovery of auxin action in the nucleus. However, this did not account for the diversity and versatility of plant responses to auxin.

The recent discovery of an auxin sensing receptor complex on the plasma membrane provides the framework to investigate the diverse modes of action of auxin (Xu et al., 2014). Auxin signal is perceived at the cell surface by a complex formed by a well known auxin receptor, ABP1, and the newly uncovered plasma membrane localized transmembrane kinase (TMK) receptor, and this signal is then translated into cytoskeletal changes that regulate cell shape in the plant cell epidermis. ABP1 perceives auxin and activates the small molecular switches, ROPs, that initiate a cascade of events including the remodeling of the inside of the cell leading to changes in leaf cells morphology. It was not known how ABP1 could transmit the auxin signal to regulate the cellular responses (including cytoskeletal remodeling, endocytosis of auxin carriers) responsible for leaf cell patterning. To activate an intracellular signal, it was hypothesized that the auxin receptor ABP1 communicates with the cytoplasm through a transmembrane docking protein. Transmembrane kinase (TMK) members of the receptor-like kinase family were excellent candidates due to their reported involvement in auxin mediated processes. *Tmk* knock out plants share many similarities with *abp1* mutant plants. In addition, introducing a weak allele of ABP1 in the *tmk* knock out mutant plants enhanced the *tmk* phenotype, suggesting an interaction between ABP1 and TMK.

Leaf epidermal cells typically display a jigsaw appearance. *tmk* mutant leaf epidermal cells showed interdigitation defects resulting in fewer lobes. Auxin treatment promotes interdigitation. However, *tmk* epidermal cells were not rescued by auxin treatment, suggesting that TMK are required for auxin dependent interdigitation. Auxin is known to activate two ROP proteins/pathways through APB1. Biochemical assays of ROP activity revealed that auxin does not promote the activation of ROP proteins in *tmk* mutant plants, whilst it increases the activity of ROPs nearly fourfold in wild-type plants. Localization studies revealed cytoskeletal elements were altered in *tmk* mutant plants. In *tmk* mutant plants actin filaments did not accumulate in the lobes and microtubules in *tmk* mutant plants were disorganized compared to wild-type plants. Visualization of TMK and ABP1 revealed that both TMK and ABP1 localize to the plasma membrane of leaf epidermal cells and that the majority of ABP1 is actually found in the endoplasmic reticulum. The hypothesis that secreted ABP1 and TMK form a complex at the cell surface to perceive extracellular auxin signaling was verified

by immunoprecipitation experiments. Auxin treatment increased the amount of complex that was detected. Using a mutant in the auxin binding pocket of ABP1, demonstrated that auxin perception by ABP1 is important for the formation of the TMK-ABP1 complex. Further work demonstrated that ABP1 interacts with the extracellular domain of TMK.

The findings by Xu et al. (2014) that involved authors from six countries across the globe (USA, Singapore, China, Belgium, Austria, Czech Republic) highlight the many exciting prospects in elucidating the roles of cell surface auxin perception. In addition to explaining how jigsaw-piece shaped cells are formed in the plant leaf epidermis, this study constitutes a landmark in auxin biology. The discovery of a novel auxin sensing receptor complex that perceives and translates an auxin signal is an entirely novel concept in auxin biology and opens up new avenues of research including the modulation of auxin signaling. The formation/need of a complex may contribute to answering this question.

Xu T, Dai N, Chen J, Nagawa S, Cao M, Li H, Zhou Z, Chen X, De Rycke R, Rakusová H, Wang W, Jones AM, Friml J, Patterson SE, Bleecker AB, Yang Z (2014) Cell surface ABP1-TMK auxin-sensing complex activates ROP GTPase signaling. *Science*. 343(6174):1025-8.

Structural requirements for a pathogen effector detector

By Jonathan Jones (The Sainsbury Laboratory, Norwich Research Park, U.K.)

Plant disease resistance genes usually encode nucleotide-binding, leucine-rich repeat (NB-LRR) proteins that structurally and functionally resemble mammalian Nod-like receptors (NLRs), which are also involved in immunity. NB-LRR proteins enable plants to detect, directly or indirectly, specific pathogen effectors from among the repertoire of effector molecules that pathogens secrete into host cells to attenuate host immunity. How NB-LRR proteins convert recognition of an effector into defense activation is still mysterious. There are several examples in which two distinct NB-LRR proteins are both genetically required for a plant to be able to recognize and respond to a particular effector. A subset of NB-LRR proteins carry a TIR (Toll, Interleukin-1 receptor, Resistance protein) domain at their N-termini. Arabidopsis RPS4 and RRS1 TIR-NB-LRR proteins are both required for Arabidopsis to respond to the *Pseudomonas syringae* effector AvrRps4, and the *Ralstonia solanacearum* effector PopP2. RRS1 also carries a C-terminal WRKY DNA binding domain.

In Williams et al. (2014) researchers from Australia, UK, Germany and New Zealand collaborated to significantly advance our understanding of how RPS4 and RRS1 work together to achieve recognition of and responsiveness to the AvrRps4 and PopP2 effectors. They defined the structures of the TIR domains of RPS4 and RRS1, and also of a co-crystal of these TIR domains. They also established an assay in

which *Agrobacterium*-mediated transient coexpression in tobacco leaves of RPS4, RRS1 and PopP2 or AvrRps4 results in defense activation. This enabled tests of whether mutations in the amino acids in the TIR-TIR interface interfered with function. A serine and a highly conserved histidine in both the RPS4 and RRS1 TIR domains were essential for AvrRps4 responsiveness in the transient assay. Transient expression of the RPS4 TIR domain alone activates defense; interestingly this is abolished by coexpression of the RRS1 TIR domain, but not by a RRS1 TIR domain that is mutated in the amino acids at the TIR:TIR heterodimer interface. Mutations at these positions in the RPS4 TIR domain also abolish its constitutive activation of defence. How do full length RPS4 and RRS1 function together? From co-immunoprecipitation experiments after transient expression in tobacco, RPS4 and RRS1 strongly associate with each other, both before and after provision of AvrRps4 and PopP2. Mutations that abolish TIR-TIR interactions have no effect on association of RPS4 and RRS1 full length proteins, so other domains must contribute to RPS4/RRS1 interactions. The effectors associate much more strongly with RRS1 than with RPS4.

A picture emerges of an RPS4/RRS1 protein complex that perceives effectors via their interactions with the RRS1 component of the complex, and then via inter- and intra-protein domain reconfigurations, activates defense via the RPS4 TIR domain.

Williams SJ, Sohn KH, Wan L, Bernoux M, Sarris PF, Segonzac C, Ve T, Ma Y, Saucet SB, Ericsson DJ, Casey LW, Lonhienne T, Winzor DJ, Zhang X, Coerd A, Parker JE, Dodds PN, Kobe B, Jones JD (2014) Structural basis for assembly and function of a heterodimeric plant immune receptor. *Science* 18;344(6181):299-303.

Plasticity constraints and developmental evolution in root architecture

By Ulises Rosas (New York University, USA), Angelica Cibrian-Jaramillo (Laboratorio Nacional de Genómica para la Biodiversidad, Guanajuato, México), & Gloria Coruzzi (New York University, USA)

As sessile organisms, diversity and phenotypic plasticity in response to a changing environment are key to plant survival. Rosas et al. (2013) question whether mechanisms controlling this plasticity “life style” are likely determined by the flexibility and constraints of the developmental and genetic programs within an individual, and their relationship to plasticity mechanisms across natural populations.

The authors from USA, Mexico, UK and France addressed the question of how root system architecture (RSA) varies within a laboratory accession of *Arabidopsis thaliana* (Col-0), compared to the variation that exists across wild *Arabidopsis* accessions influenced by various environments. Their experimental strategy consisted in the comparison of changes in root systems architecture (RSA) within the lab strain Col-0 exposed to external treatments of nitrogen (N) or hormones (auxin, cytokinin, and abscisic acid), to 69 natural variants grown on a single N-environment. They

implemented a novel use of landmark-based morphometrics and Principal Component Analysis called RootScape2. This analysis uncovered two major sources of variation in RSA: root size and root allometry (the position of lateral roots on the primary root) in both Col-0 and across accessions. Interestingly, plasticity of root allometry within Col-0 broadly recapitulates phenotypic natural variation across accessions, suggesting that hormonal and nutrient activities likely underlie phenotypic variation observed across natural accessions. Using the Principal Component axes as phenotypic traits, a genome-wide association study for structured populations identified two genes (*PHO1* and *RSA1*) associated with root allometry changes. Moreover, mutants in Col-0 with impaired activity for these genes revealed genotype-by-environment (GxE) conditional phenotypes that phenocopied the root allometry of natural variants. For instance, mutants in Col-0 with impaired activity in *PHO1*, showed a GxE interaction under abscisic acid treatment, consistent with the recently reported role of *PHO1* in ABA signaling. Similarly, *rsa1* mutants showed GxE interaction in the auxin treatment, which was later supported by enrichment of auxin-regulated genes in a transcriptomic study.

Thus, the evolution of root allometry is constrained by developmental programs. This study highlights the importance of studying multivariate allometry traits in RSA, and how a comparison of plasticity phenotypes within and across natural populations can reveal common mechanisms underlying this plasticity variation

Rosas U, Cibrian-Jaramillo A, Ristova D, Banta JA, Gifford ML, Fan AH, Zhou RW, Kim GJ, Krouk G, Birnbaum KD, Purugganan MD, Coruzzi GM (2013) Integration of responses within and across *Arabidopsis* natural accessions uncovers loci controlling root systems architecture. *PNAS USA*10;110(37):15133-8.

Ristova D, Rosas U, Krouk G, Ruffel S, Birnbaum K, & Coruzzi G (2013) “RootScape: A rapid, landmark-based system for capturing root system architecture”. *Plant Physiol.* 161(3):1086-96.

Change direction - The mechanisms behind microtubule reorientation

In plant cells the deposition of cell wall material depends on the orientation of microtubules, which form a lattice transversal to the growth direction. In response to developmental or environmental stimuli the growth direction of the microtubule lattice changes. For long this reorientation of microtubules was believed to be a self-ordering process.

In 2013 Lindeboom and colleagues from USA, Netherlands and Germany were able to show that two processes guide the fast reorganization of microtubules in the cortical hypocotyl cells of blue-light shifted etiolated *Arabidopsis* seedlings. They used spinning-disk confocal microscopy to detect mCherry fused Tubulin alpha-5 and performed walking image subtraction to identify spots of microtubule formation. They observed that new microtubule formation sites were either marked by the presence of a subunit of the γ -tubulin nucleation complex or at independent sites where microtubules cross over. It was already known that

katanin (KTN) cuts or severs microtubules and the analysis by Lindeboom and colleagues revealed that in *ktn* mutants the formation of new microtubules at sites of crossover is abolished. This implies that KTN is required for microtubule severing at crossovers which was supported by the localization studies that show KTN to be at the respective sites. By analyzing the time course and angles of microtubule growth from the new formation sites the assumption was further strengthened that two processes exist for the reorientation of microtubule formation by the initiation of new microtubule sites. The early being the γ -tubulin nucleation complex dependent process forming diagonal microtubules relative to the former lattice. The later being the katanin dependent severing at crossovers forming orthogonal microtubules relative to the former lattice and subsequent longitudinal branching events relative to the new microtubule at subsequent crossover sites. Furthermore the authors provide evidence that blue light signaling by the phototropins positively influences katanin severing and katanin is required for photocurvature.

Lindeboom and colleagues provide compelling evidence that the reorganization of microtubules in plants depends on the preexisting microtubule lattice and that two processes initiate the reorganization. Katanin was also shown to be important in developmental processes in other organisms like neuron development, mitosis, cell migration etc. This study in Arabidopsis hypocotyl cells allowed for the first time to observe individual severing events in living tissue and will help to unravel the molecular processes in microtubule formation in detail.

Lindeboom JJ, Nakamura M, Hibbel A, Shundyak K, Gutierrez R, Ketelaar T, Emons AM, Mulder BM, Kirik V, Ehrhardt DW (2013) A mechanism for reorientation of cortical microtubule arrays driven by microtubule severing. *Science* 6;342(6163):1245533.

New hints why plants don't flower under salt stress conditions

Many components of the pathway that induces flowering in plants are already known but so far evidence was lacking which components are involved in the integration of abiotic stress and repression of flowering. For instance salt stress reduces the capacity of juvenile plants to flower under long day conditions.

In 2013 researchers from South Korea, Spain, USA and Saudi Arabia published first evidence that link salt stress with the flowering regulator GIGANTEA (GI) in Arabidopsis (Kim et al., 2013). Salt stress delays flowering in wild-type plants which is accompanied by reduced expression of floral regulators (CO and FT). Mutant *gigantea* plants flower late also under salt stress conditions and the expression of floral regulators is reduced. However plants overexpressing GI flower slightly earlier than wild-type under normal conditions and the salt-induced delay in flowering is suppressed in *gi* mutants and expression of floral regulators is high. The authors showed that the protein stability of GI is affected

upon salt stress and that *gi* mutant plants are more resistant whereas the GI overexpressing plants are more susceptible to salt stress than wild-type. This clearly demonstrates that GI interferes with salt tolerance in Arabidopsis. Kim et al. suggested and tested different scenarios for the involvement of GI and salt stress response. They provided evidence for the direct interaction of GI with salt overly sensitive 2 (SOS2) a kinase that phosphorylates and thus activates the Na⁺/H⁺ antiporter SOS1 important for maintaining homeostasis under salt stress. *In vivo* and *in vitro* experiments revealed that GI suppresses SOS2 dependent phosphorylation of SOS1. They showed that the phosphorylation status of SOS1 is relevant for increased protein stability of SOS1 under salt stress and that SOS1 protein abundance was higher in *gi* mutants. In addition *sos2-2 gi-1* mutant plants suppress the salt tolerance phenotype of the *gi* mutant, which strengthens the hypothesis that GI and SOS2 are in the same pathway. Interestingly the interaction of GI with SOS2 that takes place in the cytosol and the nucleus was abolished in SOS3 overexpressing plants. SOS3 is also interacting with SOS2 and the heterodimer is required for phosphorylation of SOS1. It seems that SOS3 and GI bind and thus compete for binding to the C-terminal region of SOS2. Upon salt stress GI is targeted for proteosomal degradation by an unknown mechanism and this enhances the possibility of SOS2 and SOS3 to form a functional complex that phosphorylates and stabilizes SOS1 which then leads to salt tolerance.

The suppression of flowering by salt stress can be explained by degradation of the floral regulator GI that is directly influencing salt stress tolerance in Arabidopsis. GI also regulates the circadian rhythm, which opens new interesting hypothesis e.g. that the clock possibly anticipates and integrates emerging stress conditions.

Kim WY, Ali Z, Park HJ, Park SJ, Cha JY, Perez-Hormaeche J, Quintero FJ, Shin G, Kim MR, Qiang Z, Ning L, Park HC, Lee SY, Bressan RA, Pardo JM, Bohnert HJ, Yun DJ (2013) Release of SOS2 kinase from sequestration with GIGANTEA determines salt tolerance in Arabidopsis. *Nat Commun* 4:1352.

Get it inside - New complex necessary for endocytosis identified

Endocytosis is a crucial process to internalize membrane materials like receptors and channels as well as extracellular cargos. In eukaryotes the best characterized endocytic pathway is the clathrin-mediated endocytosis. This pathway consists of many steps including nucleation, cargo selection, vesicle coat assembly, scission and vesicle uncoating. Some components of this pathway are shared across kingdoms but also kingdom specific components have diverged during evolution. In plants the molecular components of the early adaptor process before clathrin is bound to the forming vesicle were unknown until recently.

In 2014 researchers from Belgium, Germany, USA, Austria, Lithuania and The Netherlands published their work on the TPLATE adaptor complex that drives clathrin-mediated endocytosis in plants (Gadeyne et al., 2014). By using TPLATE

as bait for several rounds of tandem affinity purification in Arabidopsis cell culture, they were able to identify 7 additional proteins that build the TPLATE complex. The authors verified several of the found interactions by bidirectional approaches. It was shown previously that TPLATE itself interacts with clathrin and Gadeyne and colleagues verified also the interaction of the TPLATE complex with the heterotetrameric adaptor protein complex 2 (AP2). Mutant analysis revealed that 4 of the 7 additional TPLATE complex components were male sterile consistent with other mutants in the clathrin-mediated endocytosis pathway. All subunits of the TPLATE complex localized to the plasmamembrane in Arabidopsis root cells and showed a dynamic appearance. Furthermore a μ homology domain was identified in one subunit and could be shown to be required for its recruitment to the plasmamembrane and the complete assembly of the TPLATE complex. In depth localization studies revealed the colocalization of TPLATE with components of the AP2 complex. Silencing of TPLATE or a second component of the TPLATE complex by artificial micro RNAs resulted in a lethal phenotype. Subsequently results with estradiol-inducible artificial micro RNA knock down lines revealed that uptake of external cargo and internalization of the plasmamembrane located receptor brassinosteroid insensitive 1 and some transporters was blocked in Arabidopsis roots after induction.

The authors identified a new adaptor-related complex complexes of clathrin-mediated endocytosis in plants that has functional homologs in other organisms but lacks sufficient sequence homology.

Gadeyne A, Sánchez-Rodríguez C, Vanneste S, Di Rubbo S, Zauber H, Vanneste K, Van Leene J, De Winne N, Eeckhout D, Persiau G, Van De Slijke E, Cannoot B, Verduyck L, Mayers JR, Adamowski M, Kania U, Ehrlich M, Schweighofer A, Ketelaar T, Maere S, Bednarek SY, Friml J, Gevaert K, Witters E, Russinova E, Persson S, De Jaeger G, Van Damme D (2014) The TPLATE adaptor complex drives clathrin-mediated endocytosis in plants. *Cell* 156(4):691-704.

Fatty acid transport to the ER

By Sangwoo Kim, Youngsook Lee and Ikuro Nishida

Fatty acids, the essential components of membrane and storage lipids in all forms of life, are not only nutritious as human food, but also precious as medicinal and health-supporting supplements. In the past two to three decades, because of their potential use as a renewable, energy-dense, post-petroleum fuel, attentions have been paid to the biotechnological improvement of lipid production. Photosynthetic organisms including plants and algae are autonomous for fatty acid and lipid production. In plants, fatty acids are synthesized in plastids from atmospheric CO₂. Fatty acids are then exported, in the form of acyl-CoAs, a water-soluble carrier of fatty acids, to the endoplasmic reticulum (ER) for lipid assembly. Acyl-CoA may be utilized in both sides (cytoplasmic and luminal) of ER, but a question has remained how such water-soluble molecules could penetrate

through the hydrophobic ER membranes for lipid assembly in the luminal side. ABC proteins are a candidate that could carry out such apparently energy-requiring processes. ABC proteins are ubiquitous in all living organisms, and their structure and functions are highly conserved. In animals, many important genetic diseases are associated with defects in lipid transporting ABC proteins. Changing the activity of some animal ABCA proteins causes lipids, such as triacylglycerol (TAG) and cholesterol esters, to overaccumulate in specific tissues. In plants, several ABCG proteins secrete lipidic molecules that form cutin and wax layers. Defects in the expression of such proteins cause reduced surface lipids and/or developmental defects, such as organ fusion.

Ikuro Nishida's group from Japan and Youngsook Lee's group from South Korea together with Edgar Cahoon from the US collaborated to identify the transporters that deliver fatty acid substrates to the ER for glycerolipid synthesis. They hypothesized that ABCA proteins in plants mediate the transport of fatty acids into the ER, and that the activity of such proteins is a limiting step in TAG biosynthesis in oil seed plants during the seed-filling stage, when TAG biosynthesis is greatest, and thus the flux of acyl-CoAs from the plastid to the ER is greatest, too. This hypothesis predicts that a knockout of such a transporter would decrease TAG synthesis, resulting in a decrease in seed storage lipid content. To identify such a transporter, they collected Arabidopsis plants mutated at one of the 12 ABCA genes, analyzed seed lipid content, observed their seed shape, and grew them in the absence or presence of sucrose, and compared their early seedling growth. Their results indicated that *AtABCA9*, an ABC transporter in *Arabidopsis thaliana*, mediates the transport of fatty acids to ER. *AtABCA9* was localized to the ER, *atabca9* null mutations reduced seed triacylglycerol content by 35% compared to the wild type, developing *abca9* seeds incorporated 35% less 14C-oleoyl-CoA into TAG than did wild-type seeds, and furthermore, overexpression of *AtABCA9* enhanced TAG deposition by up to 44%, while maintaining protein and carbohydrate contents at the same level.

