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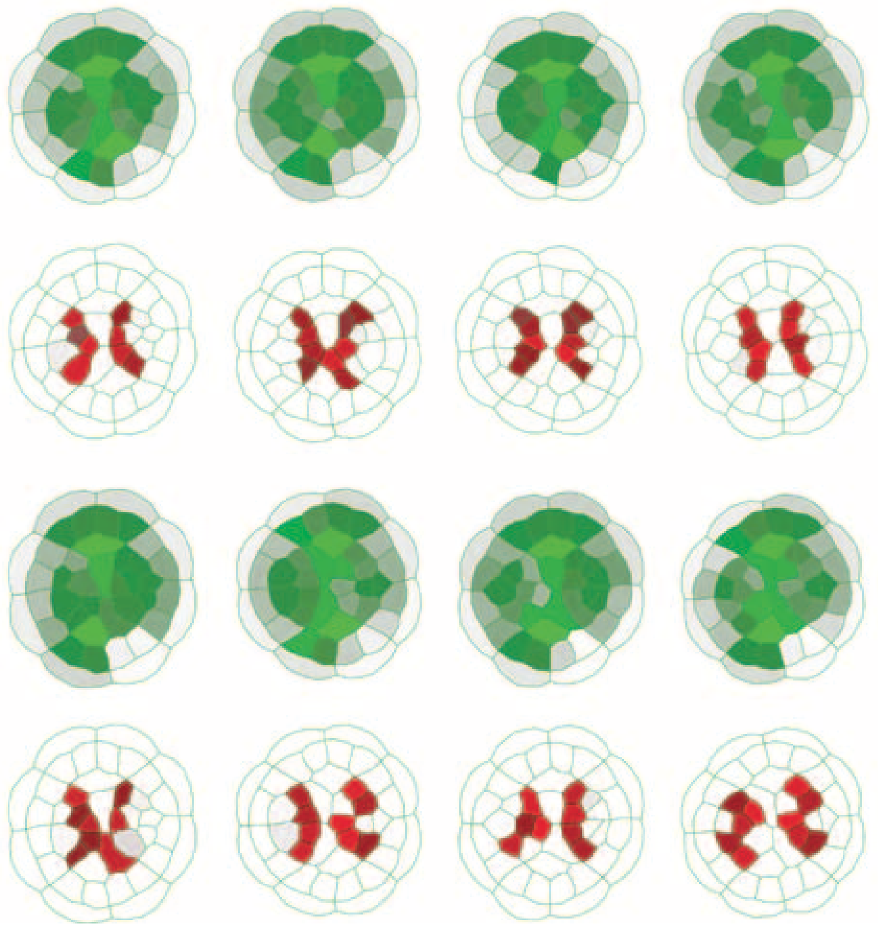
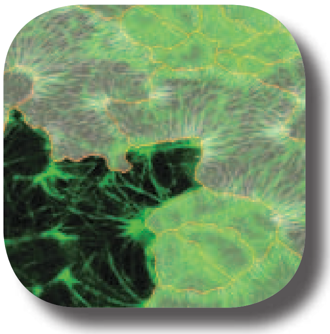
From Bench to Bountiful Harvests

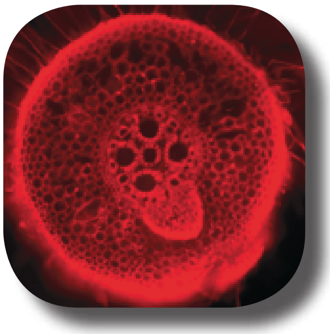
Annual Report

Multinational Arabidopsis Steering Committee (MASC)

2014/2015







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The Multinational Arabidopsis Steering Committee

Annual Report 2014/2015

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The Multinational Arabidopsis Steering Committee
July 2015

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Cover images

Modeling vascular development (top) Outcomes of simulation of auxin accumulation (green) and cytokinin (red) in a mathematical model of growth and patterning in the Arabidopsis embryonic vascular tissue. The image shows 8 independent simulations, each giving a realistic pattern of hormone response. Courtesy of Milad Adibi and Christian Fleck (page 40).

Microtubules in plant pavement cells (bottom left) Microtubule orientations (green) and mechanical tensions (white) in pavement cells. Courtesy of Arun Sampathkumar and Pawel Krupinski (page 42).

Root branch induced by water (bottom left center). Radial cross-section of a maize root showing the development of an early-stage root branch that was induced by local moisture. Courtesy of Neil E. Robbins II and José R. Dinneny (page 41).

Arabidopsis leaf axils, where branches form (bottom right center). Confocal picture of transverse section through the meristem and leaf primordia region of Arabidopsis. LAS-GFP (green) is expressed in leaf axils, where axillary buds initiate. Courtesy of Yuling Jiao (page 40).

Complex leaf shape (bottom right) From left to right: Leaf silhouette of a simple *Arabidopsis thaliana* leaf, Leaf silhouette of a complex leaf of *Cardamine hirsuta,* developing complex leaf of *Cardamine hirsuta,* where expression of the RCO gene is visualized in blue. Courtesy of Miltos Tsiantis (page 42).

Further information

www.arabidopsisresearch.org

The MASC report 2014/15 and previous reports are available online at:

MASC, The Multinational Arabidopsis Steering Committee:

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

uNASC, The Nottingham Arabidopsis Stock Centre:

http://arabidopsis.info/progreports.html

TAIR, The Arabidopsis Information Resource:

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

Dr. Luise Brand and Prof. Dr. Nicholas Provart wrote articles with input from Dr. Loïc Lepiniec, if no author is stated.

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Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2014/2015. This report has been written by MASC chair, co-chair, coordinator, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community.

The MASC community has been coordinated by Luise Brand. MASC thanks Luise Brand for overseeing the production of the MASC annual report 2014/2015.

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Foreword to the Report

The Multinational Arabidopsis Steering Committee (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*. One of the main aims of the committee was and still is to strengthen international collaboration and coordination, to reduce redundancy and to help in guiding the community in making progress on projects that can be successful only by combined international efforts. This 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 as being one of the most active research communities. Arabidopsis researchers can look back on more than 40 successful years - having published the first fully sequenced plant genome, functionally annotated most genes, and developed a plethora of techniques, tools and resources. Within the previous 20 years two MASC road maps 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. The third MASC road map was published in 2012 '*The Multinational Arabidopsis Steering Committee - From bench to bountiful harvests*' (Lavagi et al., 2012, Plant Cell, 24:2240-2247). The main aim of the Arabidopsis community stated in the third road map is to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants to be able to build a predictive model of an Arabidopsis plant, which is accompanied by the development of big data management systems. Additionally, Arabidopsis researchers have put increased effort into outreach to other plant communities and into translational approaches to allow effective exchange of information.