These data strongly support a role for *AtABCA9* as a supplier of fatty acid substrates for TAG biosynthesis at the ER during the seed-filling stage. *AtABCA9* can be a new and powerful molecular tool to increase lipid production in oilseeds.

Kim S, Yamaoka Y, Ono H, Kim H, Shim D, Maeshima M, Martinoia E, Cahoon EB, Nishida I, Lee Y (2013) *AtABCA9* transporter supplies fatty acids for lipid synthesis to the endoplasmic reticulum PNAS USA 110(2):773-8.

Impact on Applied Research and Industry

Within the last 20 years Arabidopsis was established as reference plant for basic and applied research possible due to the great efforts of the plant research community and the strong support by funding bodies. Already in 1999 the number of peer-reviewed publications referring to rice, corn or Arabidopsis reached comparable levels and since then publications on Arabidopsis and rice exceed those on maize (Figure 3). During the last decades the Arabidopsis community leveraged the applied research fields with their achievements like for example the first sequenced plant genome, which was followed by functional genomics studies, today's prosperity of omics and network approaches and concomitant the development of a plethora of new technologies, which should not be underestimated. The prevalent focus of applied research is on the development of applications 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 the freedom to explore a broad range of hypothesis, to develop new techniques and approaches is most important. 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 plant biology.

To measure the impact and evaluate 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 minimum ten years elapse between the discovery and the subsequent successful application. Therefore, in most cases the actual origins of real world applications remain obscure to a large extend unless published e.g. in peer-reviewed journals or mentioned in the patent application. An option to estimate the impact of Arabidopsis research in the past and estimate what we might expect from translating Arabidopsis research into crop species and commercial products in future, can be roughly estimated by consulting patent data bases (Figure 4). In the United States since 1994 more than 12,000 utility patents referring to Arabidopsis were published compared to more than 44,000 on rice and 93,000 on maize (Figure 4A). But the success of Arabidopsis as non-agricultural plant is tremendous and increasing, having published 1,576 utility patent in 2013 compared to 23 in 1994 in the U.S. The trend in published applications in Europe is comparable, although the general situation for especially genetically modified crops is more difficult in Europe than in the United States (Figure 4B). Last year 204 applications were published in Europe referring to Arabidopsis, 1,073 to rice and 1,605 to maize. It is peculiar that the strong increase in 2011 for European applications was followed by general decrease in 2012. This drop in filed applications is also seen for international patent

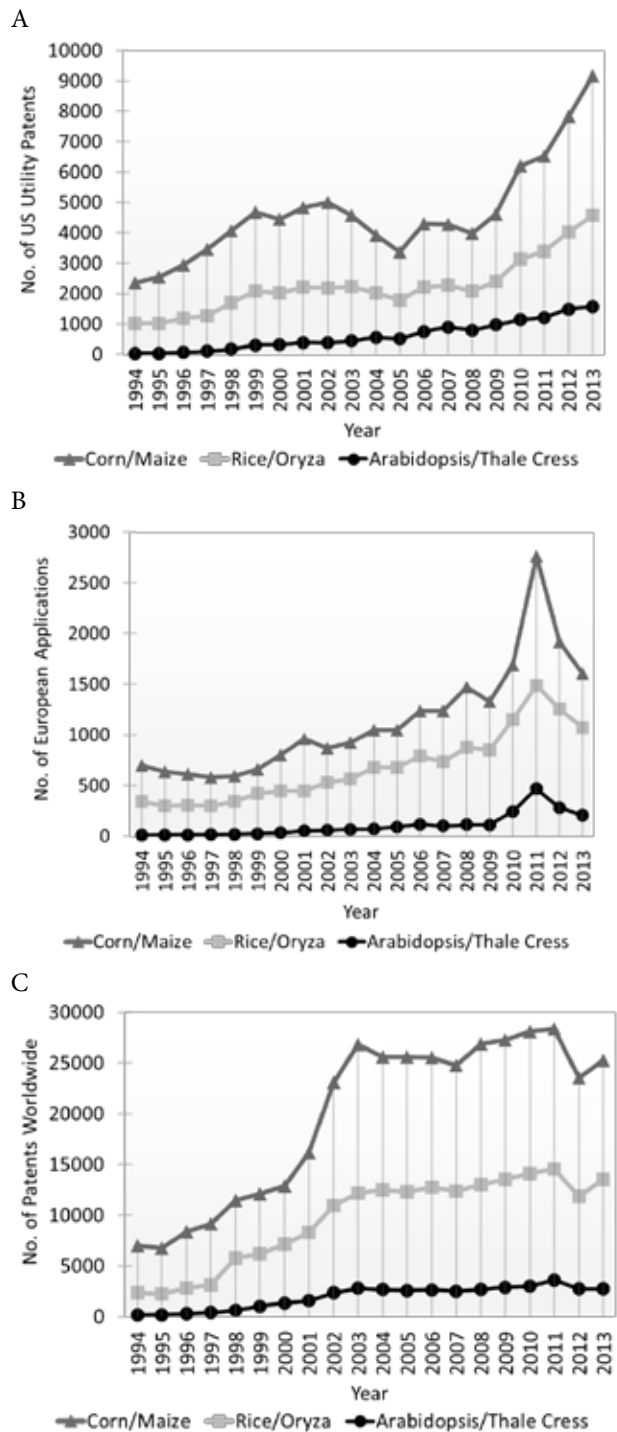


Figure 4 Trends of patents referencing model organisms (maize, oryza, Arabidopsis) from 1994 until 2013; (A) number of utility patents in the United States; (B) number of published applications in Europe; (C) number of patents worldwide, Patent and Cooperation Treaty applications (PCT) according to the World Intellectual Property Organization (WIPO, 187 contracting states). Searches were performed (2014-05-14): A) <http://patft.uspto.gov/netathtml/PTO/search-adv.htm>, e.g. query: SPEC/rice OR SPEC/oryza AND ISD/20130101->20131231; B) http://worldwide.espacenet.com/advancedSearch?locale=en_EP, select EP collection, e.g.: Keyword(s) in full text: rice OR oryza, Publication date: 2013; C) <http://patentscope.wipo.int/search/en/structuredSearch.jsf>, select any field, e.g. English all: rice OR oryza, Publication date: 2013.

applications or Patent and Cooperation Treaty (PCT) applications according to the World Intellectual Property Organization (WIPO, 187 contracting states, Figure 4C) in 2012. Nevertheless, the general trend of European and International filed applications seems to be constantly positive over the last 20 years. Since 1994 a total of 38,777 international patent applications were published referring to Arabidopsis compared to 191,586 on rice and 394,597 on maize. More and more applications consider Arabidopsis and the number increased by 19-fold within 20 years (1994 -144 patents, 2013 - 2,753). In general it can be expected that the number of filed patents or published applications will continue to increase at least concerning US utility patents, European published applications and international patents.

Although patents on corn and rice far exceed those citing Arabidopsis, the translation of Arabidopsis knowledge and technologies to crop species cannot be underestimated. A plethora of laboratories around the world exist that study Arabidopsis and a crop species in parallel. Arabidopsis is often the first choices for plant researchers to test hypothesis and develop new methods. The continuous funding of Arabidopsis basic research by funding bodies like government agencies is crucial to further develop the basic understanding of plant processes in order to leverage applied studies with other plant species. In the following section just a few recent examples of translational research are summarized to demonstrate that Arabidopsis serves as invaluable source for applied research and to show how knowledge gained in this reference organism can be translated to other species, real world applications or applied research in general.

Transporters as toolkits for improved plant growth under nutrient limiting conditions

The composition of micro- and macronutrients in soil has direct impact on proper plant growth and limited or excess supply of nutrients can cause both deleterious effects. For example boron as essential micronutrient impairs growth and reduces fertility supplied in excess or limited concentrations. Plants exhibit specific borate transporters, which facilitate uptake and translocation within the plant. Boron-deficiency-tolerant cultivars of rice, maize and wheat exhibit increased expression levels of an efflux boron transporter (BOR1) that mediates xylem loading. In Arabidopsis it was shown that increased expression of *AtBOR1* or *AtNIP5;1*, a boric acid channel, improves vegetative and reproductive growth under boron deficient conditions.

To test the boron transport in fruit-bearing crops Uraguchi and colleagues applied the knowledge gained from Arabidopsis to tomato. They generated *p35S::AtBOR1* transgenic tomato by Agrobacterium-mediated stable transformation. Out of eleven independent lines bearing the T-DNA insertion three overexpressing lines with normal fruit set were chosen for further analyses. Two out of the three lines exhibited normal growth and *AtBOR1* transcripts were detectable. One of these lines however showed reduced root growth and exhibited lower expression levels compared to the other two transgenic lines. The next generation (T1) including wild type control was grown hydroponically under normal and boron-deficient conditions. In general no phenotypic differences were detectable under normal growth conditions. Phenotypic differences were visible under boron deficient conditions although no significant difference in shoot dry weight was observed and measurement of fruit yield was impossible due to large variations. The boron concentration was enriched in plants expressing *AtBOR1* at high levels under boron limiting conditions but equal to wild type under normal conditions. The authors conclude that overexpression of borate transporters positively influences plant shoot growth in tomato under boron limiting conditions but further analyses are required especially to obtain sufficient information on fruit yield in *AtBOR1* overexpressing plants.

This work is important for the understanding of borate transport in fruit-bearing crops and Arabidopsis can be used as reference plant. Further experiments to improve plant health under boron-deficient conditions need to be done, but the boron transporters have the potential to be a great toolkit for improvement of crop growth.

Uraguchi S, Kato Y, Hanaoka H, Miwa K, Fujiwara T (2014) Generation of boron-deficiency-tolerant tomato by overexpressing an Arabidopsis thaliana borate transporter *AtBOR1*. *Front Plant Sci* 5:125.

Conserved function of Nod factors in legumes and nonlegumes

By Yan Liang and Gary Stacey (Divisions of Plant Science and Biochemistry, National Center for Soybean Biotechnology, Christopher S. Bond Life Sciences Center, University of Missouri, Columbia, MO 65211, USA)

The rhizobial-legume symbiosis, due to the ability to fix atmospheric nitrogen, is agronomically and ecologically important. This symbiosis is almost exclusively restricted to the family of leguminous plants (Fabaceae). However, it has long been the dream of researchers to transfer this ability into non-legumes (e.g. corn). A long-standing assumption is that non-leguminous plants cannot establish a symbiotic relationship with rhizobia due to an inability to recognize Nod factors, the key symbiotic signals produced by rhizobia. Although the rhizobial-legume symbiosis is beneficial and benign, data suggest that the plant responds initially with a pathogen defense response, which then is suppressed, likely through active processes initiated by the bacterial symbiont.

In 2013, Liang and colleagues demonstrated that, at least in part, this active suppression of the plant defense response was mediated by Nod factors. Interestingly, in contrast to the symbiotic interaction, this ability of Nod factors to suppress plant innate immunity is conserved in both legumes and non-legumes. Indeed, this response was found in soybean, Arabidopsis, corn and tomato. The mechanism of Nod factor-induced immunosuppression in Arabidopsis involves the more rapid turnover of the pattern recognition receptors that recognize pathogen-associated molecules that normally induce plant immunity.

In legumes, Nod factors are recognized by Nod factor receptors, termed Nod factor receptor 1 (NFR1) and NFR5 in soybean. These Nod factor receptors belong to the lysin motif (LysM)-containing receptor-like kinase (LYKs) family. Liang and colleagues found that Nod factor suppression of innate immunity was independent of the Nod factor receptor genes (NFR1 and NFR5) when tested in soybean. However, an examination of mutants defective in each of the five LYK genes in Arabidopsis showed that *Atlyk3* mutant plants did not respond to Nod factor, suggesting that Nod factors are recognized by *AtLYK3* resulting in activation of the intracellular kinase domain, which triggers suppression of innate immunity.

The study of Liang and colleagues shows that Nod factor recognition is very widespread in plants but is coupled to a suppression of innate immunity, not symbiotic development as is the case in legumes. The authors suggest that this immunosuppression ability of Nod factors might have evolved first with further co-evolution leading to a more profound developmental role for these molecules.

Liang Y, Cao Y, Tanaka K, Thibivilliers S, Wan J, Choi J, Kang Ch, Qiu J, Stacey G (2013) Nonlegumes respond to rhizobial Nod factors by suppressing the innate immune response. *Science* 341(6152):1384-7.

Don't shatter your pods - Lignified fibre cap cells make the difference in soybean

Domestication of wild species for agriculture was prevalent during the Neolithic Revolution about 10,000 years ago. Evidence exists that soybean was domesticated in East Asia about 5,000 years ago. A major milestone in the history of soybean domestication was the pod shattering resistance or fruit indehiscence that allows a more efficient cultivation by less yield loss. The mechanism that causes seed shattering in wild species (*Glycine soja*) and resistance in domesticated soybean (*Glycine max*) was unknown until lately.

Yang Dong and colleagues (2014) provide evidence for a new mechanism to control pod shattering in soybean. By in depth anatomical and phenotypic analyses of wild and cultivated soybean they found that pod shattering resistance was accompanied by excessive secondary cell wall formation in the fibre cap cells. No modifications in the abscission layer were detected, which is the site of dehiscence described for rice, sorghum or tomato. In order to identify putative candidate genes that might induce lignin deposition in the fibre cap cells in soybean, the authors took advantage of the possibility to study this process in Arabidopsis. They identified orthologues of Arabidopsis genes involved in seed shattering in soybean and characterized these by sequence analysis. The results indicated that *Glyma16g0220/Shattering1-5* (*SHAT1-5*) a NAC transcription factor might be involved in the process of cell wall deposition in fibre cap cells in soybean. Indeed this was supported by its presence in a previously described quantitative trait loci relevant for pod shattering. Expression analyses in soybean revealed that *GmSHAT1-5* was expressed 15-fold compared to *GsSHAT1-5* at a certain stage of pod development in the fibre cap cells. Translational analyses in Arabidopsis showed that both genes restore the phenotype of the respective Arabidopsis mutant. Furthermore the authors provide evidence for artificial selection of a ~116 kb region around the *SHAT1-5* locus in domesticated soybean haplotypes compared to wild soybean. Finally, the authors compared the 5' non-coding region of *SHAT1-5* in wild and domesticated soybean and showed that an InDel ~4kb upstream causes differential expression in transiently transformed Arabidopsis protoplasts. The authors propose that the GARP-binding site in the InDel of wild soybean represses *SHAT1-5* expression whereas the InDel of domesticated soybean leads to strong induction, which results in differential cell wall deposition in fibre cap cells of domesticated soybean.

The described mechanism and the genetic regulation of pod shattering in soybean can probably be transferred to other legumes and might be usefully for crop improvement. The work offers insights into domestication of wild species and is an excellent example of the use of Arabidopsis as reference plant.

Dong Y, Yang X, Liu J, Wang BH, Liu BL, Wang YZ (2014) Pod shattering resistance associated with domestication is mediated by a NAC gene in soybean. *Nat Commun* 5:3352.

Single gene hybrid vigor in oil palm

The most important traits in modern oil palm *Elaeis guineensis* are *dura*, *pisifera* and their hybrid *tenera*. The major difference between these traits is the thickness of the shell (endocarp) surrounding the kernel (endosperm). While the *pisifera* trait exhibits no endocarp and is usually female sterile, the *dura* trait exhibits a big endosperm surrounded by thick endocarp. *Tenera*, the hybrid of *dura* and *pisifera*, shows single gene hybrid vigor due to co-dominant inheritance and exhibits big endosperm surrounded by thin endocarp. The exact gene and the mechanism that cause the phenotypic difference were unknown until recently.

In 2013 Singh and colleagues identified the SHELL gene and the two co-dominant alleles responsible for the phenotypic differences of the traits. The authors used pheno- and genotyping of a mapping population of 240 F1 progenies of self-pollinated *tenera* hybrids to identify the linking region, which is a 450 kb region at the end of chromosome 2. Subsequently, 43 *pisifera* palms, chosen based on a pedigree, were analyzed by sequencing to identify the homozygous region that causes the loss of proper endosperm development in *pisifera*. The combination of traditional mapping and homozygosity mapping led to the identification of the SHELL gene, a homologue of Arabidopsis SEEDSTICK and SHATTERPROOF. In Arabidopsis these genes are involved in proper ovule, seed and lignified endocarp development suggesting a comparable role in oil palm. The allelic differences were verified by yeast-two hybrid assays with the SHELL genes from different oil palm haplotypes. Sequencing revealed amino acid substitutions in the DNA-binding domain and the nuclear localization signal of *pisifera* SHELL. These regions were shown in Arabidopsis to prevent dimerization and DNA-binding. The *tenera* hybrid is heterozygous for SHELL. The authors propose that in *tenera* productive and non-productive dimers compete, which accounts for single gene hybrid vigor.

The results by Singh et al. (2013) provide the basis for accurate phenotyping of oil palm which will reduce space requirements for plantations. This study also paves the way for molecular strategies to modulate the SHELL gene and thereby change fruit forms. Results gained in Arabidopsis and other model organisms will provide basic background to design appropriate strategies.

Singh R, Low ET, Ooi LC, Ong-Abdullah M, Ting NC, Nagappan J, Nookiah R, Amiruddin MD, Rosli R, Manaf MA, Chan KL, Halim MA, Azizi N, Lakey N, Smith SW, Budiman MA, Hogan M, Bacher B, Van Brunt A, Wang C, Ordway JM, Sambanthamurthi R, Martienssen RA (2013) The oil palm SHELL gene controls oil yield and encodes a homologue of SEEDSTICK. *Nature* 500(7462):340-4.

The global “flowering” of the potato tuber crop

By Christian W.B. Bachem

Plants regulate their reproductive cycles by perceiving the change in day-length during the seasons. For *A. thaliana*, which flowers in the long days of spring and summer, a large body of research shows the linkage between the diurnally regulated genes and the transition from vegetative to reproductive development. The knowledge of this pathway in *A. thaliana* has been successfully translated into the elucidation of reproduction in many other plants. At the heart of this regulatory pathway is the CYCLING DOF FACTOR (CDF), which acts as suppressor of CONSTANS (CO) that in turn is a regulator of the florigen FLOWERING TIME LOCUS-T (FT). CDF belongs to the DOF-family of transcription factors that itself is post-transcriptionally regulated by the clock output proteins GI and FKF1. The binding of GI and FKF1 to CDF targets it for degradation, leading to increased transcription of CO and thus, during long-days, of FT.

Recently, the map-based cloning of a potato CDF homologue (*StCDF1*) has implicated its role in day-length regulation of the initiation of vegetative reproduction in potato (Kloosterman et al, 2013). Potato, which evolved in the equatorial regions of the Andes, is dependent on short-days for tuberization. Wild South American clones do not form tubers in the long-days of spring and summer that prevail during the growing season in northern latitudes. Through the analysis of *StCDF1* alleles of potato, Kloosterman et al. have shown that truncated variants of *StCDF1*, have lost the *FKF1* binding domain and thus evade diurnal regulation. Presence of *StCDF1* throughout the day, leads to a constitutive repression of the potato CONSTANS genes. Low *StCO* indirectly induces expression of the tuberigen FT homologue *StSP6A*. The presence of truncated alleles of *StCDF1* closely correlates with the early tuberization in commercial potato varieties. The implication of this finding is, that the production of potato in the northern latitudes has only been made possible through the introduction of the mutant, day-length insensitive *StCDF1* alleles into modern tetraploid potatoes.

Development of markers for this important locus and further analysis of allelic variation in *StCDF1* will allow more rapid breeding for cultivars that are better tailored to specific geographic regions and new markets of this third most important world food crop.

Kloosterman B, Abelenda JA, Gomez Mdel M, Oortwijn M, de Boer JM, Kowitzwanich K, Horvath BM, van Eck HJ, Smaczniak C, Prat S, Visser RG, Bachem CW (2013) Naturally occurring allele diversity allows potato cultivation in northern latitudes. *Nature* 495(7440):246-50.