The MASC annual report 2014/2015 is the third report on progress made under to the current road map. The community was very successful in establishing the International Arabidopsis Informatics Consortium (IAIC), which helped to establish the new Arabidopsis Information Portal (www.araport.org), which by its flexible design allows researches to access a multitude of big data sets in one interface. This report also outlines progress and activities of the MASC in general (page 9) as well as analysis and recommendations for the Arabidopsis community for the next year according to the current road map (page 11). Almost all MASC members contributed to this year's report (Figure 1, page 9): the eight MASC subcommittee chairs (page 15 ff.), the major Arabidopsis projects and resources directors including three affiliated plant projects and resources (page 31 ff.), and 22 of 26 country representatives (page 47 ff.). Today Arabidopsis researchers are challenged by massive amounts of data and translating Arabidopsis research to the field and *vice versa* while maintaining hypothesis driven basic research. It seems that Arabidopsis researchers manage this balancing act, as the activity of the community regarding publishing of peer-reviewed articles is continuously increasing (page 39 ff.). In this report the high impact of Arabidopsis research is demonstrated by six featured publications. The increasing applicability of Arabidopsis research to industry and agriculture is shown by constant number of filed patents and four examples of translational and applied research. It is more important than ever to generally invest more both in applied and basic plant research to be able to meet society's demands. It must be ensured that information, tools and resources generated using Arabidopsis are not wasted and that financial support of basic research continues, to provide the innovation that agriculture will need in the years ahead.

The MASC report 2014/2015 is published at the 26th 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. The next 27th ICAR will be in Gyeongju, South Korea: June 29th-July 3rd 2016. Save the date! MASC thanks the local organizers of the ICAR and all MASC members who contributed to this report. If you would like to know more about MASC please visit our new web site: www.arabidopsisresearch.org or the former site at TAIR (www.arabidopsis.org/portals/masc/index.jsp).

The Multinational Arabidopsis Steering Committee
July 2015

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Executive Summary

50 years after the 1st ICAR: Arabidopsis as a Model for Plant Biology

The first International Conference on Arabidopsis Research (ICAR) was held in Göttingen, Germany, in 1965. Several well-known factors – small genome, ease of crossing, short generation time, fecundity, and the ability to do saturating mutational screens – have all led to a huge increase in the volume of Arabidopsis research since then. In the past 50 years, approximately 54,000 Arabidopsis papers – those having Arabidopsis in the title, abstract or keywords (Thomson Reuter's BIOSIS database) have been published, mostly in the past 25 years. While recent funding trends have nudged plant biologists to do more "translational" work directly on crops species, it should be pointed out that this collection of Arabidopsis papers has been widely cited outside of the Arabidopsis community. Of 41,682 Arabidopsis papers published in the past 50 years that have been cited one or more times 15,388 of these have been cited by a non-Arabidopsis paper. We believe that this important plant model species will continue to be used for cutting edge research in the next 50 years. What remains is the question how this research will be coordinated?

Therefore, MASC appointed a "MASC Future Subcommittee" during the MASC meeting 2014 in Vancouver, whose progress is summarized in the Analysis and Recommendation section of this report. General information about MASC can be found in the Progress and Activities section and progress of the Arabidopsis community towards the road map goals are highlighted throughout this MASC report.

International Conference on Arabidopsis Research (ICAR)

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

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

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

Save dates for the upcoming ICAR:

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

Progress and Activities of MASC

- MASC chair 2014/2015: Nicholas Provart (University of Toronto, Canada)
- MASC co-chair 2014/2015: Loïc Lepiniec (Jean-Pierre Bourgin Institute, France)
- MASC coordinator: Luise Brand (University of Tübingen, Germany) funded by the German Science Foundation (DFG)
- 25th ICAR 2014: 625 attendees and 334 submitted poster abstracts (http://arabidopsisconference2014.org/, Figure 2, page 10)
- MASC web pages: www.arabidopsisresearch.org

Analysis and Recommendations of MASC

Currently, we are in the middle of the road map, which means that most objectives are currently ongoing and those are recommended to be continued. Detailed information on progress and recommendations can be found throughout this report. A list of current and adjusted goals can be found in this section (page 11), the categories are:

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

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

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

(D) Build the International Arabidopsis Informatics Consortium (IAIC)

(E) Deepen international cooperation and coordination

New goals for 2021 road map:

(E) Deepen international cooperation and coordination

- Develop a permanent online system for International Conference on Arabidopsis Research (ICAR) i.e. registration and abstract submission system
- Establish MASC as e.g. not-for-profit organization to ensure international coordination of Arabidopsis research, to minimize duplication of efforts and maximize efficient use of resources through collaboration
- Better integrate websites, portals and information resources either via www.arabidopsisresearch.org or via a subdomain at Araport
- Participate in ASPB and GPC's new Plantae.org digital communication platform.

MASC Subcommittees

A new Epigenetics and Epigenomics Subcommittee was formed following 25th ICAR 2014. Currently 8 MASC Subcommittees monitor progress and activities as well as point out future directions of the respective field of Arabidopsis research, stay in close contact with the community and promote international cooperation (page 15 - 30).

- Bioinformatics (page 15)
- ORFeomics (page 16)
- Epigenetics and Epigenomics (page 18)
- Metabolomics (page 19)
- Natural Variation and Comparative Genomics (page 20)
- Phenomics (page 23)
- Proteomics (page 27)
- Systems and Synthetic Biology (page 28).

Arabidopsis Community Projects and Resources

The Arabidopsis community and the whole plant community thrive and profit from resource and stock centers, i.e. uNASC, ABRC and RIKEN-BRC as well as from informatics and data sharing projects and resources like the International Arabidopsis Informatics Consortium (IAIC), Arabidopsis Information Portal (AIP, now Araport) and The Arabidopsis Information Resource (TAIR). Information on progress and activities of the above mentioned resources can be found in this report (page 31 ff.). Besides the above mentioned traditional community projects and resources, information on major international collaborative research projects and resources that focus not solely on Arabidopsis but profit from great support by Arabidopsis researchers is included, i.e. Bio-Analytic Resource for Plant Biology (BAR), BrassiBase, European Plant Phenotyping Network (EPPN).

Arabidopsis Basic Research and its Impact on Applied Research

Scientific Highlights in 2014/2015

Arabidopsis researchers published 4,337 peer-reviewed papers in 2014, this is 66 publications more than in 2013, an almost 2-fold increase within the last decade and more than 10-fold increase within the last 20 years (Figure 3, page 39). This report includes summaries of only a few research highlights published in 2014 and early 2015 with contributions from at least three different countries (page 39 ff.):

- Plant development. Integration of growth and patterning during vascular tissue formation in Arabidopsis (Science, 345(6197):1255215).
- The stem cell niche in leaf axils is established by auxin and cytokinin in Arabidopsis (Plant Cell, 26(5):2055-2067).
- Dynamics of chromatin accessibility and gene regulation by MADS-domain transcription factors in flower development (Genome Biology, 15, R41).
- Plant roots use a patterning mechanism to position lateral root branches toward available water (PNAS, 111(25):9319-24).
- Subcellular and supracellular mechanical stress prescribes cytoskeleton behavior in Arabidopsis cotyledon pavement cells (Elife. 3:e01967).
- Leaf shape evolution through duplication, regulatory diversification, and loss of a homeobox gene (Science, 343(6172):780-3).

Impact of Arabidopsis Research on Applied Research and Industry in 2014/2015

A way of demonstrating the increasing applicability of Arabidopsis research to applied research, industry and agriculture is to look at the number of filed patents (Figure 4, page 43). In 2014 2,479 international patent applications were published referring to Arabidopsis, which is a 16-fold increase over the previous 20 years. Another way to point out the interdependency of basic and applied research is to highlight examples published in peer-reviewed journals and patents. This report includes summaries of some applied studies vitally dependent on Arabidopsis data and resources published in 2014 and early 2015 (page 43 ff.):

- Overexpression of an ABA biosynthesis gene using a stress-inducible promoter enhances drought resistance in petunia (Horticulture Research 2, 15013).
- Identification of the transporter responsible for sucrose accumulation in sugar beet taproots (Nature Plants 1, 14001).
- Arabidopsis dual resistance proteins, both RPS4 and RRS1, are required for resistance to bacterial wilt in transgenic Brassica crops (Plant Signaling & Behavior, 9:e29130).
- Plant nanobionics approach to augment photosynthesis and biochemical sensing (Nature Materials 13).

Country Highlights

The wider Arabidopsis and plant community supports MASC by appointing individual country representatives, who are nationally and internationally well connected Arabidopsis researchers. To date 26 countries support MASC and the international Arabidopsis community, out of these 22 countries contributed to this MASC annual report (page 47 ff.). Researchers from all over the world, who are working with Arabidopsis, are highly encouraged to get involved in MASC in order to further strengthen the network, international collaboration and data sharing.

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Progress and Activities of MASC

In 2014, Nicholas Provart succeeded Barry Pogson to become **MASC chair** and Loïc Lepiniec became **co-chair** (Figure 1). Loïc Lepiniec will become new MASC chair when Nicholas Provart steps down following the 26th International Conference on Arabidopsis Research (ICAR) July, 2014 in Paris, France. 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, www.dbg-afgn.de). The coordinator position was established in 2002 and has been previously supported by NSF (US) for six years, by DFG (Germany) for one year and BBSRC (UK) for three years. The MASC coordinator provides help and coordination to MASC, and the larger Arabidopsis research community. The coordinator's duties include:

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

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

MASC subcommittees, proposed in 2002, were established to help track the progress and advances made by the international Arabidopsis community. Following the ICAR 2014 the new Epigenetics and Epigenomics subcommittee was established. This report includes contributions from all eight current subcommittee chairs/co-chairs: Bioinformatics, ORFeomics, Epigenetics and Epigenomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics and Systems and Synthetic Biology (page 15 ff.). The requirements for a subcommittee to be considered active were formulated in 2009:

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

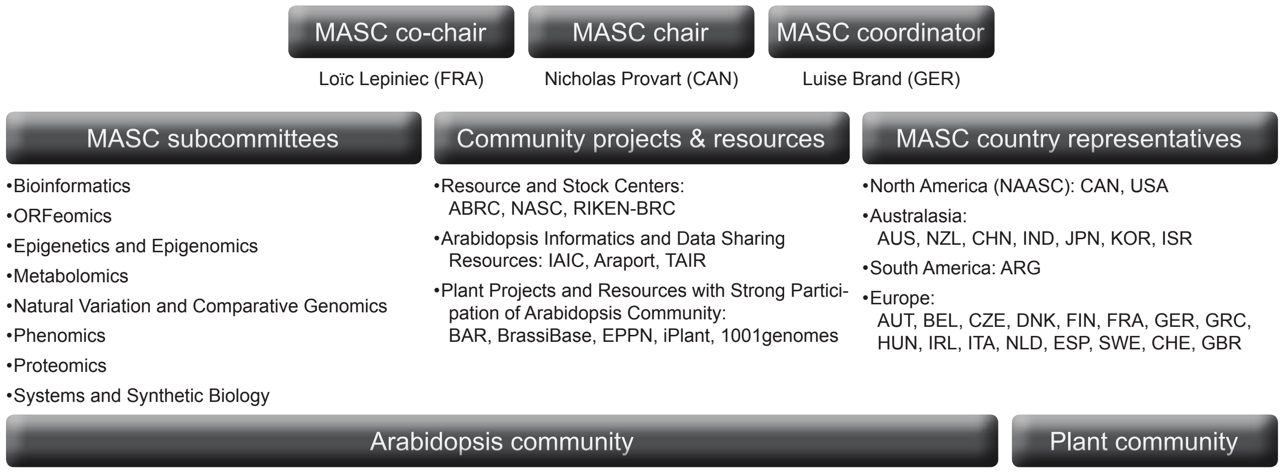

Figure 1. Multinational Arabidopsis Steering Committee (MASC). For explanation of abbreviations see MASC subcommittee (page 15 ff.), Arabidopsis community projects and resources (page 31 ff.) and MASC country reports (page 47 ff.)

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Representatives of **Arabidopsis community projects and resources** attend the annual MASC meeting and contribute to the annual MASC report to broadcast their progress, activities and goals to the community (page 31 ff.). The three resource and stock centers, i.e. Arabidopsis Biological Resource Center (ABRC, US), the Nottingham Arabidopsis Stock Centre (uNASC, UK) 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, i.e. the International Arabidopsis Informatics Consortium (IAIC), the Arabidopsis Information Portal (AIP - now Araport) and The Arabidopsis Information Resource (TAIR). Many features were added to the Araport websites over the previous year and recently an article about "Araport: the Arabidopsis Information Portal" was published. Efforts of three community projects and resources with strong participation of the Arabidopsis community can be found in this report (page 36 ff.).

Country representatives attend the annual MASC meeting held during ICARs and contribute to the annual MASC report by submitting country reports. In 2014/2015 26 countries have been involved in MASC and 22 contributed to this year's report. In 2014 Kentaro Shimizu succeeded the Swiss country representative Wilhelm Gruissem, Sigal Savaldi-Goldstein succeeded the Israeli country representative Shaul Yalovsky, Moritz Nowack succeeded the Belgian country representative Lieven De Veylder, Michael Wrzaczek succeeded the Finnish country representative Ykä Helariutta and Lynette Brownfield supports Barry Pogson by representing New Zealand. MASC thanks the former country representatives for their valuable contributions and highly encourages researchers working on Arabidopsis to get involved in MASC activities e.g. subcommittees, projects and resources or as country representatives.