Blue light switch - Interfering transcription in mammalian cells

Functional genomics are sometimes hampered by the fact that either mutation or overexpression of single genes cause lethal or pleiotropic phenotypes, which hampers tissue specific analysis. This problem is not confined to plant research but mammalian research, too. New methods have to be developed to unravel tissue specific gene function of a single locus.

In 2013 Konermann and colleagues made efficient use of the Arabidopsis blue light receptor Cryptochrome 2 (CRY2) and generated a system to modulate mammalian endogenous transcription and epigenetic states in mouse cell culture and primary neurons *in vivo*. The authors developed a system called light-induced transcription effectors (LITE or epiLITE) and applied a combination of three systems: one - the CRY2 receptor including its interaction partner Cryptochrome-Interacting Basic-helix-loop-helix 1 (CIB1), two - programmable designer Transcription Activator Like Effectors (TALE) from *Xanthomonas sp.* that bind to DNA in a sequence specific manner, and three - effector domains like the viral VP16 transcription activator domain or histone methyltransferases or deacetylases. The authors tested different versions of the LITE system i.e. TALE fused to CRY2 and CIB1:NLS fused to VP16 or TALE fused to CIB1:NLS and VP16 fused to CRY2. In all cases they observed blue-light dependent transcriptional up regulation compared to non-stimulated control. Within 30 minutes strong up-regulation was observed reaching saturated states after 12 hours. Within 3 hours after blue light treatment the mRNA expression level reached background level. They analyzed parameters like wavelength, cycle and light intensity and could show that LITE is faster than the comparable abscisic acid receptor derived system. Additionally, they were able to reduce background activity by mutagenesis of specific residues in CIB1. Finally they could show that the LITE system is also versatile to introduce epigenetic changes by fusion of histone modifying enzymes instead of a transactivation domain (epiLITE).

The LITE and epiLITE systems allow the precise spatio-temporal modification of gene expression and histone modifications, respectively and allow to test the role of genes in diverse processes in mammals. This data by Konermann et al. exemplifies the wide appreciation and application of Arabidopsis research and it can be estimated that many more applications like this exist and will be developed.

Konermann S, Brigham MD, Trevino AE, Hsu PD, Heidenreich M, Cong L, Platt RJ, Scott DA, Church GM, Zhang F (2013) Optical control of mammalian endogenous transcription and epigenetic states. *Nature* 500(7463):472-6.

Winter beet - A new way of cultivating sugar beet

By Luise H. Brand (University of Tuebingen, Germany) and Katia Schütze (KWS, Einbeck, Germany)

Sugar beet is used for sugar production and is one of two crops (besides sugar cane) which contain large amounts of sucrose. As biennial plant sugar beet builds a taproot for sucrose storage in the first vegetation period and after vernalization in winter, bolting and flowering is induced, which leads to the consumption of the sugar in the roots. Traditionally sugar beet is sown in April and taproots are harvested in October and November. KWS is working on a project called "Winter Beet" to change the way of sugar beet cultivation. The general idea is to extend the growth period by sowing sugar beet seeds in autumn instead of spring. It is estimated that this could lead to a yield increase of up to 30%. Therefore, bolting and flowering need to be repressed after winter, a flowering switch system for seed production has to be developed and enhancing freezing tolerance in sugar beet is required.

KWS was successful in generating a non-bolting *Beta vulgaris* by overexpressing an RNAi construct that reduces the expression of vernalization *VIN3-like 1* (*BvVIL1*) by 60% or more. *BvVIL1* is a homolog of the Arabidopsis *Vernalization Insensitive 3* (*AtVIN3*) and both genes share 57.2% sequence identity. Although *BvVIL1* is not differentially regulated during the vernalization process, as described for *AtVIN3*, it was clearly demonstrated that *BvVIL1* has a role in the induction of flowering after vernalization in sugar beet. Currently, researchers at KWS use two different switch systems to generate condition dependent flowering of sugar beets. Both systems were also employed previously in Arabidopsis. One switch system is based on the crossing of two flowering parental lines, one expressing a transcriptional activator and the second carrying the correspondent promoter combined with a *BvVil1*-RNAi cassette, thereby creating a nonflowering F1 progeny. The other approach is to introduce a version of the *BvVIL1* gene, which is not targeted by the RNAi, under control of an inducible system. Bolting and flowering can be specifically induced for seed production in this system.

The *BvVIL1* approach seems to be very promising for generation of a new sugar beet variants. However, there are several challenges that have to be solved in order to realize winter beets. The winter beet project involve also test with additional potential target genes that were shown in Arabidopsis to play roles in flowering, vernalization and frost tolerance. The functional genomics and network data generated as well as the plethora of methods established in Arabidopsis are important for the generation of new hypothesis and variants in agricultural research.

Presentation by Katia Schütze, KWS Saat AG (2013) Winter beet - a new way of cultivating sugar beet. During the German Botanical Conference, 29th September - 04th October, Tübingen, Germany

Stable targeted genome modifications in plants

The progress of Arabidopsis molecular biology and its impact on applied research and crop breeding would be massive, if a system would be available that allows gene specific modification of plant genomes independent of the plant species with high efficiency. Standard methods to introduce non directional mutagenesis are physical and chemical perturbation or T-DNA and transposon insertion. RNAi is an gene specific approach but down regulation is possible only. In recent years great progress was made in the field of targeted genome modification by employing zinc finger nucleases, transcription activator effectors (TALE), which all were shown to have their limitations. In 2012 the clustered regulatory interspaced short palindromic repeat (CRISPR)/ associated protein 9 nuclease (Cas9) system from *Streptococcus pyogenes* for targeted genome modifications was published and it seems to be a new promising approach. The general mechanism of CRISPR/Cas9 is: a 18-23 bp RNA guides Cas9 to the specific locus in the genome and causes a double strand break that leads to either non-homologous end-joining or homology-dependent recombination.

In 2014 Feng and colleagues could show for the first time results on the efficiency, specificity, inheritance and type of single gene mutations induced by the CRISPR/Cas9 system in *Arabidopsis thaliana*. They analyzed 12 different target sites in the genome of Arabidopsis and assayed the efficacy and type of induced mutations over three generations after T-DNA insertion of the CRISPR/Cas9 transgene. After the selection procedure 71.2% of T1, 58.3% of T2 and 79.4% of T3 plants carried a mutation in the desired locus. Leaves of T1 plants were not homozygous for gene modification events but chimeric, heterozygous or biallelic leading to the assumption that no mutagenesis event took place in the early stages of embryo development. But plants homozygous in T2 (22% of analyzed plants) were also homozygous in T3 and carried no additional mutation in the site of interest. All analyzed plants followed Mendelian inheritance. The majority of mutation events were 1bp deletions and 1bp insertions. The ratio of homologous recombination versus non-homologous end-joining was assayed by a designed GUS construct. 11% of T1 plants showed mosaic GUS-staining pattern. The rate of homozygous T2 plants was 13%. On average non-homologous end-joining was more frequent than homologous recombination. Finally, they analyzed the specificity of the CRISPR/Cas9 system in plants by deep sequencing of T1 and T2 plants and direct PCR amplification of 48 predicted off targets. Only the target site carried mutations but no mutations in off targets were detectable. The results by Feng and colleagues show that the CRISPR/Cas9 system is highly efficient and specific in plants.

They suggest that screening of mutants should be performed in T2 or later generations and that the use of germ line specific promoters might increase mutation rate in T1. It should be noted, that in vertebrates it was shown that off targets were edited, too. Thus further analysis are required

to validate the observations by Feng et al, which is the first multigeneration analysis in plants although some studies have been performed in other plant species. Arabidopsis will serve as the reference plant to further analyze and improve this system for plants. The CRISPR/Cas9 system has the potential to revolutionize basic and applied plant research including the possibly to dispense the need for transgenes as markers in future.

Feng Z, Mao Y, Xu N, Zhang B, Wei P, Yang DL, Wang Z, Zhang Z, Zheng R, Yang L, Zeng L, Liu X, Zhu JK (2014) Multigeneration analysis reveals the inheritance, specificity, and patterns of CRISPR/Cas-induced gene modifications in Arabidopsis. *PNAS USA* 111(12):4632-7.

Sander D and Joung K (2014) CRISPR/CAS system for editing, regulation and targeting genomes. *Nature* 32(4)347-355.

Country Reports of the International Arabidopsis Community

Country Highlights

Argentina

- 3 new CONICET grants funded in 2013
- The 16th International Congress of Photobiology will be held in Córdoba, Argentina, 8-12 September, 2014, with strong participation of Arabidopsis researchers

Australia & New Zealand

- Two new Australian Research Council Centres of Excellence were funded on “Translational Photosynthesis” and “Plant Energy Biology”
- 24th ICAR was held in Sydney, Australia, 24th – 28th June 2013 and was great success and enjoyed by all attendees

Austria

- New WWTF project (2014-2018) awarded “Quantitative Live Imaging to Determine the Regulatory Impact of Chromatin Dynamics.”
- New EU project funded (2013-2017) “CALIPSO - Calcium and Light Signals in Photosynthetic Organisms”

Belgium

- Collaboration between 4 Belgian institutes and one international partner (Malcolm Bennett) to develop MultiScale Simulation Models of plant growth incorporating experimental results from Arabidopsis and Maize
- Heyman J et al. (2013) ERF115 controls root quiescent center cell division and stem cell replenishment. *Science* 342(6160):860-3.

Canada

- Nicholas Provart, Stephen Wright and 8 others were awarded a Genome Canada grant to develop modules for the NSF-funded Arabidopsis Information Portal
- Carl Douglas and Xin Li will be the local hosts at the University of British Columbia for the 25th ICAR meeting set for July 28th-August 1st, 2014

China

- New institution, the Center for Plant Biology was established in Tsinghua University
- Web-based software GOEAST-Gene Ontology Enrichment Analysis Software Toolkit has been developed by Dr. Xiujie Wang's group

Czech Republic

- Mandáková T et al. (2013) The more the merrier: recent hybridization and polyploidy in Cardamine. *Plant Cell* 25 (9):3280-3295
- In 2013 twenty projects using Arabidopsis as a model were funded by the Czech Science Foundation (GACR)

Denmark

- Rasmussen S et al. (2013) Transcriptome responses to combinations of stresses in Arabidopsis. *Plant Physiol.* 161: 1783-94.
- Hackenberg T et al. (2013) Catalase and NO CATALASE ACTIVITY1 promote autophagy-dependent cell death in Arabidopsis. *Plant Cell.* 25:4616-26.

Finland

- Centre of Excellence “Molecular Biology of Primary Producers” (2014 - 2019) directed by Prof. Eva-Mari Aro
- National Plant Phenotyping Infrastructure project accepted on the FIRI roadmap (2014-15)

France

- The French society of Plant Biology (SFBV) together with members of the Saclay Plant Science LabEx will organize the 26th ICAR at the Palais des Congrès in Paris, 5th-9th July 2015
- Besnard F et al. (2013) Cytokinin signalling inhibitory fields provide robustness to phyllotaxis. *Nature* 505(7483): 417-21

Germany

- New collaborative research center - SFB 1101 and new priority program - SPP 1710 funded by DFG in 2014
- 9th Tri-National Arabidopsis Meeting (TNAM) 24-26th September 2014, Heidelberg

Greece

- A research Grant in Excellence (“ARISTEIA”) was awarded by General Secretariat of Research and Technology (GSRT) for Arabidopsis research (P. Hatzopoulos).
- A Greek consortium has been created (PMBB_GR, Plant Molecular Biology and Biotechnology) to link agricultural producers to plant biologists/biotechnologists.

India

- Three new grants were awarded for Arabidopsis research in 2013
- Abbas N et al. (2014) Arabidopsis CAM7 and HY5 physically interact and directly bind to HY5 promoter to regulate its expression to promote photomorphogenesis. *Plant Cell*

Ireland

- The 1st Irish Arabidopsis Meeting is being organised in NUI Galway in June 2014
- Kleessen S et al. (2014) Metabolic efficiency underpins performance trade-offs in growth of *Arabidopsis thaliana*. *Nat Commun.* 2014 Mar 28;5:3537

Italy

- Large project in 2013 funded by the Italian Ministry of Education, University and Research on “The control of plant root growth: a systems biology approach”
- Moubayidin L, Di Mambro R, Sozzani R, Pacifici E, Salvi E et al. (2013) Spatial coordination between stem cell activity and cell differentiation in the root meristem. *Dev Cell.* 26:405-15.

Japan

- World Premier International Research Center (WPI) Institute of Transformative Bio-Molecules (ITbM) ITbM has launched in Nagoya University as one of institutes of MEXT WPI program
- The RIKEN Center for Sustainable Resource Science (CSRS) was established in April 2013. RIKEN will continue to contribute to basic research, but will also have a special focus on Green Innovation, or sustainable production of energy, and resources

Netherlands

- De Rybel et al. (2013) *Developmental Cell* 24, 426-437
- Galvan-Ampudia et al. (2013) *Current Biology* 23, 2044-2050

South Korea

- iNID: a web-based tool for identifying network models for interplays among developmental signaling in Arabidopsis
- Lee JH et al. (2013) Regulation of temperature-responsive flowering by MADS-box transcription factor repressors. *Science.* 342(6158):628-32
- 27th ICAR will be hosted by local organizers at June 29th-July 3rd 2016

Spain

- Two large successful coordinated projects involving Arabidopsis functional genomic activities funded by the Ministry of Economy and Competitiveness of Spain ended in 2013: “TRANSPLANTA” and “The Center for Agrigenomics”
- Boer DR et al. (2104). Structural basis for DNA binding specificity by the auxin-dependent ARF transcription factors. *Cell* 156: 577-589

Sweden

- The Swedish Metabolomics Centre in Umeå was inaugurated in March 2013
- Boutté Y et al. (2013) ECHIDNA-mediated post-Golgi trafficking of auxin carriers for differential cell elongation. *PNAS USA* 110:16259 -16264.

United Kingdom

- OpenPlant is one of three synthetic biology multi-disciplinary research centres announced in 2014 by UK funding councils BBSRC, EPSRC and TSB
- Haydon MJ et al. (2013) Photosynthetic entrainment of the *Arabidopsis thaliana* circadian clock. *Nature* 502(7473):689-92

United States

- NAASC members, led by co-chairs Jose Alonso and Nick Provart, are organizing the 2014 ICAR at the University of British Columbia in Vancouver (July 28 - August 1)
- The Arabidopsis Information Portal (AIP)-development funding proposal, submitted by PI Chris Town and colleagues, received NSF support in fall 2013

Argentina

<http://arabidopsisresearch.org/index.php/countries/argentina>

Jorge J. Casal (casal@ifeva.edu.ar) IFEVA (University of Buenos Aires and CONICET) and Instituto Leloir (FIL and CONICET); Marcelo J. Yanovsky (mjyanovsky@gmail.com) Instituto Leloir (FIL and CONICET)

General Activities

Current Arabidopsis Projects

New CONICET grants

- PIP 2013-2015 11220120100349 Functional analysis of sHSPs in Arabidopsis and tomato plants under stress. Estela Marta Valle. IBR, Rosario (www.ibr.gov.ar)
- PIP 2013-2015 11220120100037 Role of mitochondrial Mn SOD in the development of the female gametophyte in *Arabidopsis thaliana*. Eduardo Julian Zabaleta. IIB, Mar del Plata (www.iib.org.ar)
- PIP 2013-2015 11220120100455 Functional analysis of the profile of light induced phospho-proteins in plants. María Agustina Mazzella. INGEBI, Buenos Aires (www.ingebi-conicet.gov.ar)

New ANPCYT grants

- PICT-2012-2117. Effects derived from activation of proline dehydrogenase on the hypersensitive response in Arabidopsis. María Elena Alvarez, Universidad Nacional de Córdoba.
- PICT-2012-1780. Regulation of cell proliferation and differentiation by microRNAs in *Arabidopsis thaliana*. Javier Palatnik. IBR, Rosario.
- PICT-2012-1396. Light signals and temperature stress in plants. Jorge José Casal. CONICET-Facultad de Agronomía-Universidad de Buenos Aires.
- PICT-2012-267. Role of Chromatin in plant responses to UV-B. Paula Casati. CONICET, Universidad Nacional de Rosario.
- PICT-2012-955. Understanding the regulation of gene expression mediated by HD-ZIP I transcription factors in plants. Raquel Chan. CONICET-Universidad Nacional del Litoral.
- PICT-2012-1203. Role of mitochondria in metal homeostasis and stress responses in plants. Daniel Gonzalez. CONICET-Universidad Nacional del Litoral.
- PICT-2012-7. Polarized growth in the pollen tube; Molecular components in the cell wall: Role of P4Hs, EXTs and PERKs. Jorge Muschietti. INGEBI-CONICET.
- PICT-2012-317. Regulation of light and hormone signaling pathways in jasmonate mediated defense responses in plants. Carlos Ballaré. IFEVA, CONICET-Facultad de Agronomía-Universidad de Buenos Aires.

- PICT-2012-1686. Identification and characterization of mechanisms promoting post-embryonic growth in plants. Ramiro Rodriguez Virasoro. IBR, Rosario.

Conferences and Workshops

- The 16th International Congress of Photobiology will be held in Córdoba, Argentina, 8-12 September, 2014, with strong participation of Arabidopsis researchers.

Selected Publications

- Casadevall, R, Rodriguez, RE, Debernardi, JM, Palatnik, JF et al. (2013) Repression of growth regulating factors by the MicroRNA396 inhibits cell proliferation by UV-B radiation in Arabidopsis leaves. *Plant Cell* 25(9):3570-83..
- Karayekov, E, Sellaro, R, Legris, M, Yanovsky, MJ et al. (2013) Heat shock-induced fluctuations in clock and light signaling enhance phytochrome B-mediated arabidopsis deetiolation. *Plant Cell* 25:2892-906.
- Rugnone, M.L., Soverna, A.F., Sanchez, S.E., Schlaen, RG et al. (2013) LNK genes integrate light and clock signaling networks at the core of the Arabidopsis oscillator. *PNAS* 110: 12120 -12125.
- Gangappa, SN, Crocco, CD, Johansson, H, Datta, S et al. (2013) The Arabidopsis B-BOX protein BBX25 interacts with HY5, negatively regulating BBX22 expression to suppress seedling photomorphogenesis. *Plant Cell* 25:1243-57.
- Bologna, NG, Schapire, AL, Zhai, J, Chorostecki, U et al. (2013) Multiple RNA recognition patterns during microRNA biogenesis in plants. *Genome Res.* 201323:1675-89.
- Martin, MV, Fiol, DF, Sundaresan, V, Zabaleta, EJ et al. (2013) oiwa, a female gametophytic mutant impaired in a mitochondrial manganese-superoxide dismutase, reveals crucial roles for reactive oxygen species during embryo sac development and fertilization in Arabidopsis. *Plant Cell* 25:1573-91.

Australia & New Zealand

<http://arabidopsisresearch.org/index.php/countries/australia-new-zealand>

Barry Pogson (Barry.Pogson@anu.edu.au), The Australian National University, Canberra

General Activities

Country Highlights and News

New Academic Appointments: Christopher Cazzonelli, University of Western Sydney; Gonzalo Estavillo, CSIRO; Ryan Lister, University of Western Australia and Andrew Eamens (Uni. Newcastle).

Notable Awards: The 2013 Goldacre award was to Min Chen (Uni. Sydney) and the 2013 Australian Academy of Science Fenner Medal to Ulrike Mathesius (ANU). The ASPS and FPB 2012 best paper award was to Hollie Webster (Murdoch Uni). The JG Wood lecture was given by Jim Reid (Uni. Tasmania). Harvey Millar (Plant Energy Biology Deputy Director, UWA) was the first Australian to receive the American Society of Plant Biology Charles Shull Award. John Evans (ANU) and David Day (Flinders U) were elected to the Australian Academy of Science and Graham Farquhar (ANU) as a Foreign member of the USA National Academy of Science.

Research Highlights: Two new Australian Research Council Centres of Excellence were funded on “Translational Photosynthesis” and “Plant Energy Biology”.