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

The **25th International Conference on Arabidopsis Research** (ICAR) was held in Vancouver, Canada from July 28th- August 1st 2014 and was organized by the North American Arabidopsis Steering Committee (NAASC). The meeting was very successful and there was a great atmosphere celebrating the 25th anniversary of the ICAR. 625 people attended the 25th ICAR in Vancouver and almost 70% of the attendees (434) submitted a poster abstract (Figure 2). On average 61% of the attendees presented a poster during the ICARs over the last 10 years. The MASC report 2013/14 was distributed to every attendee at the 25th ICAR. Around 50% of ICAR attendees looked at this report, and find especially the sections on "Arabidopsis Community Resources and Projects", "Arabidopsis Basic Research and its Impact on Applied Research", and "Arabidopsis International Community - Country Reports" to be relevant. Many MASC members were involved in the program of the 25th ICAR e.g.:

- ABRC and NASC booth, BAR booth, TAIR booth;
- 6 community workshops: "IAIC-International Arabidopsis Informatics Consortium", "Arabidopsis Information Portal (AIP) Developer and User Workshop", "EPIC - Epigenomics of Plants International Consortium", "TAIR: A Sustainable Community Database for International Arabidopsis Research", "Abiotic stress: MASC workshop", "Phenomics in Arabidopsis: from phenes to genes";
- and many sessions related to road map goals, e.g. "Translational Biology", "Novel Tools and Techniques", "Biotechnology, Food Security, Bioenergy", "Synthetic Biology", "Under-Represented Minority and Early Career Workshops", just to name a few.

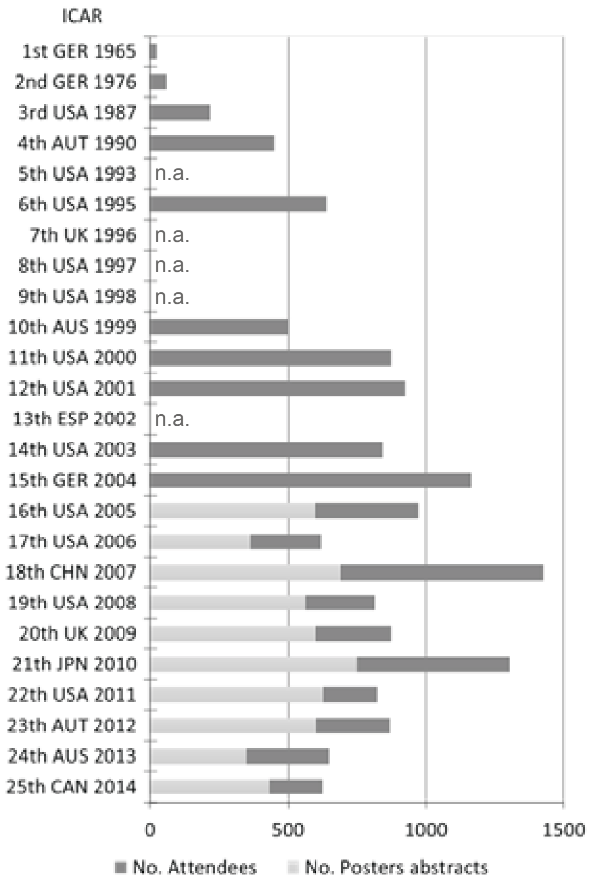

Figure 2. Number of attendees (dark grey) and number of posters presented (light grey) at the International Conference on Arabidopsis Research since 1965 (n.a. - no data available,1965-2004 no number of posters available).

Analysis and Recommendations by MASC

Compiled by Nicholas Provart with input from "MASC Future Subcommittee" members Ruth Bastow, Siobhan Brady, Keiko Sugimoto, Barry Pogson, Ana Cano Delgado, Luise Brand, Joanna Friesner, and Klaus Harter, along with comments from the wider Arabidopsis community.

Coordinating Arabidopsis Research

Let us briefly have a look at the history of coordinating Arabidopsis research. Since 1990 MASC has served as umbrella organization for worldwide Arabidopsis research. During the first decade (1991-2000) of coordinated efforts, researchers from 14 countries collaborated to sequence the Arabidopsis genome. The efforts were mainly led by the North American Arabidopsis Steering Committee (NAASC) and researchers from Australia, Europe and Japan. The second decade was manifested by the functional characterization of Arabidopsis genes through 19 supporting countries. Coordination of such an effort necessitated support by administrative staff. Thus, the role of the MASC coordinator was established in 2002. The MASC coordinator also accompanied and guided the community into the third decade and today 26 supporting countries are part of MASC. This phase can be considered as transition phase for Arabidopsis research because the current challenge is to preserve, develop and translate Arabidopsis research, which is a multifaceted task. The past successes of MASC suggest that maintaining it (via a coordinator position) in the future is something the community should aspire to. It is important to note here that the long-established work of other national and supranational coordinators cannot be underestimated (e.g. those for NAASC, GARNet, AFGN, etc., see below) as they serve as vital hubs and resources and ensure that various mid- and long-term goals are reached. The MASC coordinator's efforts to link these groups has, in the past 13 years, been funded by federal funding agencies i.e. NSF (US), BBSRC (UK) and DFG (Germany) but this is not sustainable as this entails new grant applications to be written every couple of years. In the present funding landscape focusing on translational plant research, it is unlikely that a purely Arabidopsis-focused coordinator position would be funded.

Coordination of the international Arabidopsis community by MASC is achieved through four instruments: (1) the International Conference on Arabidopsis Research (ICAR), (2) the annual MASC meeting, (3) the annual MASC report and (4) the MASC websites. This concept of coordinating Arabidopsis research has proven very successful, and can be reviewed in this current and previous MASC reports.

ICAR Meetings

The first and second Arabidopsis conferences were held in Germany in 1965 and 1976, and then more regularly (either annually or biannually) from 1987 onwards (see page 10). In 2007 it was agreed that the annual ICAR meeting would rotate between three geographical areas (Americas, Europe and Asia). The location for each meeting is determined and agreed via MASC but the organization of each meeting is completely autonomous and reliant upon the activities of the host country. There is no single bank account associated with the ICAR and as a result there is no financial link between each meeting, meaning that there is no mechanism to transfer profits from one meeting to the next one. There is also limited organizational crossover between meetings; current and previous MASC coordinators always pass on their knowledge and assist local organizers where possible, but there is no formal shared organizational structure, website, registration system, or a database of previous attendees. The exception to this situation is when the meeting is held in North America, and organized by NAASC. This is in contrast to other organizations, like International Society for Computational Biology (ISCB), which mounts a big yearly conference on bioinformatics and computational biology (ISMB) at locations around the world.

MASC's Future

The MASC has its origin in multiple countries and therefore it is important to respect and encourage national initiatives to take part in MASC. During the past 25 years several coordinated national Arabidopsis consortia have been established, like the North American Steering Committee (NAASC; since 1992 in the US), GARNet (since 2000, UK) and the Arabidopsis Functional Genomics Network (AFGN; since 2000, Germany). The NAASC and MASC histories are entwined, as the first MASC Coordinator was funded by the US National Science Foundation to simultaneously coordinate NAASC. Only NAASC has managed transform itself into a sustainable not-for-profit organization supporting a part-time coordinator. The NAASC coordinator has been funded, since 2010, via proceeds from every third ICAR, which are organized by the NAASC Coordinator in North America. A major task for the international Arabidopsis community is to develop a new model for a sustainable future for MASC to enable the international community to continue to effectively cooperate and collaborate. In this respect, during the 25th ICAR in 2014, a “MASC Future Subcommittee” was appointed consisting of senior and junior investigators and Arabidopsis research coordinators from North America, Europe and Australasia.

The MASC Future Subcommittee first assessed the relevant expenses necessary to maintain MASC in its current structure (Table 1); based on this, it considered three support scenarios.

The first was the establishment of a Multinational Arabidopsis Society with an annual membership fee, but informal discussions with the community suggested that there is “society fatigue”, that is, there are already too many societies to which one ought to belong. A society option would have an additional operational load of collecting and managing yearly fees for little perceived community benefit.

The second option would be to seek affiliation with an established national or international organization, like the American Society of Plant Biologists (ASPB, US), the Society of Experimental Botany (SEB, UK) or the Global Plant Council (GPC, Switzerland). The MASC Future Subcommittee members were in close contact with all three organizations in order to discuss the possibilities. Ultimately, it seemed that such an association would not be more beneficial than the third option.

The third option would be for MASC to register as charity or not-for-profit organization with a small executive board in a manner similar to how NAASC functions. This would require a certain amount of seed capital depending on the country of registration (US$ 2,500-5,500) and additional accounting costs per year (US$ 500). The registration of MASC as not-for-profit organization would, at the very least, help MASC to stay independent and enable it to carry funds forward to subsequent years, which could help provide surety (down payment) for future ICAR organizers.

The MASC Future Subcommittee would recommend that MASC establishes itself as not-for-profit organization (scenario three). First MASC would have to get suffiecient seed capital e.g. contributions from previous ICAR organizers or by fund raising. Second MASC would have to establish a small executive board and a larger members board including representatives from all MASC Subcommittees, Projects and Resources as well as Countries. Third MASC would have to decide about its functional structure, meaning the evaluation of all options from having a MASC coordinator (50% or less), to a flex-time position where graduate students could help produce the report, with most of the report production devolved to the MASC subcommittees and moving all content online, etc. or even an option of having no MASC personnel.

It should be noted that the current work load to coordinate MASC cannot be undertaken by the research faculty. In case there would be a MASC coordinator in place, who would be funded out of yearly conference profits, it would be expected that the coordinator contributes substantially towards conference organization, in consultation with the local organizing committee, which has primary organizational authority for each ICAR. This would include, for example:

1. Covering some of the upfront costs - to be reimbursed after the conference
2. Organizing registration and abstract submission system
3. Organizing conference website at www.arabidopsisresearch.org or www.araport.org
4. Abstract book assembly in cooperation with local organizers
5. Speaker selection logistics in cooperation with local organizers
6. Fund raising in cooperation with local organizers.

The local organizers would still be responsible for site selection, program and speaker selection, but would work much more closely with MASC than in the past. This would help raise the profile of MASC. The MASC coordinator would also continue to produce the yearly MASC report (with the possibility of charging for advertisements, an activity that is only possible if MASC has an official banking mechanism) and to liaise with country representatives and granting bodies.

In case there is no MASC coordinator it can be expected that the workload for individual MASC members will increase and the coordination efforts will probably be reduced to holding of an annual MASC meeting and preserving a semi-static MASC website. Whether it will still be possible to generate a MASC report, perhaps a shortened version, is up for discussion. The ICAR organization would continue to rely completely on local organizers.

Table 1. Overview of current MASC costs. (*Profits of Australasian and European ICARs; every third year’s profits support NAASC, although some amount might be shared if the MASC coordinator substantively assisted the NAASC coordinator in running the North American ICARs, such as with external fund-raising, which is the source of NAASC’s ICAR profits.)

Item	Costs (estimates US$)	Funding	Purpose
MASC coordinator (50%)	40,000/year	Profits of ICARs* - increased fund raising to keep fees low	ICAR organization, MASC report, MASC websites, MASC meeting
MASC annual report (print)	3,000/year	Advertising, fundraising in the report	
Public Relations	500/year	Profits of ICARs*	MASC website, posters, flyers…
Travelling costs for coordinator	5,000/year	Profits of ICARs*	Travels to conferences, meetings, workshops…

The MASC Future Subcommittee recommends that MASC in any case reduces duplication of efforts regarding the ICAR organization by establishing an ICAR registration and abstract submission system that is hosted by the MASC websites (either independently at www.arabidopsisresearch.org or at www.araport.org). Currently there is duplication of efforts as every year that year's ICAR website has to be set up *de novo*. How and who will establish this system is up for debate. MASC also will have to decide if it wants to have a unique web interface or would want to host its websites at an Araport subdomain. In order to leverage community resources, we recommend that MASC considers participating in the ASPB and GPC's new Plantae.org digital communication platform for the plant science community to manage outreach and social media activities, depending on the cost of participation.

Finally, the MASC Future Subcommittee wants to point out that careful and considerate discussions have to take place during the 2015 MASC meeting in order to collaboratively create an agreeable solution for the future coordination of international Arabidopsis research.

Ongoing and adjusted road map goals for 2015/2016

The community has made continuous progress on all goals in the five categories as outlined in the road map 2021. Building of the International Arabidopsis Informatics Consortium was completed as well as great progress was made towards the improvement of the recently established Arabidopsis Information Portal (Araport). Currently, we are in the middle of the road map, which means that most objectives are currently ongoing and those are recommended to be continued. Detailed information on progress and recommendations can be found throughout this report and a list of the current and adjusted road map goals can be found below.

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

Subcommittees (SCs), page 15 ff.; Resource and Stock Centers, page 32 ff.; IAIC and Araport, page 33 ff.; Country reports, page 47 ff.

1. Collect and collate accurate quantifiable data obtained at multiple levels of abstraction (organelle, cell, tissue, organ, organism - genomics, epigenomics, metabolomics, proteomics, phenomics, systems biology)
2. Continue to develop collections of mutants and mutant lines
3. Translation of quantitative data into functional networks computational/mathematical models across scales
4. Develop new research tools and experimental methods to address the lack of global assays for a number of plant processes and fully exploit existing technologies
5. Provide training for plant scientists in computational science and theoretical approaches and encourage further collaboration between plant biologists and theoretical scientists

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

SCs, page 15 ff.; IAIC and Araport, page 33 ff.; Arabidopsis Basic Research, page 39 ff.

1. Continue to develop genomic sequencing and computational resources in order to understand and utilize the natural variation of Arabidopsis and related species and to infer biological networks
2. Develop tools and techniques to facilitate the identification of QTLs that have subtle effects on plant genotypes
3. Utilize the information gathered in Arabidopsis and related species to undertake comparative genomics/comparative evolution/comparative ecological genomics
4. Develop appropriate open access informatics and data infrastructure for storage, retrieval and analysis of variation and QTL data
5. Analyze ecotypes and Arabidopsis relatives in association with their rhizosphere, endophyte and epiphyte communities in various ecological settings
6. Develop a multi-scale artificial field model towards natural conditions and develop high-throughput methods for measuring phenotypes in the lab and in the fiel

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

Progress and Activities, page 9 ff.; SC, page 15 ff.; IAIC and Araport, page 33 ff.; Impact on Applied Research and Industry, page 43 ff.; Country reports, page 47 ff.