Current Arabidopsis Projects

The best source of information about plant research in Australia is the Australian Society of Plant Physiologists (www.asps.org.au/). Other information is at www.arabidopsis.org/info/2010_projects/Australia.jsp or contact Barry Pogson, The Australian National University, Canberra, Email: barry.pogson@anu.edu.au

- Major areas of Arabidopsis research and functional genomics are Canberra, Melbourne, Adelaide and Perth. Major sites of plant science with foci on crops include Queensland, Tasmania, South Australia, ACT and NSW. Institutes with a strong focus on Arabidopsis include the Australian Research Council (ARC) Centres of Excellence in Plant Energy Biology (www.plantenergy.uwa.edu.au/) and Plant Cell Walls (www.plantcellwalls.org.au) and CSIRO Plant Industry (www.pi.csiro.au), plus numerous researchers across all the Universities.
- Increasing numbers of New Zealand plant scientists are incorporating *Arabidopsis thaliana* into their research, and several are using functional genomics approaches. In addition to the projects being conducted at the universities, research programs are carried out at the Government-owned Crown Research Institutes.

Conferences and Workshops

- Arabidopsis 2013, Sydney, 24th – 28th June. The 24th International Conference on Arabidopsis Research was held in Sydney, Australia and was enjoyed by all attendees. Highlights were the Simon Chan Memorial Symposium, the support of all sponsors, both domestic and international and the science.
- COMBIO – Combined Biology Societies Annual Conference. See <http://www.asps.org.au/> for details.

Road Map Related Activities

Arabidopsis Tools and Resources

- NCRIS Plant Phenomics (www.plantphenomics.org.au). This offers cutting-edge growth and automated non-invasive analytical facilities. Analyses include root and shoot growth, photosynthetic rates, infra-red and hyper-spectral imaging of Arabidopsis and crop plants in growth chambers, glasshouses and field sites. The Facility is available to national and international researchers. For more information please contact Bob Furbank (Robert.Furbank@csiro.au). More details can be found in the Phenomics Subcommittee section of this annual report.
- SUBA (a SUBcellular location database for Arabidopsis proteins). The SUBA database provides a powerful means to assess protein subcellular localisation in Arabidopsis (<http://www.suba.bcs.uwa.edu.au>).
- Anno-J: Interactive web-based genome browsing in Arabidopsis for large datasets in functional genomics
- Julian Tonti-Filippini and A. Harvey Millar (hmillar@cyllene.uwa.edu.au), ARC Centre of Excellence in Plant Energy Biology, M316. The University of Western Australia, Perth, WA, 6009, Australia.

Major Funding Sources

Major Funding Agencies: Australian Research Council (www.arv.gov.au)

Austria

<http://arabidopsisresearch.org/index.php/countries/austria>

Marie-Theres Hauser (marie-theres.hauser@boku.ac.at), University of Natural Resources and Life Sciences BOKU, Vienna; Andreas Bachmair (andreas.bachmair@univie.ac.at) University of Vienna, Austria; Andrea Pitzschke (andrea.pitzschke@boku.ac.at), University of Natural Resources and Life Sciences BOKU, Vienna; Peter Schlögelhofer (peter.schloegelhofer@univie.ac.at), Department of Chromosome Biology, Max F. Perutz Laboratories, University of Vienna, Austria; Thomas Friese (thomas.friese@gmi.oeaw.ac.at), Gregor Mendel Institute of Molecular Plant Biology

General Activities

Arabidopsis Research Facilities

- University of Natural Resources & Life Science Vienna, Department of Applied Genetics & Cell Biology (www.dagz.boku.ac.at/en/)
- Gregor Mendel Institute of Molecular Plant Biology (<http://www.gmi.oeaw.ac.at/>)
- Max F. Perutz Laboratories (<http://www.mfpl.ac.at/en/home.html>)
- Campus Science Support Facilities at the Vienna Biocenter Campus - Plant Science (<http://www.csf.ac.at/facilities/PlantS/>)
- Institute of Science and Technology, Austria (<https://ist.ac.at/en/>)
- University of Vienna, Molecular Systems Biology (<http://www.univie.ac.at/mosys/>)

Research Groups

Population Genetics

Magnus Nordborg (www.gmi.oeaw.ac.at/research-groups/magnus-nordborg), Scientific Director of the GMI, genome-wide association (GWA); 1001 Genomes project; Genomic analysis of genotype:phenotype map; Adaptation to the abiotic environment; Molecular evolution of Arabidopsis; Statistical methodology for association mapping.

Systems biology

Wolfram Weckwerth (www.univie.ac.at/mosys/wolfram_weckwerth.html): largest proteomics database resource for Arabidopsis <http://promex.pph.univie.ac.at/promex/>

Molecular Biology and signalling

Andrea Pitzschke (<http://www.dagz.boku.ac.at/arbeitsgruppen/ag-pitzschke/>): stress signalling and Mitogen-Activated Protein Kinases

Markus Teige (www.univie.ac.at/ibmz/groups/teigeov.html): signal transduction and physiology

Andreas Bachmair (<http://www.mfpl.ac.at/mfpl-group/group/bachmair.html>): SUMO conjugation to plant proteins, Ubiquitin, involvement of the pathway in nitric oxide sensing, tobacco retrotransposon Tto1 in Arabidopsis

Chromosome Biology

Karel Riha (www.gmi.oeaw.ac.at/research-groups/karel-riha). Telomeres and genome stability.

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). Genetic and epigenetic aspects of abiotic stress effects; Genetic and epigenetic aspects of polyploidy.

Hisashi Tamaru (www.gmi.oeaw.ac.at/research-groups/hisashi-tamaru). Control of chromatin fates in pollen.

Development

Wolfgang Busch (www.gmi.oeaw.ac.at/research-groups/wolfgang-busch). Regulation of root development in Arabidopsis

Thomas Greb (www.gmi.oeaw.ac.at/research-groups/thomas-greb). Growth and cell fate regulation.

Claudia Jonak (www.gmi.oeaw.ac.at/research-groups/claudia-jonak). Stress signaling and adaptation.

Michael Nodine (www.gmi.oeaw.ac.at/research-groups/michael-nodine). Small RNA functions in plant embryos.

Eva Benkova (<http://ist.ac.at/de/forschung/forschungsgruppen/benkova-gruppe/>): hormonal cross-talk and root architecture

Jiri Friml (<http://ist.ac.at/de/forschung/forschungsgruppen/friml-gruppe/>): Auxin transport, cell polarity and endocytic trafficking

Molecular Genetics & Cell Biology

Marie-Theres Hauser (www.dagz.boku.ac.at/en/research-groups/ag-hauser/): development, stress

Lindy Abas (www.dagz.boku.ac.at/en/research-groups/ag-abas/): membrane proteins, hormone transport

Jürgen Kleine Vehn (www.dagz.boku.ac.at/en/research-groups/ag-kleine-vehn/): phytohormonal crosstalk, differential growth regulation

Barbara Korbei (www.dagz.boku.ac.at/en/research-groups/ag-korbei/): membrane protein transport in plants

Christian Luschnig (www.dagz.boku.ac.at/en/research-groups/ag-luschnig/): auxin, chromatin

Glycobiology

Lukas Mach (www.dagz.boku.ac.at/en/research-groups/ag-mach/): glycosylation enzymes, proteinases, vacuolar proteins

Georg Seifert (www.dagz.boku.ac.at/en/research-groups/ag-seifert/): arabinogalactan proteins, cell elongation biosynthesis of nucleotide sugars for cell wall polymers

Richard Strasser (www.dagz.boku.ac.at/en/research-groups/ag-strasser/): N-glycosylation

Doris Lucyshyn (www.dagz.boku.ac.at/en/research-groups/ag-abas/project-lucyshyn/): O-GlcNAcylation

RNA metabolism

Andrea Barta (www.mfpl.ac.at/mfpl-group/group/barta.html): splicing and alternative splicing in plants, SR proteins in development and stress response, non-sense mediated RNA decay

Mariya Kalyna (www.dagz.boku.ac.at/en/research-groups/ag-hauser/project-kalyna/): Alternative splicing

Current Arabidopsis Projects

SFB projects

- since 2010 "RNA Regulation of the transcriptome" SFB 43, coordinated by Renee Schroeder, Max F Perutz Labs (www.mfpl.ac.at/rna-biology/focus-regulatory-rna/)
- 2009-2016 "Fusarium Metabolites and Detoxification Reactions" SFB 37 coordinated by Gerhard Adam, University of Natural Resources & Life Sciences, Vienna

WWTF projects "New Ventures Beyond Established Frontiers"

- 2014-2018 "Quantitative Live Imaging to Determine the Regulatory Impact of Chromatin Dynamics." coordinated by Ortrun Mittelsten Scheid, GMI (http://wwtf.at/projects/research_projects/details/index.php?PKEY=4148_DE_O&lang=EN)

EU-projects

- 2010 - 2014 "MeioSys-Systematic analysis of factors controlling meiotic recombination in higher plants", a collaborative project funded by the EU (FP7) (www.meiosys.org/)
- 2010 - 2014 "UV-B radiation: A specific regulator of plant growth and food quality in a changing climate" (www.ucc.ie/en/uv4growth/)
- 2011-2014 "MERIT - Metabolic Reprogramming by Induction of Transcription", Marie-Curie Initial Training Network funded by the EU (FP7) (<http://theory.bio.uu.nl/MERIT/html/index.html>)
- 2013-2017 "CALIPSO - Calcium and Light Signals in Photosynthetic Organisms", Marie-Curie Initial Training Network funded by the EU (FP7) (<http://itn-calipso.univie.ac.at/>)

ERA-CAPS projects (2014-2017; www.era-caps.org/joint-calls/era-caps-funded-projects)

- "N-virionment on ubiquitin-dependent protein degradation (N-end rule pathway)" Andreas Bachmair among 4 PIs from 4 European countries
- "Delineating the crossover control networks in plants" (speaker Peter Schlögelhofer, 6 PIs from 3 European countries).
- "Dimorphic fruits, seed and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments" (Ortrun Mittelsten Scheid among 6 PIs from 4 European countries)
- "European Plant Embryology Consortium" Michael Nodine among 5 PIs from 3 European countries

Road Map Related Activities

Arabidopsis Tools and Resources

- The Campus Science Support Facilities at the Vienna Biocenter Campus - Plant Sciences (<http://www.csf.ac.at/facilities/PlantS/>) is currently establishing protocol for CRISPR/CAS9 mediated gene knock-out/ targeting.
- Established a novel system for transient expression in plant tissue; suitable also for research on Arabidopsis genes: Pitzschke A (2013) *Tropaeolum tops tobacco* - simple and efficient transgene expression in the order brassicales. *PLoS One* 8: e73355

Outreach Activities

Within the COST action UV4growth the brochure "Exploiting ultraviolet light and other external factors for sustainable food security" was made for stakeholders and recommendation of funding bodies. This brochure has been distributed European wide.

Several activities for the International Fascination of Plants Day 2013 such as Movie Night at the GMI: an evening of award-winning documentaries

Several activities for the "Lange Nacht der Forschung" at the University of Natural Resources and Life Sciences, Vienna, 4.4.2014

Conferences and Workshops

- The MeioSys research consortium (<http://www.meiosys.org/>) had its yearly meeting in Vienna (VBC 2.6.-4.6.2013), organized by Karl Mechtler and Peter Schlögelhofer
- Viennese Plant Networkers Meetings at the IST Austria, 9. 10. 2013 and at the GMI, 29.4.2014

Selected Publications

- Meijón M, Satbhai SB, Tsuchimatsu T, Busch W (2013) Genome-wide association study using cellular traits identifies a new regulator of root development in *Arabidopsis*. *Nature Genetics* 46: 77-81
- Long Q, Rabanal FA, Meng D, Huber CD et al. (2013) Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden. *Nature Genetics* 45: 884-890
- Rosquete MR, von Wangenheim D, Marhavý P, Barbez E et al. (2013) An auxin transport mechanism restricts positive orthogravitropism in lateral roots. *Curr Biol* 23: 817-822
- Pitzschke A, Datta S, Persak H (2014) Salt Stress in *Arabidopsis*: Lipid Transfer Protein AZI1 and Its Control by Mitogen-Activated Protein Kinase MPK3. *Mol Plant* 7, 722-738
- Korbei B, Moulinier-Anzola J, De-Araujo L, Lucyshyn D et al. (2013) *Arabidopsis* TOL proteins act as gatekeepers for vacuolar sorting of PIN2 plasma membrane protein. *Curr Biol*. 23:2500-2505
- Uanschou C, Ronceret A, Von Harder M, De Muyt A et al. (2013) Sufficient amounts of functional HOP2/MND1 complex promote interhomolog DNA repair but are dispensable for intersister DNA repair during meiosis in *Arabidopsis*. *Plant Cell* 25:4924-40

Major Funding Sources

- FWF Austrian Science Fund <http://www.fwf.ac.at/en/index.asp>
- WWTF Vienna Science and Technology Fund <http://www.wwtf.at/index.php?lang=EN>
- OeAD Scholarship database <http://www.grants.at/home/>
- New Frontiers Programme (NFP) <http://www.oeaw.ac.at/deutsch/forschung/new-frontiers.html>
- FFG-Austrian Research Promotion Agency <https://www.ffg.at/en/funding>
- ÖAW Austrian Academy of Sciences <http://www.oeaw.ac.at/english/home.html>

Education

Vienna Biocenter Summer School is a ten week research and teaching programme for undergraduates from around the world. Supported by four Vienna Biocenter institutes, including the Gregor Mendel Institute of Molecular Plant Biology (www.vbcphdprogramme.at/summer-school/).

Vienna Biocenter International PhD Programme allows outstanding students to undertake PhD studies using *Arabidopsis* projects at the Gregor Mendel Institute of Molecular Plant Biology. (www.vbcphdprogramme.at)

Belgium

<http://arabidopsisresearch.org/index.php/countries/belgium>

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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 (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 Dijk; F. Roland), membrane proteins (M. Boutry), abiotic stress (N. Verbruggen; C. Hermans, Y. Guisez; M. Hanikenne), flowering (C. Périlleux; P. Tocquin) and plant pathogen interaction (G. Angenon, B. Cammue, L. Gheysen; P. du Jardin, J. Vanderleyden, P. Delaplace, J. Dommes).

Current Arabidopsis Projects

Belgian *Arabidopsis* projects are funded by university-, regional- or federal-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. More info, see 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, 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.

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

Conferences and Workshops

- European Network of Plant endomembrane Research (ENPER) 2013 meeting, 27-30/08, Ghent

Selected Publications

- Heyman J, Cools T, Vandenbussche F, Heyndrickx KS et al. (2013) ERF115 controls root quiescent center cell division and stem cell replenishment. *Science* 342(6160):860-3.
- Di Rubbo S, Irani NG, Kim SY, Xu ZY et al. (2013) The clathrin adaptor complex AP-2 mediates endocytosis of brassinosteroid insensitive1 in Arabidopsis. *Plant Cell* 25(8):2986-97.

- De Storme N, De Schrijver J, Van Criekinge W, Wewer V et al. (2013) GLUCAN SYNTHASE-LIKE8 and STEROL METHYLTRANSFERASE2 are required for ploidy consistency of the sexual reproduction system in Arabidopsis. *Plant Cell* 25(2):387-403.
- Bhosale R, Jewell JB, Hollunder J, Koo AJ et al. (2013) Predicting gene function from uncontrolled expression variation among individual wild-type Arabidopsis plants. *Plant Cell* 25(8):2865-77.

Major Funding Sources

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

Canada

<http://arabidopsisresearch.org/index.php/countries/canada>

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General Activities

Current Arabidopsis Projects

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

Nicholas Provart, Stephen Wright and 8 others were awarded a Genome Canada grant to develop modules for the NSF-funded Arabidopsis Information Portal. Over the three year term of the grant modules for transcriptomics, protein-protein interactions, expressologs/syteny, protein structures, and visualization will be developed for use in the AIP and other cyberinfrastructure portals. The Bio-Analytic Resource, on which these modules are based, continues to be used by approximately 70,000 plant researchers per month from around the world.

Conferences and Workshops

- Carl Douglas and Xin Li will be the local hosts at the University of British Columbia for the 2014 ICAR meeting set for July 28th-August 1st, 2014.

Major Funding Sources

Funding for Arabidopsis research is largely from NSERC, one of the three federal funding agencies in Canada.

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

China

<http://arabidopsisresearch.org/index.php/countries/china>

Wei-Cai Yang (wcyang@genetics.ac.cn) Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences, Beijing

General Activities

Current Arabidopsis Projects

In 2013, the main Arabidopsis research focus is on stem cell biology and reproductive biology, witnessed by continuous support from the Ministry of Science and Technology of China. Three group projects were funded for 5 years, they are “molecular network of stem cell maintenance and reprogram in meristem microenvironment” (coordinated by Dr. Yu-Xin Hu, Institute of Botany, CAS), “molecular mechanisms controlling embryo and seed development in plants” (coordinated by Dr. Chun-Min Liu of Institute of Botany, CAS), and “molecular network controlling the establishment of leaf polarity” (coordinated by Dr. Yu-Ling Jiao, Institute of Genetics and Developmental Biology, CAS). In addition, three key projects using Arabidopsis model system to study plant reproduction and epigenetics were funded by National Science Foundation of China.

It is worth to notice that a new institution, the Center for Plant Biology was established in Tsinghua University. The center currently hosts 10 groups covering a variety of research topics in plant science, including structural biology, bioinformatics, proteomics, plant-microbe interactions, stress biology, and epigenetics.

Good news is that the funding of NSFC continues to increase as public spending is shrinking in other areas. The budget for NSFC is 19b RMB in 2014, about 11.7% increment compared to 2013. This will undoubtedly promote Arabidopsis research in 2014.

Road Map Related Activities

Arabidopsis Tools and Resources

Additional Information

A web-based software GOEAST-Gene Ontology Enrichment Analysis Software Toolkit has been developed by Dr. Xiujie Wang's group at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. GOEAST provides an easy to use, visualizable, comprehensive and unbiased Gene Ontology (GO) analysis for high-throughput experimental results, especially for results from microarray hybridization experiments. The main function of GOEAST is to identify significantly enriched GO terms among given lists of genes using accurate statistical methods. For more information, please visit <http://omicslab.genetics.ac.cn/GOEAST/>.

Major Funding Sources

The National Science Foundation of China:

No. 83 Shuangqing Road, Haidian District, Beijing 1000085.
Tel: (086) 010 62327087.

<http://www.nsf.gov.cn/Portal0/default106.htm>

The Ministry of Science and Technology of China

Department of Basic Research

No. 15 Fuxing Road, Beijing 100862. Tel: 86-10-58881515

<http://www.most.gov.cn/eng/index.htm>

Czech Republic

<http://arabidopsisresearch.org/index.php/countries/czech-republic>

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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 and cytogenetics/genome biology. Traditional centers of experimental plant research exist at the institutes of the Academy of Sciences of the Czech republic : esp. Institute of Experimental Botany - <http://www.ueb.cas.cz/en>, Institute of Biophysics - <http://www.ibp.cz/en/> and Institute of Plant Molecular Biology - <http://www.umbr.cas.cz/> and universities: Charles University in Prague - <http://kfrserver.natur.cuni.cz/english/index.html>, Masaryk University - <https://www.muni.cz/sci/314010> and Mendel University - <http://ubfr.af.mendelu.cz/en/?lang=en> , both in Brno and Palacky university in Olomouc - <http://www.prf.upol.cz/en/menu/departments/>. Over last several years new joint research centers are established in Moravian cities Olomouc and Brno - both of them with plant biology as one of the crucial foci of research.

1. 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.
2. 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.

Both of these centers opened new institutes and labs working in plant biology and using Arabidopsis as a crucial model.

Current Arabidopsis Projects

Arabidopsis research in the Czech republic is funded on the individual grants basis and in the year 2013 twenty projects using Arabidopsis as a model were funded by the Czech Science Foundation (GACR). Among the biggest ones there were - "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 RNA splicing in protoxylem cell fate", "Nonspecific phospholipase C", "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" and "Functions of the plant exocyst tethering complex in exocytosis, cell division and cell wall biogenesis".

Outlook on Arabidopsis Research

Especially due to great plant research infrastructure development supported by the EU over last several years it is to be expected that Arabidopsis driven research will be very important part of especially basic but also applied research funding in the Czech republic.