1. Undertake the approaches outlined in sections A and B to help us understand important complex traits
2. Promote active dialogue, knowledge and data exchange between plant communities and various fields of expertise
3. Develop a data and informatics infrastructure in which underpinning knowledge generated in Arabidopsis can flow easily to plant breeding
4. Showcase examples of the role of Arabidopsis in rational improvement of plant species for agriculture and other plant-based industries through the annual MASC report and the annual International Conference on Arabidopsis Research (ICAR)
5. Promote exchanges of information and personnel between Arabidopsis groups and those working on other plant species and vice versa
6. Promote knowledge exchange with data providers/users of other model organism communities and facilitate interactions with computational/theoretical researchers

(D) Build the International Arabidopsis Informatics Consortium (IAIC)

Bioinformatics SC page 15 ff.; IAIC and Araport, page 33 ff.

1. Continue to develop Araport; use it to establish widespread use of appropriate data standards
2. Generate an infrastructure that promotes data exchange and collaboration. For example to ensure that integration of data allows users to move vertically between Arabidopsis associated data as well as horizontally to other plant species and model organisms
3. Ensure all data and resources generated are available via the appropriate public data repositories
4. Ensure there is interoperability between the data and resources generated by the Arabidopsis community and those generated by other communities
5. Establish strong links with other data providers/users and computational experts to allow exchange of information and best practice

(E) Deepen international cooperation and coordination

Progress and Activities, page 9 ff.; Analysis and Recommendations, page 11 ff.

1. Continue to represent each country that is undertaking Arabidopsis research around the globe
2. Increase awareness of the richness of international Arabidopsis research via the production and distribution of the annual MASC report and the ICAR
3. Help coordinate international Arabidopsis research to minimize duplication of efforts and maximize efficient use of resources through collaboration
4. Promote open communication and free exchange of data, materials resources and ideas among the Arabidopsis research community
5. Liaise with funding agencies supporting Arabidopsis research
6. Provide coordination for the road map
7. Periodically assess the status of the road map and adjust goals

New goals for 2021 road map:

(E) Deepen international cooperation and coordination

- Develop a permanent online system for International Conference on Arabidopsis Research (ICAR) i.e. registration and abstract submission system
- Establish MASC as e.g. not-for-profit organization to ensure international coordination of Arabidopsis research, to minimize duplication of efforts and maximize efficient use of resources through collaboration
- Better integrate websites, portals and information resources either via www.arabidopsisresearch.org or via a subdomain at www.araport.org
- Participate in the ASPB and GPC's new Plantae.org digital communication platform.

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.

Tools and Resources

Using TDNA-seq, a next-generation sequencing approach for generating T-DNA flanking sequence tags established by the Ecker laboratory at the Salk Institute, 166,439 insertions in 100,013 existing segregating T-DNA insertion lines were identified and are now are now available at TAIR/ABRC. The TDNA-seq method on mainly existing lines from the SALK, SAIL, WISC, and GABI-kat collections (distinguishable by the presence of a "seq" after the T-DNA line identifier, i.e. SALKseq, SAILseq, GABIseq, WISCseq) identified approximately 120,000 new T-DNA insertions, and these represent a large set of potential new loss-of-function mutants for the Arabidopsis community.

New RNA-seq data sets continue to be generated, such as Hong Ma and colleague's floral transcriptome (Zhang et al., 2014). Complementary papers looked at alternative splicing (Wang et al., 2014) and methylation (Yang et al., 2015) during floral development. Transcriptomic and metabolomic changes were documented in response to sulfur starvation by the Hoefgen lab (Bielecka et al., 2014), while Kim et al. (2015) used large-scale perturbations guided by a genome-scale metabolic network to identify patterns of metabolite changes. Christine Queitsch at University of Washington in Seattle 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 and were officially published by Sullivan et al. (2014). A data set of approximately 800 Arabidopsis transcription factor binding specificities, from Matthew Weirauch, Tim Hughes, Joe Ecker and collaborators (Weirauch et al., 2014) is available on CisBP at http://cisbp.ccbr.utoronto.ca. Heyndrickx et al. (2014) published a functional and evolutionary perspective on transcription factor binding in *Arabidopsis thaliana*, and close colleagues also published a paper which used an ensemble approach to reverse-engineer gene regulatory network to identify interconnected transcription factors in oxidative stress (Vermeirssen et al., 2014). A "FlowerNet" of coexpressed genes involved in flower development was published (Pearce et al., 2015). The Brady lab used a yeast one hybrid approach to identify gene regulatory networks involved in secondary cell wall synthesis (Taylor-Teeples et al., 2015), while Van de Velde et al. (2014) inferred transcriptional networks in Arabidopsis through conserved non-coding sequence analysis across the higher plants. Relatedly, Jamie Waese and coworkers at the Bio-Analytic Resource released conserved non-coding regions from the *Brassicaceae* from Haudry et al. (2013) into a visualization tool called GeneSlider at http://bar.utoronto.ca/geneslider/ (manuscript in preparation). Lai and Ge (2014) undertook a nice meta-analysis of gene expression signatures from hundreds of gene expression profiling studies to uncover hidden links between biological processes.

Araport.org: Work towards creating a new Arabidopsis Information Portal by the International Arabidopsis Informatics Consortium continued (International Arabidopsis Informatics Consortium, 2012), with community meetings held at ICAR in Vancouver and ASPB in Portland last summer, and at the PAG Conference in San Diego in January 2015. The new portal has been online since April 2014 at http://araport.org. Araport also hosted a Developers' Workshop at the University of Texas – Austin in November 2014. The first "app" to come out of this workshop appeared on Araport in March 2015. More are planned for this year and next – stay tuned! The Araport team has also mapped more than 100 RNA-seq data sets from the Short Read Archive at NCBI in order to identify novel splice variants for the next Arabidopsis genome release later this year or early next year (Araport 11).

Eva Huala and colleagues at TAIR moved to a subscription-based model, and have set up a non-profit company, Phoenix Bioinformatics Inc., to continue TAIR's annotation work. TAIR added a total of 677 gene symbols, new and updated gene summaries, and new GO and PO annotations to 17,876 genes, including experiment-based annotations from published research articles to 2,936 genes. The updated annotations will be available after a delay on Araport.

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Clone-Based Functional Genomics Resources (ORFeomics)

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

By Motoaki Seki (Chair) and Joe Ecker (Co-Chair) with contributions from subcommittee members, Masatomo Kobayashi (RIKEN BRC), Satoshi Takahashi (RIKEN CSRS), David J. Gifford (RIKEN CSRS), Eric Grotewold (ABRC) and Debbie Christ (ABRC)

Progress Towards Road Map Goals

The major goal 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.

Future Goals

To continue 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.

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

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

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

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

Tools and Resources

We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Table 2).

The revised ones are shown in bold. New clones include Gateway clones for about 2000 transcription factor and about 400 glycosyltransferase genes.