Road Map Related Activities

Arabidopsis Tools and Resources

"Plant Cell Morphogenesis, Methods and Protocols" Springer Protocols vol. 1080 (Žárský V. and Cvrčková F. eds.) - ISBN 978-1-62703-643-6 (eBook) - comprehensive resource for plant cell morphogenesis analysis from classical anatomy approaches to EM tomography. - <http://www.springer.com/life+sciences/plant+sciences/book/978-1-62703-642-9>

Outreach Activities

Olomouc Biotech 2013 PLANT BIOTECHNOLOGY: Green for Good II, June 17 - 21, 2013 Olomouc, Czech republic <http://www.cr-hana.eu/G4G2/>

Conferences and Workshops

- Auxins and Cytokinins in Plant Development, International Symposium 2014, June 29 - July 4, 2014, Prague www.acpd2014.org

Selected Publications

- Mandáková T, Kovařík A, Zozomová-Lihová J et al. (2013) The more the merrier: recent hybridization and polyploidy in Cardamine. *Plant Cell* 25 (9):3280-3295.
- Žďárská M, Zatloukalová P, Benitez M et al. (2013) Proteome analysis in Arabidopsis reveals shoot- and root-specific targets of cytokinin action and differential regulation of hormonal homeostasis. *Plant Physiology* 161 (2):918-930.
- Drdová E, Synek L, Pečenkova T et al. (2013) The exocyst complex contributes to PIN auxin efflux carrier recycling and polar auxin transport in Arabidopsis. *Plant Journal* 73 (5):709-719.
- Kulich I, Pečenkova T, Sekereš J et al. (2013) Arabidopsis exocyst subcomplex containing subunit EXO70B1 is involved in the autophagy-related transport to the vacuole. *Traffic* 14 (11):1155-1165.

- Černý M, Kuklova A, Hoehenwarter W et al. (2013) Proteome and metabolome profiling of cytokinin action in Arabidopsis identifying both distinct and similar responses to cytokinin down- and up-regulation. *Journal of Exp. Botany* 64(14):4193-4206.

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 also recently supported by the Technology Agency of the Czech Republic (TACR) and Arabidopsis is accepted as model to be a driver for applications.

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

Denmark

<http://arabidopsisresearch.org/index.php/countries/denmark>

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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 2016. CPSC will be rooted in the Department of Plant and Environmental Sciences at the Faculty of Science at Frederiksberg Campus 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 among which Arabidopsis is employed as a model organism in two centers, Centre for Membrane Pumps in Cells and disease (Pumpkin) and Center for Dynamic Molecular Interactions (Dynamo).

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

- Rasmussen S, Barah P, Suarez-Rodriguez MC, Bressendorff S et al. (2013) Transcriptome responses to combinations of stresses in Arabidopsis. *Plant Physiol.* 161: 1783-94.
- Hackenberg T, Juul T, Auzina A, Gwizdz S et al. (2013) Catalase and NO CATALASE ACTIVITY1 promote autophagy-dependent cell death in Arabidopsis. *Plant Cell.* 25:4616-26.
- Hoffmann RD, Palmgren MG (2013) Epigenetic repression of male gametophyte-specific genes in the Arabidopsis sporophyte. *Mol Plant.* 6:1176-86
- Knoch E, Dilokpimol A, Tryfona T, Poulsen CP et al. (2013) A β -glucuronosyltransferase from *Arabidopsis thaliana* involved in biosynthesis of type II arabinogalactan has a role in cell elongation during seedling growth. *Plant J.* 76:1016-29.
- Andersen TG, Nour-Eldin HH, Fuller VL, Olsen CE et al. (2013) Integration of biosynthesis and long-distance transport establish organ-specific glucosinolate profiles in vegetative Arabidopsis. *Plant Cell* 25:3133-45.

Finland

<http://arabidopsisresearch.org/index.php/countries/finland>

Yrjö Helariutta (yrjo.helariutta@helsinki.fi) University of Helsinki, Finland

General Activities

Arabidopsis Research Facilities

Our Academy of Finland funded research group is working on Arabidopsis Flower related Ubiquitin Proteasome System unraveling the molecular networks acting on post translational modifications of regulators of flowering time and flower development.

University of Eastern Finland, the research group of plant biotechnology

University of Helsinki, Finland

University of Turku, Finland

Current Arabidopsis Projects

Professor Kärenlampi S: Mechanisms of metal hyperaccumulation and hypertolerance in plants. Funded by Academy of Finland 2012-2016, <http://www.uef.fi/en/plant-biotechnology/metal-hyperaccumulation>

Center of Excellence Academy of Finland, Centre of Excellence "Molecular Biology of Primary Producers" (2014 - 2019), Directed by Prof. Eva-Mari Aro

Road Map Related Activities

Arabidopsis Tools and Resources

Prof Tapio Palva will probably also report on National Plant Phenotyping Infrastructure project that was accepted on the FIRI roadmap and has got funding to be installed during 2014-15. As a project manager I am involved in the planning and setting up phase and will also prepare the future development and expansion plans. This phenomics project is first of its' kind in Scandinavia and will hopefully grow to serve the whole Baltic region. The facility will be designed to serve Arabidopsis research and translational research to crops and trees.

New generation sequencing, bioinformatics, functional genomics, cell and tissue specific expression

Outreach Activities

The Academy of Finland has recently initiated a think-tank to develop a vision for research strategies for the support of Finnish Bioeconomy.

Conferences and Workshops

- Plant Science Days 2013 (<http://www.helsinki.fi/plantsci-days2013/>), brought together 180 plant researchers of Finland including many who work on Arabidopsis.

- Plant Vascular Biology 2013 (<http://pvb2013.org/>), in Helsinki 26-30 July 2013, brought together some 180 plant researchers mainly from abroad, mostly working on Arabidopsis.

France

<http://arabidopsisresearch.org/index.php/countries/france>

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General Activities

Arabidopsis Research Facilities

About ten research centers conduct research with *Arabidopsis thaliana* despite increasing pressure in favor of crop plants. These centers are supported by research organizations like the Centre National de la Recherche Scientifique (CNRS, with Institutes of Biological Sciences and Ecology and Environment), the Institut de la Recherche Agronomique (INRA, with divisions of Plant Biology and Breeding, and Plant health and the environment) in association with French Universities and higher education establishments (Ecole Normale Supérieure, AgroParisTec, SupAgro). Research projects including some work with Arabidopsis are funded by the Agence Nationale de la Recherche (ANR). Technological platforms and equipment receive also funding from French regions.

Among the tools developed in the context of the program "Investing for the future", sponsored by the French government, Laboratory of Excellence (LabEx) supports research activities, training, teaching, innovation and transfer to applied research. Arabidopsis projects were represented in various multidisciplinary LabEx. In addition, two plant LabEx, including a large number of Arabidopsis teams, were funded: one is the Saclay Plant Science LabEx (SPS) gathering 4 plant sciences labs in the Paris area (Versailles, Gif sur Yvette, Orsay and Evry) that develop research activities mainly in genetic, molecular and cellular mechanisms that control plant physiology and development, as well as their interactions with fluctuating biotic or abiotic environments; the other LabEx is TULIP that networks 5 labs in the Midi-Pyrénées region of France. TULIP strengthens the link between communities working on plant biology, agrobiosciences, biodiversity or ecology.

Current Arabidopsis Projects

An ERC advanced grant was attributed to Pascal Genschik for PHAGORISC, a project connecting RNA and protein degradation machineries. Olivier Hamant received an ERC consolidator grant for his MechanoDevo project that aims to identify the role of mechanotransduction in plant development. ERC starting grants were successful for VariWhim, by Sylvain Raffaele that focuses on plant-Sclerotinia sclerotiorum fungus interactions and for APPL, by Yvon Jaillais that focus on anionic phospholipids in plant receptor kinase signaling.

In 2013, funded ANR projects with Arabidopsis were from non-thematic AAP as well as from applications to the thematic BIOADAPT programme. Among these: Reglisse, Regulation of glycerolipids interconversion in plants in response to environmental variations, Laurent Nussaume; Fe-S traffic: The cellular trafficking of iron-sulfur (Fe-S) clusters in plants, Nicolas Rouhier; InaSeed: Investigating the Role of Innate Immunity in Arabidopsis Seed Development, Gwyneth Ingram.

For young researcher: Bugspit: Molecular mechanisms underlying plant specification in the pea aphid complex, Akiko Sugio; Extrachrom, epigenetic control of extrachromosomal forms and neoinsertions of transposable elements in plants, Marie Mirouze.

Outlook on Arabidopsis Research

There are presently no visibility on future funding options for fundamental research programmes, whatever model species. In 2014, France's participation to ERA-CAPS, that aims at sustaining fundamental and cooperative research programs in plants, was first posted with additional constraints (involvement of a company, and no model plant) and was finally retracted.

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>).

Functional Genomics on Arabidopsis is developed at the URGV-Genopole at Evry providing expertise and access to transcription profiling methods with microarrays and high-throughput sequencing (HTS) technologies (contact S. Balzergue, <http://www-urgv.versailles.inra.fr/microarray/index.htm>).

Two high-throughput automated phenotyping platforms, PHENOSCOPE at Versailles (contact O. Loudet, <http://www.ijpb.versailles.inra.fr/en/plateformes/ppa/index.html>) and PHENOPSIS at Montpellier (contact C. Granier, www1.montpellier.inra.fr/ibip/lepse/english/ressources/phenopsis.htm) 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>).

Outreach Activities

The Scientific Group of Interest "Plant Biotechnologies" (GIS BV) was created following the "Genoplante" network (<http://www.genoplante.com>). The GIS BV is built on a large public-private partnership community, which gathers public research institutes (including work performed on model plants as Arabidopsis), seed companies, technical institutes, sector representatives, and competitive clusters. The ambition of the GIS BV is to further support the development of large-scale research programs, while measuring up to the current international initiatives in plant biotechnologies.

Conferences and Workshops

- The XIIIth Cell Wall Meeting - Nantes, France, July 7 - 12, 2013
- Graines 2013, 4th National Symposium of the French Seed Biology Network, Dijon, France, October 30 - 31, 2013
- SFBV International Congress, Créteil, France, December 12-13, 2013

Selected Publications

- Tisné S, Serrand Y, Bach L, Gilbault E et al. (2013) Phenoscope: an automated large-scale phenotyping platform offering high spatial homogeneity. *Plant J* 74(3):534-44.
- Besnard F, Refahi Y, Morin V, Marteaux B et al. (2013) Cytokinin signalling inhibitory fields provide robustness to phyllotaxis. *Nature* 505(7483): 417-21.
- Uyttewaal M, Burian A, Alim K, Landrein B et al. (2012) Mechanical stress acts via katanin to amplify differences in growth rate between adjacent cells in Arabidopsis. *Cell* 149(2):439-51.

Major Funding Sources

Agence Nationale de la Recherche (ANR), "BLANC" non-thematic program, BIOADAPT: Adaptation: from genes to populations. Genetics and biology of adaptation to stresses and disturbances;

Ministère de l'éducation nationale, de l'enseignement supérieur et de la recherche: programmes investissements d'avenir

European fundings: ERC, ERA-CAPS, Mari-Curie fellowships

Germany

<http://arabidopsisresearch.org/index.php/countries/germany>

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General Activities

Arabidopsis Research Facilities

Arabidopsis research in Germany is very broad and projects cover all aspects of the functional genomics of Arabidopsis development and interaction with the biotic and abiotic environment. Places of Arabidopsis research are distributed across Germany at Universities, Max-Planck-Institutes, Helmholtz Centers and Leibniz-Institutes. From 2001 to 2010 the Arabidopsis Functional Genomics Network (AFGN) was funded by the German Science Foundation (DFG) to enhance coordination and collaboration between German Arabidopsis researchers. AFGN continues its coordinating function and works as a section under the umbrella of the German Botanical Society (DBG). AFGN is coordinated by Luise Brand (University of Tuebingen) and the new AFGN homepage will be online soon (<http://www.zmbp.uni-tuebingen.de/plant-physiology/afgn.html>). The new homepage will serve as information portal for German Arabidopsis research.

Current Arabidopsis Projects

Funding of basic Arabidopsis functional genomics research is and will be provided by the DFG via several funding instruments (<http://gepris.dfg.de/gepris/OCTOPUS?language=en>). Selected examples are given below:

Individual Funding

Currently a total number of 182 individual projects concerning Arabidopsis research are funded by the DFG, of these are 7 projects funded by the Emmy Noether Program, 1 project is funded by the Heisenberg Program, 10 projects are research fellowships and 164 individual research grants.

Priority Programs

Arabidopsis researchers are involved in 8 priority programs, three examples are:

- SPP 1710 (since 2014): Dynamics of thiol-based redox switches in cellular physiology (<http://www.thiolswitches.de/>)
- SPP 1529 (since 2011): “Evolutionary plant solutions to ecological challenges: molecular mechanisms underlying adaptive traits in the Brassicaceae s.l.” (<http://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html>)
- SPP 1530 (since 2011): “Flowering time control: from natural variation to crop improvement” (<http://www.flowercrop.uni-kiel.de/en>)

- SPP 1212 (2007-2014): “Microbial reprogramming of plant cell development” (<http://www.plant-micro.de/>)

Collaborative Research Centers

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

- SFB 1101 (since 2014): “Molecular encoding of specificity in plant processes” (<http://www.uni-tuebingen.de/en/research/core-research/collaborative-research-centers/sfb-1101.html>)
- SFB 973 (since 2012): “Priming and memory of organismic responses to stress” (<http://www.sfb973.de/>)
- SFB 648 (since 2005): “Molecular mechanisms of information processing in plants” (<http://www.sfb648.uni-halle.de/>)

Research Training Groups

- GPK 1525 (since 2009): “The dynamic response of plants to a changing environment” (<http://www.igrad-plant.hhu.de/>)
- GPK 1342 (since 2007): “Molecular and functional analysis of lipid-based signal transduction systems” (<http://www.gk-1342.uni-wuerzburg.de/>)

Research Units

- FOR 948 (since 2009): “Nitrogen uptake, metabolism and remobilization in leaves during plant senescence” (<http://dfg-for948.ipk-gatersleben.de/>)
- FOR 1186 (since 2009): “Photorespiration: Origins and metabolic integration in interacting compartments”
- FOR 804 (since 2007): “Retrograde signaling in plants”
- FOR 964 (since 2008): “Calcium signaling via protein phosphorylation in plant model cell types during environmental stress adaption” (<http://www.uni-muenster.de/FOR964/>)
- FOR 1061 (since 2008): “Dynamic storage functions of plant vacuoles during cold and osmotic stress” (<http://www.uni-kl.de/for1061/>)

Cluster of Excellence

- EXC 1028 (since 2012): “Cluster of Excellence on Plant Sciences - from complex traits towards synthetic modules Excellence on Plant Sciences - from complex traits towards synthetic modules” (<http://www.ceplas.eu/en/>)

Arabidopsis functional genomics research is and will be performed within the ERA-NETs ERA-PG (<http://www.erapg.org/>) and ERA-CAPS (<http://www.eraCaps.org/>) for coordinating action in plant sciences, which is supported by the European Commission 6th and 7th Framework Programs.

14 projects were funded following the first ERA-CAPS call (<http://www.era-caps.org/joint-calls/era-caps-funded-projects>). German Arabidopsis researcher participate in three of them:

- “Plasticity of flowering time in response to environmental signals in *Arabidopsis thaliana*”
- “Identifying and exploiting genetic variation controlling seed yield and quality in oilseed crops”
- “European Plant Embryology Consortium”

Road Map Related Activities

Arabidopsis Tools and Resources

- Arabidopsis Functional Genomics Network (<http://www.zmbp.uni-tuebingen.de/plant-physiology/afgn.html>)
- 1001 genomes platform (<http://1001genomes.org/>)
- German Plant Phenotyping Network (DPPN, <http://www.dppn.de/en>)

There are new methods developed by Arabidopsis researchers every year, only a few can be highlighted here:

- Kleessen S et al. (2013) Data integration through proximity-based networks provides biological principles of organization across scales. *Plant Cell* 25(6):1917-27.
- Nordström et al. (2013) Mutation identification by direct comparison of whole-genome sequencing data from mutant and wild-type individuals using k-mers. *Nat Biotechnol* 31(4):325-30.
- Brand LH et al. (2013) Screening for protein-DNA interactions by automatable DNA-protein interaction ELISA. *PLoS One* 8(10):e75177.
- Brennecke P et al. (2013) Accounting for technical noise in single-cell RNA-seq experiments. *Nat Methods* 10(11):1093-5.
- Szecowka M et al. (2013) Metabolic fluxes in an illuminated Arabidopsis rosette. *Plant Cell* 25(2):694-714.

Outreach Activities

Projects that use knowledge gained from Arabidopsis for translational research are funded by the BMBF, some examples:

- PLANT-KBBE IV (since 2014) “Nematode susceptibility targets for a durable resistance”
- PLANT-KBBE IV (since 2014) “Genes and mutants affecting virus infection in rapeseed”
- PLANT-KBBE IV (since 2014) “Control of the abiotic stress response in plants by DELLA proteins and chemicals”
- PLANT BIOTECHNOLOGY (since 2012) “Development and use of novel gene technologies to increase biomass yield in the woody perennial *Populus spec.*”

- PLANT BIOTECHNOLOGY (2011-14) Sugar beet (*Beta vulgaris*) - Manipulation of tap root metabolism and photosynthate allocation by increasing sink and source capacities“
- PLANT-KBBE III (2011-14) “White mold *Brassica napus* resistance challenge“
- INTERNATIONAL PLANT BIOTECHNOLOGY (2011-14) „New generation techniques for genetic engineering of cultivated plants“
- PLANT BIOTECHNOLOGY (2011-14) “Development of haploids by uniparental elimination of genome“
- The German Plant Phenotyping Network (DPPN, <http://www.dppn.de/en>) aims to address the “phenotyping bottleneck”.

Conferences and Workshops

- Tri-National Arabidopsis Meeting (TNAM) biannual conference, hosted by colleagues from Germany, Austria and Switzerland: 9th TNAM 24-26th September 2014, Heidelberg (www.tnam2014.org).
- SPP1530 workshop “Floral Transition in Arabidopsis”, September 16-18, 2013, Tübingen
- Deutsche Botanikertagung 2013, September 30-October 4, 2013, Tübingen

Selected Publications

- Santiago J, Henzler C, Hothorn M. (2013) Molecular mechanism for plant steroid receptor activation by somatic embryogenesis co-receptor kinases. *Science* 341(6148):889-92.
- Wahl V, Ponnu J, Schlereth A, Arrivault S et al. (2013) Regulation of flowering by trehalose-6-phosphate signaling in *Arabidopsis thaliana*. *Science* 339(6120):704-7.
- Pick TR, Bräutigam A, Schulz MA, Obata T et al. (2013) PLGG1, a plastidic glycolate glycerate transporter, is required for photorespiration and defines a unique class of metabolite transporters. *PNAS* 110(8):3185-90.
- Völz R, Heydlauff J, Ripper D, von Lyncker L et al. (2013) Ethylene Signaling Is Required for Synergid Degeneration and the Establishment of a Pollen Tube Block. *Devel Cell* 25(3): 310 -316.
- Heckmann D, Schulze S, Denton A, Gowik U et al. (2013) Predicting C4 Photosynthesis Evolution: Modular, Individually Adaptive Steps on a Mount Fuji Fitness Landscape. *Cell* 153(7):1579 -1588.

Major Funding Sources

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

Greece

<http://arabidopsisresearch.org/index.php/countries/greece>

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

General Activities

Arabidopsis Research Facilities

PMBB_ARA_GR (Plant Molecular Biology & Biotechnology for Arabidopsis in Greece) is a greek consortium comprising research groups from six public sector institutions across Greece: The major centers of Arabidopsis research in Greece are: Agricultural University of Athens, the University of Crete, the Aristotelian University of Thessaloniki, University of Athens, Mediterranean Agronomic Institute of Chania and Technological Educational Institute of Athens.

Current Arabidopsis Projects

The research groups of the Arabidopsis community has a strong focus on aspects related to developmental biology, abiotic and biotic stress, programmed cell death in Arabidopsis immune system, biocontrol agents in activation of SAR (Systemic Acquired Resistance) and other defence mechanisms in Arabidopsis, HSP90 as a modulator for plant development, signal transduction in plant development epigenetic mechanisms and plant development and regulation, natural variation of Arabidopsis in Greece, cytoskeleton structure, photosynthesis, organelle biology, plant virology and plant microbe interactions. The community has established collaboration schemes with renowned research institutes having access to state-of the art technologies including –omics technologies such as transcriptomics and proteomics, advanced bio-imaging equipment, protein crystallography platform and instruments used for deep analysis of primary and secondary metabolites. The basic research performed on Arabidopsis has opened new perspectives to study and resolve issues associated with agronomically important crops including the olive tree, peach tree, tomato and grapevine.

Hatzopoulos' group (Agricultural University of Athens) has been awarded an Excellence grant by the General Secretariat for Research and Technology (GSRT) for Arabidopsis research.

Outlook on Arabidopsis Research

The outlook of the research directions will constitute the ones mentioned above (Current Arabidopsis Research Topics), and will establish the basis for research on plants like olives, tomato, grapes, peach etc. The Arabidopsis research is mainly supported by the General Secretariat for Research and Technology (GSRT) and the State Scholarships Foundation (IKY) grants, from European Union (EU) or from International Organizations

Road Map Related Activities

Arabidopsis Tools and Resources

Phenomics analysis of *Arabidopsis thaliana* MAGIC mapping population and chromatin remodeling mutants during drought stress. European Plant Phenotyping Network. PI: Vlachonasios KE. (2013)

Mutant analysis and genetics, transformation (Agricultural University of Athens)

Gene Atlas personal microarray system (Affymetrix), bioinformatics tools (Lemone software) for gene regulatory networks, RNAi seq bioinformatics analysis

Outreach Activities

The groups established solid collaboration bonds with SMEs involved in processing and export of peach fruit products and in biopharmaceuticals or cosmetics.

Conferences and Workshops

- Biosynthesis, Function and Biotechnology of Isoprenoids in Terrestrial and Marine Organisms. A joint Meeting of TERPNET2013, Cost Action “Plant Engine”, Cost Action “QualityFruit” and “EU-SmartCell” (2013), Kolymvari, Crete, Greece.
- 35th Hellenic Society for Biological Science (EEBE) meeting (2013), Nafplio, Greece.
- 13th Hellenic Botanical Society (EBE) meeting (2013) Thessaloniki, Greece.
- Plant phenomics – EPPN Workshop at Porto Heli 5/9/2013.
- EPSO Conference, Porto Heli 1-4/9/2013
- 36th Scientific Conference of Hellenic Association for Biological Sciences, Ioannina, Greece 8-10/5/2014
- 65th National Conference of the Hellenic Society for Biochemistry and Molecular Biology, Thessaloniki, Greece, 28-30/11/2014

Selected Publications

- Daras G, Rigas S, Tsitsekian D, Zurb H et al. (2014) Alternative transcription initiation and the AUG context configuration control dual organellar targeting and functional competence of Arabidopsis Lon1 protease. Mol Plant ePub (ahead of print).
- Rigas S, Ditengou FA, Ljung K, Daras G et al. (2013) Root gravitropism and root hair development constitute coupled developmental responses regulated by auxin homeostasis in the Arabidopsis root apex. New Phytologist, 197(4):1130-1141.
- Comment in: Dolan, L (2013) Pointing PINs in the right directions: a potassium transporter is required for the polar localization of auxin efflux carriers. New Phytologist 197(4):1027-1028.

- Solheim C, Li L, Hatzopoulos P, Millar AH (2012) Loss of Lon1 in Arabidopsis changes the mitochondrial proteome leading to altered metabolite profiles and growth retardation without an accumulation of oxidative damage. *Plant Physiology* 160(3):1187-1203.
- Hofius D, Schultz-Larsen T, Joensen J, Tsitsigiannis DI et al. (2009) Autophagic components contribute to hypersensitive cell death in Arabidopsis. *Cell* 137(4):773-783.
- Kalamaki MS, Alexandrou D, Lazari G, Merkouropoulos V et al. (2009) Over-expression of a tomato N-acetyl-glutamate synthase gene in *Arabidopsis thaliana* results in increased tolerance in salt and drought stresses. *Journal of Exp Botany* 60:1859-1871.

Major Funding Sources

- General Secretariat for Research and Technology (GSRT) www.gsrt.gr
- Grants from the European Union
- State Scholarships Foundation (IKY) www.iky.gr

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India

<http://arabidopsisresearch.org/index.php/countries/india>

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General Activities

Arabidopsis Research Facilities

In India emphasis is more on applied research but sufficient funding is available for basic research too on model systems like Arabidopsis. Invariably Arabidopsis is allowed to be used for functional validation of genes identified in crops which are not amenable for genetic transformation. Major research centres where there is greater emphasis on Arabidopsis research in India include CCMB, Hyderabad; IISc, Bangalore; University of Delhi South Campus; NIPGR, New Delhi; NRCPB, New Delhi; JNU, New Delhi; IHBT, Palampur. Some of the major thrust areas using Arabidopsis as a system include:

- Light regulation of plant development
- Hormone and sugar signalling
- Abiotic and biotic stress response pathways
- Identification of gene regulatory elements by insertional mutagenesis
- Regulation of pattern formation and differentiation, etc.

Current Arabidopsis Projects

Prof. Sudip Chattopadhyay

- Investigation of functional interrelations of bZIP transcription factors: ZBF2/GBF1, HY5 and HYH of light signaling pathways in *Arabidopsis thaliana*. Funded by Department of Science & Technology, Govt. of India; JC Bose National Fellowship award grant (2011-2016).
- Investigation of cross talk between MAP Kinase and light signaling pathways in *Arabidopsis thaliana*. Department of Science & Technology, Govt. of India (2012-2015).

Dr. Ashis Nandi

- Chromatin remodeling for activation of systemic acquired resistance in Arabidopsis. Funded by Department of Biotechnology, Govt. of India (2011-2014).
- Identification of genes involved in fine tuning of plant defense using cdd1 mutant of Arabidopsis as genetic tool. Funded by Council of Scientific & Industrial Research (2013-2016).
- Role of MEDEA, a polycomb repressor of Arabidopsis in pathogenesis. Funded by Department of Science & Technology, Govt. of India (2013-2016).

Dr. Ashverya Laxmi

- To study the interaction between glucose and cytokinin signaling pathway in model plant system *Arabidopsis thaliana*. Funded by Department of Biotechnology, Govt. of India (2011-2014).
- To study the role of glucose and its interaction with hormones in controlling *Arabidopsis thaliana* root directional responses. Funded by Department of Biotechnology, Govt. of India (2011-2014).

Dr. Girdhar Pandey

- Identification and functional characterization of targets of CIPK3, a calcineurin B-like associated protein kinase, in Arabidopsis in ABA-mediated abiotic stress signaling. Funded by Department of Science & Technology, Govt. of India (2009-2013).
- To determine the molecular basis of potassium nutrition/ Signaling and functional analysis of this calcium mediated CBL-CIPK network under potassium deficient condition. Funded by Department of Science & Technology, Govt. of India (2009-2013).

Dr. Kalika Prasad

- Regulation of patterning and regeneration in Arabidopsis. Funded by IISER-TVM intramural and Department of Biotechnology, Govt. of India (2013-2016).

Outlook on Arabidopsis Research

Essentially the work described above will be continued with Arabidopsis in the years to come. Government as such has long term commitment for funding research in plant science and agriculture. It is hoped that sufficient funding will be available for Arabidopsis research too.

Road Map Related Activities

Arabidopsis Tools and Resources

As such there is no work going on Arabidopsis in India involving NGS technologies in a major way, although high throughput expression analysis is being carried out using microarray. Some of the new tools developed were discussed in last year's report.

A small phenomics facility has been established recently at IARI, New Delhi, largely for phenotyping crop plants but will be also available for Arabidopsis work, if the need be.

Outreach Activities

Periodically suggestions are given to funding agencies for the utility of Arabidopsis as a model system for understanding regulation of various aspects of plant growth and development, including yield. Among the core group working on Arabidopsis in India, there is indeed interaction and several joint projects have been developed largely in the areas already identified and mentioned in this report. There is indeed effort being made to develop international collaborations too.

Conferences and Workshops

Every year there are several conferences organized in the country and scientists engaged in research on Arabidopsis share their findings and also share the material with other researchers interested. Recently, an International Conference on 'Plant Signalling and Behaviour' was organized (in March 2014) by University of Delhi where nearly 200 scientists participated, including ca. 40 from overseas.

Selected Publications

- Kushwaha HR, Singla-Pareek SL, Pareek A (2013) Putative osmosensor - OsHK3b - a histidine kinase protein from rice shows high structural conservation with its ortholog AtHK1 from Arabidopsis. J Biomol Struct Dyn. [Epub ahead of print] PubMed PMID: 23869567.
- Singh V, Roy S, Giri MK, Chaturvedi R et al. (2013) *Arabidopsis thaliana* FLOWERING LOCUS D is required for systemic acquired resistance. Molecular Plant Microbe Interaction 26:1079-1088
- Ram H, Priya P, Jain M, Chattopadhyay S (2014) Genome-wide DNA binding of GBF1 is modulated by its heterodimerizing protein partners, HY5 and HYH. Molecular Plant 7:448-451.
- Abbas N, Maurya JP, Senapati D, Gangappa S et al. (2014) Arabidopsis CAM7 and HY5 physically interact and directly bind to HY5 promoter to regulate its expression to promote photomorphogenesis. Plant Cell (doi:10.1105/tpc.113.122515)
- Kushwah S, Laxmi A (2014) The interaction between glucose and cytokinin signal transduction pathway in *Arabidopsis thaliana*. Plant Cell & Environment 37:235-53.

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/>)

Summary of the work done in India in 2013-2014

In India, Arabidopsis is being used as a model system to understand how light, hormones and sugars interact to regulate plant development; identify transcription factors involved in regulating regeneration and regulatory components involved in pattern formation; identify novel components

involved in host-pathogen interaction; to generate insertion lines with the aim to identify novel promoters and regulatory sequences. In addition, many laboratories are using Arabidopsis as a system to validate function of genes identified from other species like wheat and rice because of the ease with which Arabidopsis can be manipulated genetically.

Group of Prof. Sudip Chattopadhyay has been working on light controlled Arabidopsis seedling development. Their studies have established the functional interrelations of three bZIP transcription factors, GBF1 with HY5 and HYH, in Arabidopsis seedling development. The impact of heterodimerization of GBF1 with HY5 and HYH on its genome-wide binding has been analyzed. Further, it has been shown that the N-terminal domain of GBF1 inhibits its interaction with HY5 and HYH. In addition, it has been found that HY5 and CAM7 (a calmodulin) directly interact with the HY5 promoter to mediate the transcriptional activity of HY5 during Arabidopsis seedling development. Dr. Ashverya Laxmi's group has been exploring the interaction between glucose and hormones and its affect on plant growth and development in Arabidopsis. It has recently been shown by her group that along with root growth and development in general, glucose can also influence root directional responses via modulating brassinosteroid response pathway. The interaction of glucose with cytokinin has also been explored on whole genome level and in relation to their control on dark grown hypocotyl growth. Towards understanding the regulation of regeneration in cultures, Dr. Kalika Prasad's and co-workers have shown that a group of plant specific transcription factors regulate regeneration by a two-step mechanism.

In order to understand the mechanism of systemic acquired resistance (SAR) development, by screening M2 population, Dr. Ashis Nandi's team has identified a mutant with reduced systemic immunity (*rsi1*). *rsi1* has been further characterized as an allele of Flowering Locus D (FLD) and found to affect histone methylation of several WRKY promoters to activate SAR. We also identified a novel AP2 like protein that affect salicylic acid (SA) biosynthesis by modulating ICS1 (Isochorismate synthase) expression. Dr Ashwani Pareek's group has been engaged in understanding the gene circuitous functioning in plants in response to various abiotic stresses (especially salinity and drought). For this purpose, his group has utilized bioinformatics tools for comparative genomics and transcriptomics and characterized various stress responsive gene families in Arabidopsis (and rice) such as two-component system, cyclophilins and SOS pathway.

Ireland

<http://arabidopsisresearch.org/index.php/countries/ireland>

Prof. Charles Spillane (charles.spillane@nuigalway.ie), Genetics and Biotechnology Lab, Plant and AgriBiosciences Research Centre (PABC), National University of Ireland Galway, University Road, Galway, Ireland.

General Activities

Arabidopsis Research Facilities

Ireland (population > 4 million) has a relatively small and diverse plant research community (approx 30-40 research groups) all of which are members of Plant Research Ireland (a consortium comprising research groups from eight public sector institutions across the island of Ireland). There are currently no private sector institutions working with *Arabidopsis thaliana* in Ireland.

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

- Prof Charles Spillane, Genetics and Biotechnology Lab, National University of Ireland Galway (NUIG), Ireland.
- Dr. Ronan Sulpice, Plant Systems Biology Lab, National University of Ireland Galway (NUIG), Ireland.
- Prof Tony Kavanagh, Plant Molecular Genetics, Smurfit Institute of Genetics, Trinity College Dublin, Ireland.
- Dr. Frank Wellmer, Plant Developmental Genetics, Smurfit Institute of Genetics, Trinity College Dublin.
- Dr. Paul McCabe, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Carl Ng, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Fiona Doohan, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Marcel Jansen, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.
- Dr. Fuquan Liu, School of Biological Sciences, Queens University Belfast, Northern Ireland.
- Dr. Emmanuelle Graciet, School of Biology, National University of Ireland Maynooth, Ireland.

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

For more information please visit:

<http://www.plantresearchireland.org/>

Current Arabidopsis Projects

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

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

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

The lab of Prof. Charles Spillane has conducted collecting missions for *Arabidopsis thaliana* accessions across Ireland.

The following Methods have been developed for *Arabidopsis thaliana*:

- Kacprzyk J, Devine A, McCabe PF (2014) The root hair assay facilitates the use of genetic and pharmacological tools in order to dissect multiple signalling pathways that lead to programmed cell death. PLoS One. 2014 Apr 22;9(4):e94898.
- McKeown PC, Fort A, Spillane C. (2014) Analysis of genomic imprinting by quantitative allele-specific expression by Pyrosequencing(*). Methods Mol Biol. 2014;1112:85-104.
- Graciet E, O'Maoiléidigh DS, Wellmer F. (2014) Next-generation sequencing applied to flower development: ChIP-Seq. Methods Mol Biol. 2014;1110:413-29.
- O'Maoiléidigh DS, Wellmer F. (2014) A floral induction system for the study of early Arabidopsis flower development. Methods Mol Biol. 2014;1110:307-14.

Conferences and Workshops

The 1st Irish Arabidopsis Meeting is being organized in NUI Galway in June 2014.

Selected Publications

- Ansari KI, Doyle SM, Kacprzyk J, Khan MR et al. (2014) Light influences how the fungal toxin deoxynivalenol affects plant cell death and defense responses. Toxins (Basel). 2014 Feb 20;6(2):679-92.
- Diamond M, Reape TJ, Rocha O, Doyle SM et al. (2013) The fusarium mycotoxin deoxynivalenol can inhibit plant apoptosis-like programmed cell death. PLoS One. 2013 Jul 26;8(7):e69542.

- Donoghue MT, Fort A, Clifton R, Zhang X et al. (2014) CmCGG Methylation-Independent Parent-of-Origin Effects on Genome-Wide Transcript Levels in Isogenic Reciprocal F1 Triploid Plants. DNA Res. 2014;21(2):141-51.
- Duszynska D, McKeown PC, Juenger TE, Pietraszewska-Bogiel A et al. (2013) Gamete fertility and ovule number variation in selfed reciprocal F1 hybrid triploid plants are heritable and display epigenetic parent-of-origin effects. New Phytol. 2013 Apr;198(1):71-81.
- Kleessen S, Laitinen R, Fusari CM, Antonio C et al. (2014) Metabolic efficiency underpins performance trade-offs in growth of *Arabidopsis thaliana*. Nat Commun. 2014 Mar 28;5:3537.
- ÓMaoiléidigh DS, Wuest SE, Rae L, Raganelli A et al. (2013) Control of reproductive floral organ identity specification in Arabidopsis by the C function regulator AGAMOUS. Plant Cell. 2013 Jul;25(7):2482-503. .

Major Funding Sources

Science Foundation Ireland (www.sfi.ie) is currently the only funding source for Arabidopsis projects in Ireland.

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

Italy

<http://arabidopsisresearch.org/index.php/countries/italy>

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Università di Roma, Dip. Biologia e Biotecnologie, Rome

General Activities

Arabidopsis Research Facilities

Several Italian research groups utilize Arabidopsis as a model organism to study different developmental or physiological processes. Work is mainly based on individual laboratories; however, facilities for growth, handling and analysis of Arabidopsis are often shared between groups belonging to the same institution, while reagents and genetical material are continuously exchanged among laboratories. Informal multi-institutional collaborations are also common, and new networks and collaborations have started to emerge. Results related to Arabidopsis research were published in high impact journals.

Current Arabidopsis Projects

The Italian Ministry of Education, University and Research has funded several Arabidopsis Initiatives in 2013, among which a large project on "The control of plant root growth: a systems biology approach" awarded to the groups of I. Ruberti (IBPM-CNR, Rome), C. Tonelli (University of Milan) and S. Sabatini/P. Costantino (Sapienza University, Rome); this project is coordinated by Paolo Costantino and involves also other partners performing RNAseq and proteomic analysis. Other funding comes from the EU: ERC grant have been awarded S. Sabatini/P. Costantino and F. Cervone/G. deLorenzo, while M. Kater/L. Colombo have funding also from a Marie Curie staff exchange scheme.

A new collaboration 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) has been funded by the Italian Ministry of Foreign Affairs. The goal is to find common regulatory networks controlling stamen and hypocotyl growth in Arabidopsis. M. Cardarelli/P. Costantino were also members of the COST action 'Harnessing plant reproduction for crop improvement' which has been completed in 2013.

Other funding sources include private foundations such as CARIPLO to M. Kater/L. Colombo, Cenci-Bolognetti (to F. Cervone/G. deLorenzo, S. Sabatini/P. Costantino and P. Vittorioso/P. Costantino), the Italian Ministry of Agriculture (to F. Cervone/G. deLorenzo) and the AGER consortium (to C. Tonelli).

Outlook on Arabidopsis Research

Funding is being sought through the participation to proposals for collaborative projects in the Eranet ERA-CAPS 2014 call, as well as the upcoming Horizon 2020 calls.

Research in many Italian Arabidopsis laboratories is developing in the direction of generating high amount of data, thanks to the use of top experimental approaches linked to next-generation sequencing tools, that will allow to have a broad knowledge of the developmental processes in Arabidopsis. The spatial resolution of gene discovery and gene profiling will be increased by conducting these analyses at a tissue- and cell-specific level, with the overall goal to define molecular and biochemical processes occurring in individual cell types.

Future work will continue the characterization of the signalling pathways involved in oligoglacturonides-mediated resistance, ion homeostasis mechanisms, seed germination and root, hypocotyl and flower development.

Road Map Related Activities

Arabidopsis Tools and Resources

S. Sabatini/P. Costantino group has started to set up an *in silico* system for modeling the formation of an auxin gradient in response to a cytokinin input.

M. Kater/L. Colombo 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.

Outreach Activities

Several Arabidopsis researchers from Milan, Rome and Naples were involved in planning and organizing the Fascination of Plants day under the umbrella of EPSO (European Plant Science Organization) on May 18 2013.

M. Kater/L. Colombo group continued a collaboration with Keygene (a molecular genetics R&D company with a primary focus on crop improvement) and initiated a collaboration with the BIOBASE company for an European project. BIOBASE is a leading provider of expert-curated biological databases, software and services for the life sciences.

Conferences and Workshops

- C. Tonelli was the organizer of the 9th conference on the Future of Science, held in Venice on September 19-21, 2013.

Selected Publications

- Cecchetti V, Altamura MM, Brunetti P, Petrocelli V et al. (2013) Auxin controls Arabidopsis anther dehiscence by regulating endothecium lignification and jasmonic acid biosynthesis. *Plant J.* 74:411-422.
- Galbiati F, Sinha Roy D, Simonini S, Cucinotta M et al. (2013). An integrative model of the control of ovule primordia formation. *Plant Journal* 12, 1-10.