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,

TOC

Table 2. Arabidopsis ORF and cDNA clone repositories. Stock centres distributing Arabidopsis clone repertoires:

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

Creator	**Format**	**Focus**	**Validation**	**Scale**	**URL**	**Stock center**
ORF clones						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14.398	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12.114	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18.258	http://interactome.dfci.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3.041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5′ and 3′ end seq.	1.282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5′ and 3′ end seq.	15.543		ABRC
REGIA	Gateway entry	Transcription factors	5′ and 3′ end seq.	982	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5′ and 3′ end seq.	7.300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5′ and 3′ end seq.	6.448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
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
Pruneda-Paz et al.	**Gateway Entry, no stop**	**Transcription factor**	**Full sequence**	**1.956**		**ABRC**
Pruneda-Paz et al.	**Gateway Destination, no stop, pDEST22**	**Transcription factor**	**Full sequence**	**1.956**		**ABRC**
Lao et al.	**Gateway DONR, no stop, pDONR223**	**glycosyltransferases**	**Full sequence**	**429**	**http://gt.jbei.org/**	**ABRC**
Amita Kaundal et al.	**Gateway DONR, no stop, pDONR201**			**26**		**ABRC**
cDNA clones						
RIKEN/SSP/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

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.).

Selected Publications

- The plant glycosyltransferase clone collection for functional genomics. (2014) Lao J, Oikawa A, Bromley JR, McInerney P, Suttangkakul A, Smith-Moritz AM, Plahar H, Chiu TY, González Fernández-Niño SM, Ebert B, Yang F, Christiansen KM, Hansen SF, Stonebloom S, Adams PD, Ronald PC, Hillson NJ, Hadi MZ, Vega-Sánchez ME, Loqué D, Scheller HV, and Heazlewood JL. Plant J. 79:517-529.
- A Genome-Scale Resource for the Functional Characterization of Arabidopsis Transcription Factors. (2014) Pruneda-Paz, J.L., Breton, G., Nagel, D.H., Kang, S.E., Bonaldi, K., Doherty, C.J., Ravelo, Galli, M., Ecker, J.R., and Kay, S.A. Cell Reports 8: 622–632.

Epigenenetics and Epigenomics

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

By Doris Wagner

Progress Towards Road Map Goals

(A) Epigenetics is critical to elucidate the how phenotypes arise from genotypes. The work of EPIC and the epigenetics/epigenomics MASC subcommittee has raised awareness of the role of epigenetics in this.

(B) Natural epigenetic variation has been studied extensively in Arabidopsis and epiallelic variation and genomic imprinting have recently been shown to produce novel gene expression patterns in seeds.

(C) Epigenetic regulation of important traits, such as drought tolerance and hybrid vigor are being elucidated.

(D) IAIC is making use of the many Arabidopsis epigenome data sets present in the unified epigenome browser developed by EPIC (Brian Gregory) in collaboration with iPlant (Eric Lyons) and the Gordon and Betty Moore Foundation (Vicki Chandler).

(E) Yearly international meetings and workshops are being held (2013 in the UK (C. Dean), 2014 in the US (D. Wagner), 2015 in China (XF Cao).

Future Goals

The subcommittee will continue to work on the goals related to the road map in the coming year. The EPIC RCN will end in 2016 and by this time a new MASC epigenetics and epigenomics subcommittee will be formed that will work towards these gaols. In addition, the subcommittee will continue to organize yearly International meetings with workshops, as well as the yearly ICAR workshop. In addition, it will work to support further development of the CoGe epigenome browser and towards dissemination of new methods for epigenomic research. If possible, it will also redesign the EPIC website to make it more useful to the greater community.

Tools and Resources

Unified CoGe epigenome browser https://genomevolution.org/wiki/index.php/EPIC-CoGe now hosts more than 1,000 Arabidopsis epigenome data sets.

Additional analysis, and visualization tools are under development.

Conferences and Workshops

- PAG workshop on Plant Epigenetics; January 2015 (Rob Martienssen)
- Keystone symposium on RNA and chromatin; February 2015 (Craig Pikaard and Rob Martienssen)
- Cold Spring Harbor Asia meeting on Epigenetics and Plant development; June 2015 (Doris Wagner, Xiofeng Cao and Justin Goodrich)

- EPIC/MASC workshop on Plant Epigenetics; ICAR July 2015 (Doris Wagner and François Roudier) - application pending
- PAG workshop on Plant Epigenetics; January 2016 (Rob Martienssen)
- Keystone symposium on Plant Epigenetics and desirable traits; February 2016 (Scott Michaels, Doris Wagner and Nathan Springer)

Selected Publications

- Three plant journals have special issues on Plant Epigenetics Plant Physiology (D. Wagner co-editor), Plant Journal , and Molecular Plant.
- Also D. Wagner, Craig Pikaard and Vincent Colot will contribute a chapter on Plant Epigenetics for the NAASC Tansley review on 25$^+$ years of Arabidopsis research.

Metabolomics

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

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

Progress Towards Road Map Goals

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

Future Goals

To realize the goals, we aimed to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. This subcommittee website has been launched at www.masc-metabolomics.org. The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where the subcommittee members can join. A MASCM gator portal is under development comparable with the MASCP gator portal http://gator.masc-proteomics.org/. The webinterface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases.

Tools and Resources

- www.masc-metabolomics.org

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

  Metabolomic characterization of 50 Arabidopsis mutants and the database as a functional genomics tool (MeKO), Arabidopsis metabolome expression databases 'AtMetExpress development', 'AtMetExpress 20 ecotypes' and 'ReSpect for Phytochemicals'.
- 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 specializing in plant metabolism.

Conferences and Workshops

- 2014/6/23-26 Metabolomics 2014, Tsuruoka, Japan
- 2015/6/29-7/2 Metabolomics 2015, San Francisco, US
- 2015/7/19-24 Gordon Research Conference, Plant Metabolic Engineering, Waterville Valley, US
- 2015/12/15-20 Pacifichem 2015, Genomics and Metabolomics for Phytochemical Research, Honolulu, US

Selected Publications

- Metabolomic characterization of knock-out mutants in Arabidopsis - Development of a metabolite profiling database for knock-out mutants in Arabidopsis (MeKO). (2014) Fukushima A, Kusano M, Mejia RF, Iwasa M, Kobayashi M, Hayashi N, Watanabe-Takahashi A, Narisawa T, Tohge T, Hur M, Wurtele ES, Nikolau BJ, Saito K. Plant Physiol. 165: 948-961.
- Proposed quantitative and alphanumeric metabolite identification metrics. (2014) Sumner LW, Lei Z, Nikolau BJ, Saito K, Roessner U, Trengove R Metabolomics, 10: 1047-1049.
- Exploring the Arabidopsis sulfur metabolome. (2014) Gläser K, Kanawati B, Kubo T, Schmitt-Kopplin P, Grill E. Plant J. 77: 31–45.
- Meta-analysis of metabolome QTLs in Arabidopsis: trying to estimate the network size controlling genetic variation of the metabolome. (2014) Joseph B, Atwell S, Corwin JA, Li B, Kliebenstein DJ. Frontiers in Plant Science, 5:461.
- Metabolome Analysis of *Arabidopsis thaliana* Roots Identifies a Key Metabolic Pathway for Iron Acquisition. (2014) Schmidt H, Günther C, Weber M, Spörlein C, Loscher S, Böttcher C, Schobert R, Clemens S. PLoS ONE. 9(7): e102444.