- Francocci F, Bastianelli E, Lionetti V, Ferrari S et al. (2013) Analysis of pectin mutants and natural accessions of *Arabidopsis* highlights the impact of de-methyl-esterified homogalacturonan on tissue saccharification. *Biotechnology for Biofuels* 6:163.
- Franciosini A, Lombardi B, Iafrate S, Pecce V et al. (2013) The *Arabidopsis* COP9 SIGNALOSOME INTERACTING F-BOX KELCH 1 Protein Forms an SCF Ubiquitin Ligase and Regulates Hypocotyl Elongation. *Mol Plant* 6(5):1616-1629.
- Moubayidin L, Di Mambro R, Sozzani R, Pacifici E et al. (2013) Spatial coordination between stem cell activity and cell differentiation in the root meristem. *Dev Cell* 26:405-15.
- Turchi L, Carabelli M, Ruzza V, Possenti M et al. (2013) *Arabidopsis* HD-Zip II transcription factors control apical embryo development and meristem function. *Development* 140:2118-2129.

Major Funding Sources

- Italian Ministry of Education, University and Research (www.istruzione.it): National Interest Research Grants (PRIN) and FIRB
- Italian Ministry and Foreign Affairs (www.esteri.it): International Cooperation Grants
- Institut Pasteur-Cenci Bolognetti Foundation (www.istitutopasteur.it)
- Italian Consortium AGER (www.progettoager.it)
- CARIPLO Foundation (www.fondazionecariplo.it)

Japan

<http://arabidopsisresearch.org/index.php/countries/japan>

Minami Matsui (minami@riken.jp) RIKEN Center for Sustainable Resource Science

General Activities

Advances

New coordinated projects started in 2013:

1. World Premier International Research Center Institute of Transformative Bio-Molecules (WPI ITbM) (<http://www.itbm.nagoya-u.ac.jp/>)

ITbM has launched in Nagoya University as one of institutes of MEXT WPI program. ITbM is the first WPI institute studying plant science. Ambitious full-scale collaboration between synthetic chemists, plant and animal biologists, and theoreticians is led by Director Kenichiro Itami and Vice-directors Tetsuya Higashiyama and Shigehiro Yamaguchi.

2. RIKEN Center for Sustainable Resource Science (CSRS) (<http://www.riken.jp/en/research/labs/csrs/>)

The Center for Sustainable Resource Science (CSRS) was established in April 2013. RIKEN will continue to contribute to basic research, but will also seek out, identify, and work to find solutions for critical scientific technical and social issues, with a special focus on Green Innovation, or sustainable production of energy, and resources.

CSRS is merging plant scientists from the Plant Science Center (PSC: 2000-2013), chemists and chemical biologists from the Advanced Science Institute (ASI: 2008-2013), and scientists focusing on applied research from the Biomass Engineering Program Cooperative Division and the Drug Discovery Platforms Cooperation Division of the Research Cluster for Innovation (RCI: 2010-).

3. Multidimensional Exploration of Logics of Plant Development (MEXT) (2013-2017) (<http://logics.plantdev.biol.s.u-tokyo.ac.jp/en/index.html>)

In this project, they will delineate the systems that coordinate intercellular and intracellular signals, the functions of key differentiation genes, and the control of metabolism. They will combine the efforts of nine research groups and four supporting facilities/teams using multiple model species. The four supporting facilities/teams will provide assistance in metabolomics, the use of an *Arabidopsis thaliana* transcription factor library, the application of *Marchantia polymorpha* as a model system, and mathematical modeling. The multidisciplinary collaborative approach will enable to explore new research directions in unprecedented ways.

4. Core Research for Evolutional Science and Technology (JST-CREST) (<http://www.jst.go.jp/presto/plantsci/en/crest/index.html>)

A new CREST program started from 2011 and aims to create essential technologies to utilize carbon dioxide as a resource through the enhancement of plant productivity and the exploitation of plant products.

5. JST-ALCA (<http://www.jst.go.jp/alca/en/index.html>)

- A project with a research title “Genetic engineering of cyanobacterial transcriptional regulators and circadian clocks for succinate production” is led by Dr. Takashi Osanai (RIKEN, CSRS), aiming to generate cyanobacterial strains producing succinate at high levels.
- A project with a research title, “Development of Synthetic Promoters for Acceleration of Biomass Production”, has started led by Yoshiharu Y. Yamamoto (Gifu Univ.). The synthetic promoter data is released at ppdb (Plant Promoter Database, <http://ppdb.agr.gifu-u.ac.jp>).

Individual Activities

RIKEN CSRS

(<http://www.riken.jp/en/research/labs/csrs/>)

1. Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi).

CSRS established the Arabidopsis metabolomics platform (<http://prime.psc.riken.jp/>), which consists of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics. The publicly-available platform resources include Arabidopsis metabolome expression database AtMetExpress (<http://prime.psc.riken.jp/lcms/AtMetExpress/>); Arabidopsis MS/MS spectral tag (MS2T) viewer (<http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html>); standard spectrum search (http://prime.psc.riken.jp/?action=standard_index), ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (<http://spectra.psc.riken.jp/>); Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index); Drop Met (http://prime.psc.riken.jp/?action=drop_index); Annotation of metabolites by NMR from ¹³C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search). PRIMElink (<http://spectra.psc.riken.jp/menta.cgi/primelink/index>) integrates the 3 above databases (AtMetExpress, MS2T and ReSpect) to provide a bi-directional searchable function from the gene or metabolite perspective.

2. Hormonome platform and RIKEN Plant Hormone Research Network; (<http://hormones.psc.riken.jp/>) (Hitoshi Sakakibara and Yuji Kamiya)

3. Transcriptome platform by using tiling array (<http://omicspace.riken.jp/gps/>) and next generation sequencers in collaboration with RIKEN ACCC (Motoaki Seki, Keiichi Mochida, Minami Matsui, Tetsuro Toyoda, Kazuo Shinozaki)

4. Proteome platform (<https://database.riken.jp/sw/links/en/ria1021i>)

PSC (Hirofumi Nakagami, Ken Shirasu) and Keio University (Yasushi Ishihama, Naoyuki Sugiyama) developed a high-through-put shotgun phosphoproteomics tool for plants and phosphorylation site databases (<http://phosphoproteome.psc.database.riken.jp>, <http://pepbase.iab.keio.ac.jp>)

5. Phenome platform

(<https://database.riken.jp/sw/en/item/cria301u2i/>) RIKEN Activation tagging lines Database and Full-length-cDNA-overexpressing (FOX) Arabidopsis lines (Minami Matsui), Rice FOX Arabidopsis line Database (<http://ricefox.psc.riken.jp/>) (Minami Matsui), Ds-transposon tagged lines (<http://rarge.psc.riken.jp/phenome/>) (<http://rapid.psc.database.riken.jp>) (Takashi Kuromori, Tetsuya Sakurai, Tetsuro Toyoda, Kazuo Shinozaki).

6. The Chloroplast Function Database (<http://rarge.psc.riken.jp/chloroplast/>) for knockout Arabidopsis mutant lines for nuclear genes encoding chloroplast proteins (Fumiyoshi Myouga, Kazuo Shinozaki).

7. Analysis of small Open Reading Frame (Kousuke Hanada, Minami Matsui, Motoaki Seki) They identified ~8,000 sORFs with high coding potential in intergenic regions of the Arabidopsis genome. They designed array and generated an expression atlas for 16 organs and 17 environmental conditions among 7,901 identified coding sORFs and all annotated genes.

8. Mass Bank (Masanori Arita, Takaaki Nishioka, Kazuki Saito) The public repository of mass spectral data for sharing them among scientific research community. MassBank data are useful for the chemical identification and structure elucidation of chemical compounds detected by mass spectrometry. (<http://www.massbank.jp/en/about.html>)

9. Genome-wide biochemical analysis using wheat germ cell-free-based protein array technology. The method that Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) and RIKEN CSRS (Motoaki Seki and Kazuo Shinozaki) developed is useful for identification of substrates and interacting proteins for protein kinases, protein phosphatases and transcription factors.

RIKEN BMEP (Biomass Engineering Program)

(www.riken.jp/bmep/english/index.html)

RIKEN BMEP program is focusing on the establishment and innovation for plant biomass production and renewable chemical materials and Bioplastics. Brachypodium as a model of grass biomass is used besides Arabidopsis in this program. This interdisciplinary program is organized by cooperation of chemists and plant biologists. RIKEN BMEP research activities were integrated into CSRS as Biomass Engineering Cooperation Division from 2013.

RIKEN BRC

Experimental Plant Division (Masatomo Kobayashi, kobayasi@rtc.riken.jp) collects, preserves and distributes Arabidopsis resources developed in Japan through National BioResource Project (NBRP). Not only Arabidopsis seeds (mutants, insertion and FOX lines, natural accessions) and cDNA clones but also a number of plant cultured cell lines such as Arabidopsis T87 and Tobacco BY-2 have been distributed to both domestic and overseas institutions and universities. Distribution of full-length cDNA clones of a model monocot plant *Brachypodium distachyon* was launched in 2013. (<http://www.brc.riken.jp/lab/epd/Eng/>, plant@brc.riken.jp)

KAZUSA DNA RESEARCH INSTITUTE

KaPPA-View4 (<http://kpv.kazusa.or.jp/>) for integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database MassBase (<http://webs2.kazusa.or.jp/massbase/>) and KomicMarket (<http://webs2.kazusa.or.jp/komics/>), the co-expressed gene search tools KAGIANA (<http://pmnedo.kazusa.or.jp/kagiana/index.html>) and CoP (<http://webs2.kazusa.or.jp/kagiana/cop/>), and the regulatory network research RnR (<http://webs2.kazusa.or.jp/kagiana/rnr/>) (Daisuke Shibata).

Ongoing projects

1. Environmental sensing of plants: Signal perception, processing and cellular responses (2010-2014) (<http://esplant.net/index.html>) headed by Akira Nagatani, Kyoto University
2. Integrated Analysis of Strategies for Plant Survival and Growth in Response to Global Environmental Changes (2010-2014) (http://bsw3.naist.jp/JFM/English_top.html) headed by Jian Feng Ma, Okayama University, Institute of Plant Science and Resources
3. JST-NSF (http://nsf.gov/funding/pgm_summ.jsp?pims_id=503558) "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society", Research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and Kazuki Saito (RIKEN PSC). Research led by Oliver Fiehn (Univ. of California at Davis) and Masanori Arita (Univ. of Tokyo)
4. ERATO Higashiyama Live-Holonics Project (2010-2015) (<http://www.liveholonics.com/en/>) headed by Tetsuya Higashiyama, Nagoya University. This project aims to study intercellular signaling in multicellular organisms with complete control of cells and molecules under the microscope, by developing new technologies for live-cell analysis.
5. Japan Advanced Plant Science Research Network has been started in 2011. In this program nine centers of excellence in university and research institute take roles to support plant researches for green innovation.
6. NC-CARP (as a program in GRENE; Green Network of Excellence) A new program "Network of Centers of Carbon Dioxide Resource Studies in Plants: NC-CARP (organizer: Hiroo Fukuda)" started from 2011 as a 5-year project. This program aims at innovation of plant biomass technology by collaboration among Plant Science, Agriculture, Engineering and Chemistry, and at education of this new area.
7. DREB project supported by MAFF; Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat
8. SATREPS project supported by JST-JICA; Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant soybean.
9. East Asia Science and Innovation Area Joint Research Program (e-ASIA), 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).

Road Map Related Activities**Arabidopsis Tools and Resources***RIKEN resources and tools***BRC**

- Resources from RIKEN BRC (<http://www.brc.riken.go.jp/lab/epd/Eng/>)

CSRS

- RRIMe (<http://prime.psc.riken.jp/>)
- AtMetExpress (<http://prime.psc.riken.jp/lcms/AtMetExpress/>)
- Arabidopsis MS/MS spectral tag (MS2T) viewer (<http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html>)
- Standard Spectrum Search (http://prime.psc.riken.jp/?action=standard_index)
- ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (<http://spectra.psc.riken.jp/>)
- Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index)
- Drop Met (http://prime.psc.riken.jp/?action=drop_index)
- Annotation of metabolites by NMR from ¹³C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search)
- PRIMeLink (<http://spectra.psc.riken.jp/menta.cgi/primelink/index>)

- RIKEN Plant Hormone Research Network (<http://hormones.psc.riken.jp/>)
- The Chloroplast Function Database (<http://rarge.psc.riken.jp/chloroplast/>).
- RIKEN Arabidopsis Activation Tagging Line Database (<http://amber.gsc.riken.jp/act/top.php>)
- RIKEN Arabidopsis Genome Encyclopedia (RARGE) (<http://rarge.psc.riken.jp/>)
- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) (<http://rarge.gsc.riken.jp/phenome/>)
- RIKEN Plant Phosphoproteome Database (RIPP-DB) (<http://phosphoproteome.psc.database.riken.jp>)

KAZUSA resources and tools

- Kazusa Metabolomics Database KOMICS (<http://www.kazusa.or.jp/komics/>)
- The KaPPA-View4 (<http://kpv.kazusa.or.jp/>)
- MassBase (<http://webs2.kazusa.or.jp/massbase/>)
- KomicMarket (<http://webs2.kazusa.or.jp/komics/>)
- MS-MS Fragment Viewer (<http://webs2.kazusa.or.jp/msmsfragmentviewer/>)
- KAGIANA (<http://pmnedo.kazusa.or.jp/kagiana/index.html>)
- CoP (<http://webs2.kazusa.or.jp/kagiana/cop/>)
- The regulatory network research RnR (<http://webs2.kazusa.or.jp/kagiana/rnr/>).
- MFSearcher (<http://webs2.kazusa.or.jp/mfsearcher/>)

Grants

1. RIKEN is supported by MEXT.

Kazusa projects is supported by Chiba-Prefecture.

2. Grants-in-Aid for Science from MEXT, (www.jsps.go.jp/english/egrants/grants.html)
3. CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
4. Program of Promotion of Basic Research Activities for Innovative, Biosciences (www.brain.go.jp/welcome-e.html)
5. ALCA (Advanced Low Carbon Technology Research and Development Program) (<http://www.jst.go.jp/alca/en/index.html>)

A research and development-driven funding was started from 2011 for realization of low atmospheric carbon dioxide and wealthy society. For this purpose this funding supports game-change technologies leading to green-innovations.

6. Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project. (<http://www.jst.go.jp/inter/english/sicorp/index.html>)

Netherlands

<http://arabidopsisresearch.org/index.php/countries/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

From the 2013 publications of the Arabidopsis Dutch research community we highlight two:

De Rybel et al., *Developmental Cell* 24, 426-437, 2013

Using a combination of transcriptional profiling, mutant analysis and 3D-imaging, De Rybel and coworkers (Biochemistry, Wageningen and Plant Sciences, Bern) showed that the dimer between the basic helix-loop-helix transcriptional regulator TMO5 (target of Monopteros 5) and a protein from the same family, Lonesome Highway, is instrumental in initiating vascular tissue in the Arabidopsis embryo.

Galvan-Ampudia et al., *Current Biology* 23, 2044-2050, 2013

Through an assay on diagonal gradients, Galvan-Ampudia and other members of the group of Christa Testerink (Plant Physiology, University of Amsterdam) demonstrated that the roots display a directional growth response when confronted with salinity. They show that salt triggers asymmetric auxin distribution through promoting calthrin-mediated endocytosis of the auxin transporter PIN2, leading to reorientation of roots.

Ronald Pierik (Plant Ecophysiology), working on the integration of photoreceptor signals which adjusts shade avoidance responses, and Leonie Bentsink (Plant Physiology, Wageningen), studying dormancy and life span regulation, received VIDI awards from the Dutch Science Organization (NWO) to support their careers as young group leader.

South Korea

<http://arabidopsisresearch.org/index.php/countries/south-korea>

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

General Activities

Arabidopsis Research Topics

- Protein distribution system in plant cells
- System and Synthetic Agrobiotech Center
- Circadian clock regulation of environmental stress adaptation in Arabidopsis
- Function of ABC type transporter proteins
- Multi-omics approaches for systems study on plant senescence

Current Arabidopsis Projects

- Protein distribution systems in plant cells
- Circadian clock regulation of environmental stress adaptation in Arabidopsis
- Function of ABC type transporter proteins in Arabidopsis
- Multiple research projects funded from diverse sources including government, industries and research institutes.
- Systems & Synthetic Agrobiotech Center (~ 0.9 M\$/yr for 10 years by Rural Development Administration, Korea.
- Systems understanding of plant senescence and life history (~ 6 M\$/yr for 10 years by Institute of Basic Research)

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

- iNID: a web-based tool for identifying network models for interplays among developmental signaling in Arabidopsis. iNID provides 1) transcriptomes, 2) protein/genetic interactions, and 3) tools for identifying key regulators and network models for interplays among signaling pathways in Arabidopsis.
- Diverse top-level research services are easily available in Korea including new generation sequencing, RNA SEC, MALDI-TOF and antibody production services and so on.

Outreach Activities

- In Korea, Arabidopsis researchers usually carry out both basic sciences and applied plant research.
- Recently, many life science related venture companies have been established in Korea and they are accepting many plant scientists trained in Arabidopsis research.

Conferences and Workshops

- Plant Winter Conference at POSTECH
- Annual meeting of Korean Society of Plant Biologists

Selected Publications

- Xu ZY, Kim SY, Hyeon do Y, Kim DH et al. (2013) The Arabidopsis NAC transcription factor ANAC096 cooperates with bZIP-type transcription factors in dehydration and osmotic stress responses. *Plant Cell* 25:4708-24.
- Jung JH, Park JH, Lee S, To TK et al. (2013) The cold signaling attenuator HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE1 activates FLOWERING LOCUS C transcription via chromatin remodeling under short-term cold stress in Arabidopsis. *Plant Cell* 25:4378-90.
- Lee JH, Ryu HS, Chung KS, Posé D et al. (2013) Regulation of temperature-responsive flowering by MADS-box transcription factor repressors. *Science*. 342(6158):628-32.
- Kim Y, Han S, Yeom M, Kim H et al. (2013) Balanced nucleocytoplasmic partitioning defines a spatial network to coordinate circadian physiology in plants. *Dev Cell* 26(1):73-85.
- Kim WY, Ali Z, Park HJ, Park SJ et al. (2013) Release of SOS2 kinase from sequestration with GIGANTEA determines salt tolerance in Arabidopsis. *Nat Commun.* 4:1352.

Major Funding Sources

- The Next-Generation BioGreen Program (SSAC, PJ008109)
- The cooperative research program (PJ007850) supported by RDA

Spain

<http://arabidopsisresearch.org/index.php/countries/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.

General Activities

Two large coordinated projects involving Arabidopsis functional genomic activities funded by the Ministry of Economy and Competitiveness of Spain have ended in 2013: “TRANSPLANTA” (nation-wide; included 29 Arabidopsis groups coordinated by Javier Paz-Ares) aiming to study the function of Arabidopsis transcription factors, and “The Center for Agrigenomics” (Barcelona; included groups studying crop and livestock species, 10 of which using Arabidopsis, coordinated by Pere Puigdomènech). About 80 grants from the Ministry of Economy and Competitiveness of Spain fund Arabidopsis research projects at individual laboratories.

Awards and Honors

Genetics National Award: José Luis Micol; Carmen and Severo Ochoa Award for Research in Molecular Biology: Paloma Más; José Luis Riechmann and Paloma Más were elected as members of the Academia Europaea and EMBO, respectively.

Road Map Related Activities

Arabidopsis Tools and Resources

Several collections have been generated and deposited at NASC and/or ABRC: 1159 transgenic lines conditionally overexpressing genes encoding transcription factors (PIs: José León and José A. Jarillo; Valencia and Madrid, respectively; TRANSPLANTA project), 6000 transgenic lines producing artificial microRNAs (345 different amiRNAs) targeting groups of paralogous genes encoding transcription factors (María Rosa Ponce; Elche, TRANSPLANTA) and 700 genuine leaf mutants selected from the Salk Unimutant collection (José Luis Micol; Elche, AGRON-OMICS).

Conferences and Workshops

- The New Frontiers in Plant Biology Workshop, focusing on novel insights enabled by the different “omic” approaches, was held on January 31 and February 1 2013 in Madrid.
- The Society for Experimental Biology Annual Main Meeting took place in Valencia on 4-5 July 2013.
- The 3rd European Workshop on Plant Chromatin was held on 29-30 August 2013 in Madrid.

Selected Publications

- Boer DR, Freire-Rios A, van den Berg WA, Saaki T et al. (2104). Structural basis for DNA binding specificity by the auxin-dependent ARF transcription factors. *Cell* 156: 577-589.
- Gimenez-Ibanez S, Boter M, Fernández-Barbero G, Chini A et al. (2014). The bacterial effector HopX1 targets JAZ transcriptional repressors to activate jasmonate signaling and promote infection in Arabidopsis. *PLoS Biol.* 12: e1001792.
- Castrillo G, Sánchez-Bermejo E, de Lorenzo L, Crevillén P et al. (2013). WRKY6 transcription factor restricts arsenate uptake and transposon activation in Arabidopsis. *Plant Cell* 25: 2944-2957.
- González-Grandío E, Poza-Carrión C, Sorzano CO, Cubas P (2013). BRANCHED1 promotes axillary bud dormancy in response to shade in Arabidopsis. *Plant Cell* 25: 834-850.
- Locascio A, Blazquez MA, Alabadi D (2013). Dynamic regulation of cortical microtubule organization through prefoldin-DELLA interaction. *Current Biol.* 23: 804-809.
- Doblas VG, Amorim-Silva V, Posé D, Rosado A et al. (2013). The SUD1 gene encodes a putative E3 ubiquitin ligase and is a positive regulator of 3-hydroxy-3-methylglutaryl coenzyme a reductase activity in Arabidopsis. *Plant Cell* 25: 728-743.
- Fabregas N, Li N, Boeren S, Nash TE et al. (2013). Specific roles for BRL3 signalosome complex in Arabidopsis root development. *Plant Cell* 25: 3377-3388.

Major Funding Sources

Ministry of Economy and Competitiveness of Spain fund Arabidopsis research projects at individual laboratories

Sweden

<http://arabidopsisresearch.org/index.php/countries/sweden>

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

General Activities

Arabidopsis Research Facilities

Arabidopsis constitutes a first choice model species to address basic questions of plant growth and development, photosynthesis and stress related topics.

The Arabidopsis community consists of several hundred researchers and is spread between more than ten universities in Sweden, engaged in vast areas of research from cell biology to ecological research. Traditionally there has been a strong focus on aspects of developmental biology, abiotic and biotic stress, plant growth regulators and photosynthesis. The research community is highly international, with a large part of researchers being recruited from abroad and extensive collaborations with peers in other countries.

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

- Lund University (<http://www4.lu.se/molecular-plant-biology>) and the plant research resource in Southern Sweden is Plant Link (<http://www.plantlink.se/>) coordinating plant research at Lund University and University for Agricultural Sciences (SUAS) in Alnarp
- Gothenburg University, Department of Plant and Environmental Sciences, Plant Cell and Molecular
- 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; comprising Departments at Umeå University and SUAS in Umeå (<http://www.upsc.se/>)

Current Arabidopsis Projects and Topics

- Development/systems biology
- ShapeSystems - Systems Biology of Plant Cell Shape, Wallenberg funded project headed by Prof. Marcus Grebe
- Large projects in the area of plant forest biotechnology and genomics, with Arabidopsis serving a model species for many projects (<http://www.upsc.se/research/large-projects/>).
- The Berzelli Centre for Forest Biotechnology
- The Spruce Genome Project
- Funcfibre, Wood Science
- Bioimprove (<http://www.bioimprove.se/>)
- Bio4Energy (<http://www.bio4energy.se/>)

Information on individual research projects as well as Centres funded by major funding bodies can generally be obtained directly through databases from each databases (e.g. Formas, VR, SSF, Wallenberg, please see funding bodies).

Outlook on Arabidopsis Research

There is currently a strong emphasis on funding basic research with applications or end products for the stakeholders. This funding is projected to be covering plant research projects in the area of Agriculture and of Forest Biotechnology, with emphasis for instance on fiber and energy related research.

Larger research grants typically funding a small cluster of collaborating researchers can be applied for currently at:

- The Swedish Foundation for Strategic Research (<http://www.stratresearch.se>)
- The Swedish Agency for Innovation Systems (VINNOVA; <http://www.vinnova.se>)

However, most funding bodies regularly advertise or are likely to advertise such calls in the coming years.

Road Map Related Activities

Arabidopsis Tools and Resources

National resources used by the Arabidopsis research community:

- Max Lab hosted by Lund University (<http://www.maxlab.lu.se/maxlab>) a facility dedicated to high-throughput, nanovolume characterization and crystallization of biological macromolecules.
- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government (<http://www.scilifelab.se>)
- Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis (<http://www.upsc.se>) found under “resources”.
- The Swedish Metabolomics Centre in Umeå is a national resource, inaugurated March 2013, for more information (<http://www.swedishmetabolomicscentre.se/>)

Swedish research institutions have started to sign up for subscription to TAIR, in order to secure access to research tools and databases essential for Arabidopsis research.

Conferences and Workshops

- 2013, Swedish Plant Science Network, 18-19 November, Linnean Center, Uppsala

- 2014, Umeå renewable energy meeting, 17-19 March, UPSC, Umeå
- 2014, Symposium in Plant Epigenetics in Development and Disease, 23 May, SUAS, Biocenter, Uppsala
- 2014 Biocontrol of Plant Diseases: “From the field to the laboratory and back again”, 15-18 June, Uppsala
- 2014, The 8th Scandinavian Plant Physiology Society PhD Students Conference, 16-19 June, Uppsala
- 2014, Lignin 2014 Conference, 24-28 August, Umeå <http://www.lignin2014.se>
- 2014, Swedish Developmental Biology Organization (SWEDBO) 2-3 October, Umeå, <http://www.swedbo.se/>
- 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

In addition there are a plethora of private foundations where it is possible for apply for support. Each University may also have their internal calls to support curiosity driven and strategic research.

Research directions and funding possibilities

There are regular calls for Centres of Excellence and strategic research which include the possibility to fund Arabidopsis functional genomics. In recent years national funding has been mainly distributed by the funding agencies outlined above. In addition, strategic Arabidopsis research in Sweden is funded by the European Union (EU), the European Research Council (ERC), EMBO, bilateral exchange programs etc.

Selected Publications

- Boutté Y, Jonsson K, McFarlane HE, Johnson E et al. (2013) ECHIDNA-mediated post-Golgi trafficking of auxin carriers for differential cell elongation. PNAS USA 110:16259 -16264.
- Derkacheva M, Steinbach Y, Wildhaber T, Mozgová I et al. (2013) Arabidopsis MSII connects LHP1 to PRC2 complexes EMBO J 32(14):2073-85.
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Major Funding Sources

- The Swedish Research Council (VR; <http://www.vr.se>) a core funder of researcher-initiated basic research.
- 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 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>) and The Royal Academy of Agriculture and Forestry (<http://www.ksla.se>)
- The Wallenberg Foundations (<http://www.wallenberg.com>) is a private foundation supporting individual researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.

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General Activities

Arabidopsis Research Facilities

The main UK funding body for plant science, Biotechnology and Biological Sciences Research Council (BBSRC; <http://www.bbsrc.ac.uk/>) continues to be supportive of Arabidopsis research. The University of Nottingham Arabidopsis Stock Centre (uNASc; <http://arabidopsis.info/>), one of the two international Arabidopsis stock centres, is based at the University of Nottingham, UK. Over 300 research groups in Universities and Research Institutes in the UK utilize the model plant Arabidopsis in their studies.

Two BBSRC research institutes, the John Innes Centre and Rothamsted Research, have a plant science focus and *Arabidopsis thaliana* research forms a substantial part of their research output. BBSRC also funds the national Plant Phenomics Center at the Institute of Biological, Environmental and Rural Sciences.

The Gatsby Charitable Foundation support two further plant science research institutions. The Sainsbury Laboratory (Norwich) and the Sainsbury Laboratory at the University of Cambridge both have large Arabidopsis research programmes.

Current Arabidopsis Projects

Many UK research groups are leaders in their field producing world-class research and publications in high impact journals. Arabidopsis research is largely project-focused, with work based in individual laboratories, multi-institutional collaborations or national Centers and Institutes.

OpenPlant (www.openplant.org/) is one of three synthetic biology multi-disciplinary research centres announced in 2014 by UK funding councils BBSRC, EPSRC and TSB. It is a plant synthetic biology consortium based in Norwich and Cambridge, and will develop open tools and resources. It is funded until 2019.

Outlook on Arabidopsis Research

BBSRC strategic priorities include crop science, soil science, bioenergy, data driven biology, systems biology and synthetic biology.

BBSRC is leading the cross-council and cross-government Global Food Security programme. The major funding news for plant science in 2013 was the announcement of a UK Strategy for Agricultural Technologies, including £60 million for research development and £90 million for a number of Centres for Agricultural Innovation.

Road Map Related Activities

Arabidopsis Tools and Resources

The UK is co-developing the Arabidopsis Information Portal. BBSRC awarded funds to a group led by Gos Micklem (the University of Cambridge) to work with NSF-funded colleagues at US institutions the J Craig Ventor Institute, the Texas Advances Computing Centre, and the Carnegie Institution for Science on the project.

Rootnav, an image analysis tool for semiautomated quantification of complex root system architectures, was developed at the University of Nottingham. It was originally demonstrated in *Arabidopsis thaliana*, *Triticum aestivum*, *Brassica napus* and *Oryza sativa*.

Pound MP, French AP, Atkinson JA, Wells DM, Bennett MJ and Pridmore T (2013) RootNav: Navigating Images of Complex Root Architectures. *Plant Physiology* 162:1802-1814.

Three papers demonstrating the CRISPR-Cas genome editing system in plants were published back-to-back in the August 2013 issue of Nature. One, lead by researchers from The Sainsbury Laboratory, Norwich, showed targeted mutagenesis in *Nicotiana benthamiana* using Cas9 RNA-guided endonuclease.

Nekrasov V, Staskawicz B, Weigel D, Jones JDG and Kamoun S (2013) Targeted mutagenesis in the model plant *Nicotiana benthamiana* using Cas9 RNA-guided endonuclease. *Nature* 31: 691-693

Outreach Activities

The UK Plant Sciences Federation released a report, UK Plant Science: Current Status and Future Challenges, in January 2014. The report calls for a doubling of funding for UK plant science. It is being followed up by working groups focusing on Funding, Training & Skills, Portfolio Balance, Translation, and Regulation.

GARNet launched a report on plant synthetic biology, Opportunities and Recommendations for UK Plant Synthetic Biology, in April 2014. GARNet will work with other groups to implement the recommendations in the report, including the establishment of a UK Plant Synthetic Biology Steering Group and explore ways to develop a community facility for sharing biological parts.

Several UK Arabidopsis researchers are members of the Plant Science Panel, an outreach enterprise organized by the charity Sense About Science. Members of the public email or tweet questions and receive a response from one of the scientists on the Panel. The Panel regularly has one-off Question and Answer sessions on topical issues such as GM crops and pesticide use (<http://www.senseaboutscience.org/pages/plant-science-expert-panel.html>).

Early career Arabidopsis researchers have been volunteering for the 'I'm a Scientist Get me Out of Here' online schools outreach event (<http://imascientist.org.uk/>).

Conferences and Workshops

- The Sixth Mathematics in the Plant Sciences Study Group was hosted by the Centre for Plant Integrative Biology at the University of Nottingham on 25-28 March 2013.
- The third annual UK Plant Sciences Federation meeting, PlantSci 2013, took place on 16-17 April 2013 at the University of Dundee.
- GARNet's 2013 meeting An Introduction to Opportunities in Plant Synthetic Biology, was held at the University of Nottingham on 21-22 May 2013.
- Data Mining with iPlant was a GARNet training workshop hosted at the University of Warwick on 17-20 September 2013.
- PlantSci 2014 was on 31 March-1 April and the University of York.
- Software Carpentry for Plant Scientists, an introduction to programming workshop, is on 9-10 April at the University of Warwick.
- SEB2014 will be in Manchester on 1-4 July.
- Arabidopsis: The Ongoing Green Revolution will be on 9-10 September 2014 at the University of Bristol.

Selected Publications

- Vanholme R, Cesarino I, Rataj K, Xiao Y et al. (2013) Caffeoyl Shikimate Esterase (CSE) Is an Enzyme in the Lignin Biosynthetic Pathway in Arabidopsis. *Science* 341 (6150):1103-06
- Noordally Z, Ishii K, Atkins K, Wetherill S et al. (2013) Circadian control of chloroplast transcription by a nuclear-encoded timing signal. *Science* 339 (6125):1316-1319
- Haydon MJ, Mielczarek O, Robertson FC, Hubbard KE and Webb AAR. (2013) Photosynthetic entrainment of the *Arabidopsis thaliana* circadian clock. *Nature* 502(7473):689-92
- Gibbs DJ, Isa NM, Movahedi M, Lozano-Juste J et al. (2013) Nitric Oxide Sensing in Plants Is Mediated by Proteolytic Control of Group VII ERF Transcription Factors. *Molecular Cell* 53(3):369-379.
- Sun Y, Li L, Macho AP, Han Z et al. (2013). Structural Basis for flg22-Induced Activation of the Arabidopsis FLS2-BAK1 Immune Complex. *Science* 342 (6158): 624-628.

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 Union - http://ec.europa.eu/research/era/index_en.htm

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North American Arabidopsis Steering Committee (NAASC)

NAASC is an elected body composed primarily of U.S. researchers that provides North American representation to MASC and serves as the main organizing and fundraising body for the International Conference on Arabidopsis Research (ICAR) when it is held in North America. NAASC's community service efforts include: (1) fundraising to support all ICARs including participation by young scientists and under-represented scientists, (2) serving on relevant advisory committees and boards, (3) acting as leaders and participants for community-related initiatives, such as the International Arabidopsis Information Consortium (IAIC) and (4) acting as liaison between researchers, funders, and other relevant community resources such as the Arabidopsis Biological Resource Center (ABRC) and the Arabidopsis Informatics Portal (AIP).

1. The eight NAASC members serve four-year terms with two rotating off annually. Wolf Frommer (Carnegie Institution for Science) and Dominique Bergmann (Stanford University) conclude their terms in fall 2014 after the next election. Continuing members include Nick Provart (University of Toronto), Jose Alonso (North Carolina State University), Siobhan Brady (University of California, Davis), Keiko Torii (University of Washington), Erich Grotewold (the Ohio State University/ABRC) and Sarah Assmann (Pennsylvania State University.)
2. NAASC members solicit funding support for US researchers, including early career, under-represented minorities, faculty at US minority-serving institutions, and sometimes invited speakers, to facilitate participation by North American scientists in ICARs. In support of the 2014 ICAR, organized by NAASC in Vancouver, Canada, Keiko Torii secured funding from the US National Science Foundation (NSF) to fully support 10 US under-represented minorities and faculty from minority-serving institutions; 10 early-career researchers; 8 invited speakers, including 5 at the early career level and 3 for a new Synthetic Biology session; and 4 speakers to lead new career development workshops. Siobhan Brady submitted a funding proposal to the US Department of Agriculture (USDA) to support early career researchers and invited speakers (funding decision not yet made.)

3. Joanna Friesner, NAASC Coordinator, supports all NAASC efforts including, among other duties, acting as lead conference organizer for North American ICARs and assistance with NAASC-led community initiatives such as the IAIC (see below).
4. Committee service: Jose Alonso, Nick Provart, and Blake Meyers serve on the Arabidopsis Biological Resource Center (ABRC) advisory committee. Jose Alonso and Nick Provart are the conference organizing committee co-chairs for ICAR 2014 (see below). Nick Provart is member of the IAIC Steering Committee.

NAASC Organizes 2014 International Conference on Arabidopsis Research

NAASC members, led by co-chairs Jose Alonso and Nick Provart, are organizing the 2014 ICAR at the University of British Columbia in Vancouver (July 28 - August 1). This is the second Canadian ICAR NAASC has organized, following ICAR 2008 in Montreal. Members of the local UBC faculty, led by co-chairs Xin Li and Carl Douglas, are participating as the local organizing committee. 2014 is notable because it is the 25th convening of the meeting, which was first held in 1965 in Germany. In the 1980s, the research qualities of Arabidopsis became more apparent which led to broader adoption in plant science and renewed interest in holding an Arabidopsis conference, which came to be known as the ICAR. ICARs were held regularly starting in 1987 and annually since 1995, sparked in large part by the internationally funded Arabidopsis Genome Project that concluded in 2000 with the public release of the Arabidopsis genome sequence. This powerful tool accelerated research and led to the NSF's Arabidopsis 2010 Project, which aimed to determine a function for all Arabidopsis genes by the year 2010. The AT2010 project and associated funding facilitated the development of innovative new tools, a broad array of genomics resources, and led to an expanded understanding of the function and evolution of plant genomes. Importantly, the enabling resources developed through the project inspired new research directions and collaborations. The ICAR serves as the annual main Arabidopsis research meeting and nucleates numerous community discussions. More recently, discussions at ICAR 2009 sparked the development of the International Arabidopsis Informatics Consortium (IAIC), which led to community development of the new bioinformatics resource, the Arabidopsis Informatics Portal (AIP). An AIP-development funding proposal, submitted by PI Chris Town and colleagues, received NSF support in fall 2013.

In recognition of the significance of this meeting being the 25th Conference, NAASC organizers have asked the three Arabidopsis keynote speakers to include these points: (1) How Arabidopsis research has impacted their field, (2) the history of how that happened, (3) how continued focus

on a deeply developed model will contribute to answering remaining key problems in biology, and (4) how that will impact food security and crop production in a changing climate. The two opening keynote speakers are Jeff Dangl (USA) and Xuemei Chen (USA) and the two closing keynote speakers are Peter McCourt (Canada) and Brenda Andrews (Canada) a yeast researcher.

NAASC members have developed several additional new activities for ICAR 2014:

1. Under-Represented Minority (URM) career development program- to advance personal and professional development of US URM's via networking and research presentation events, and specific career workshops, including one held jointly with the Early-Career Researchers.
2. Early-Career Researcher (ECR) career development program- to advance personal and professional development of scientists in earlier career stages via networking and specific career workshops, including one held jointly with the URM's.
3. Synthetic Biology plenary session
4. Oral posters- these presentations are brief introductions to the research poster the speaker will present during poster sessions. Early-career participants are prioritized to give these short talks, which will give them exposure in a platform session and ideally, drum up interest for further interactions in the meeting. The presentations are at most 2 minutes long and contain a maximum of 5 slides.

The International Arabidopsis Informatics Consortium (IAIC)

(www.arabidopsisinformatics.org/)

The IAIC is a community-led consortium initiated in 2010 in response to growth in the size and complexity of Arabidopsis data the need for new resource sustainability models. The overarching goal of the IAIC is to develop a novel, integrated, international framework with which to address the informatics needs of the Arabidopsis community, while providing a smooth transition from the current TAIR-based central database structure to this stable, long-term structure. In the past year, IAIC leaders, including Blake Meyers, IAIC Interim Director and former NAASC member, and others from the North American and Multinational Arabidopsis Steering Committees, monitored progress on the submission of an AIP-funding proposal to NSF, and provided input to the process, including to the proposal PI (Chris Town) and colleagues, as needed. Additional activities revolved around community outreach and engagement such as (1) the development and distribution of an electronic newsletter to disseminate IAIC and AIP progress and activities, (2) initiating planning of an AIP satellite workshop to be held in conjunction with the 2014 ICAR, (3) working with

international community members that submitted AIP module funding proposals in their home countries (UK, Canada, and Germany), and (4) the convening of several IAIC workshops at major conferences (ICAR 2013 and Plant and Animal Genome (PAG) 2014). The AIP satellite workshop at ICAR 2014 will include a public preview release of the Portal. There is expected to be a second IAIC workshop at ICAR 2014 to include presentations by module developers and community discussions on further involvement. Based on the outcomes of these community interactions at ICAR 2014, the IAIC Steering Committee and Director will consider holding a longer module-focused workshop in fall 2014.

Notable Awards and Honors for US Researchers Using Arabidopsis

- Elected to the National Academy of Sciences, April 2013: Xuemei Chen (former NAASC), Xing Wang Deng (former NAASC)
- Elected as Fellows of the American Association for the Advancement of Science, November 2013: David Meinke (former NAASC), Richard M. Clark, Katie Dehesh, Julin Maloof
- ASPB 2013: Adolph E. Gude Jr. Award: Natasha Raikhel; Martin Gibbs Medal: Jen Sheen; Excellence in Education Award: Erin Dolan

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