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 Arabidopsis 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 metabolic analyses. Joseph et al. (2015) show that the metabolic network has genetically programmed stochastic variance controlled by all the genomes and is node specific. For example, a gene can control phenylalanine noise across individuals without influencing shikimate or sinapate.

(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. Major milestones were made in the economically important genus Brassica, including the publication of *Brassica napus* (Chalhoub et al. 2014) and *Brassica oleracea* (Liu et al. 2014, Parkin et al. 2014). These analyses are now being followed up with sequencing across the diversity of these important crops (canola, broccoli, cauliflower, kale, kohlrabi, Brussels sprouts, and so forth; for example Wang et al. 2014). Numerous other comparative genomic analyses are ongong across the order *Brassicales* (Grewe et al. 2014). These studies in comparative genomics and natural variation illuminated several aspects of Arabidopsis biology.
- Progress in the natural variation of Arabidopsis was made. The sequencing of 1000 Arabidopsis genomes is ongoing, and various studies are investigating variation within a subset of the sequenced lines (for example, Li et al. 2014). Joseph et al. (2014) show from a meta-analysis that any RIL population under 1000 lines is too small for even dissecting the genetic architecture of a biparental cross. These results indicate that much larger populations need to be developed by the community then are currently being generated for multiparental trait dissection and suggests that GWA hits will be population dependent (with no population ever being the “Best”).

(E) Deepen international cooperation and coordination

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

(F) Subcommittee specific goals (if applicable)

- Progress was made toward agreeing on gene naming conventions across the Brassica species, with planned discussions among the Arabidopsis and Brassica communities to coordinate various standards and ontologies, as well an 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.
- Developing systems biology and -omics resources parallel to those available in Arabidopsis in crops like Brassica and Camelina and phylogenetically related model species that exhibit traits not present in Arabidopsis (e.g., both C3 and C4 photosynthesis in Cleome, woodiness in Caper).

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

Future goals include:

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

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

Future goals include

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

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

Future goals include:

- Integrating -omics data and informatics infrastructure in Arabidopsis with other species.
- Developing international standards for population genomics (Arabidopsis 1001 genomes, Brassica 100 genomes) and comparative genomics (BMAP 100 genomes) to maintain high-quality reference genomes and re-sequenced genomes.
- Developing open access ontology-driven database tools and promote the adoption of uniform vocabularies and machine-readable formats for describing experimental data and metadata. Subcommittee member Nick Provart is further developing Arabidopsis-centric view of BMAP data via a tool called GeneSlider at the Bio-Analytic Resource (BAR). Updated versions of the tool will include predicted transcription factor binding sites with links to Regulome (genome-wide DNAse I sensitivity data), see http://bar.utoronto.ca/~asher/GeneSlider_New/?datasource=CNSData&agi=At1g01010&before=1000&after=1000&zoom_from=779&zoom_to=879

(E) Deepen international cooperation and coordination

Future goals include:

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

(F) Subcommittee specific goals

Future goals include:

- Studying natural variation within Arabidopsis and comparative ‘omic and systems biology investigations in related species is central to understanding plant biology and plant environment interactions.
- Coordinating gene naming conventions across the Brassica species, with planned discussions among the Arabidopsis and Brassica communities to coordinate various standards and ontologies, as well an 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 planned for 2015-2016:

- Plant Genome Evolution in Amsterdam, Netherlands will meet again in September 2015.
- The next Crucifer Genetics Workshop will be in September 2016 in Melbourne, Australia; and Brassica 2018 will meet in St. Malo, France.

Selected Publications

- Early allopolyploid evolution in the post-neolithic *Brassica napus* oilseed genome. (2014) Chalhoub B, Denoeud F, Liu S, Parkin IAP, Tang H, et al. Science. 345: 950-953.
- Genetic Variation for Life History Sensitivity to Seasonal Warming in *Arabidopsis thaliana*. (2014) Li Y, Cheng R, Spokas KA, Palmer AA, and Borevitz JO. Genetics. 196: 569-577
- The *Brassica oleracea* genome reveals the asymmetrical evolution of polyploid genomes. (2014) Liu S, Liu Y, Yang X, Tong C, Edwards D, et al. Nature Communications. 5: 3930.
- Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid *Brassica oleracea*. (2014) Parkin IAP, Koh C, Tang H, Robinson SJ, Kagale S, et al. Genome Biology. 15: R77.
- Genome-wide investigation of genetic changes during modern breeding of *Brassica napus*. (2014) Wang N, Li F, Chen B, Xu K, Yan G, Qiao J, Li J, Gao G, Bancroft I, Meng J, King GJ, Wu X. heoretical & Applied Genetics. 8: 1817-1829.

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Chalhoub B, Denoeud F, Liu S, Parkin IAP, et al. (2014) Early allopolyploid evolution in the post-neolithic Brassica napus oilseed genome. Science 345: 950-953.

Grewe F, Edger P, Keren I, Sultan L, et al. (2014) Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of Brassica oleracea. Mitochondrion 19 : 135-143.

Joseph B, Corwin JA and Kliebenstein DJ. (2015) Genetic variation in the nuclear and organellar genomes control stochastic variation in the metabolome. PLoS Genetics 11(1)e1004779.

Joseph B, Atwell S, and Kliebenstein DJ. (2014) Meta-analysis of metabolome QTLs in Arabidopsis: Can we estimate the network size controlling genetic variation of the metabolome. Frontiers in Plant Science 5(1) 461.

Li Y, Cheng R, Spokas KA, Palmer AA, Borevitz JO. (2014) Genetic Variation for Life History Sensitivity to Seasonal Warming in Arabidopsis thaliana. Genetics 196: 569-577

Liu S, Liu Y, Yang X, Tong C, et al. 2014. The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications 5: 3930.

Parkin IAP, Koh C, Tang H, Robinson SJ, et al. 2014. Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. Genome Biology 15: R77.

Wang N, Li F, Chen B, Xu K, et al. (2014) Genome-wide investigation of genetic changes during modern breeding of Brassica napus. Theoretical & Applied Genetics 8: 1817-1829.

Phenomics

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

By 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 2014 there has been a continued development of automated platforms and methods including new software for non-invasive phenotyping of Arabidopsis and crop phenotyping increasing the capacity and the number of research centers that are engaged in large-scale phenomics research.
- There were significant examples of comprehensive pipeline approaches to link genome to phenome and enable multi-trait analysis towards this goal.
- Comprehensive efforts have continued within The International Plant Phenotyping Network, the European Plant Phenotyping Network (providing access to external users) and the implementation of national phenotyping networks in Germany (DPPN), France (Phenome), UK (UKPPN), and Australia (APPF) in particular.

Future Goals

- Coordination of experimentation across phenotyping centers regarding germplasm used for sequencing within the 1001 genome project and mutant collections would be desirable.
- Promote best practices in phenotyping experimentation
- 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: Nelissen et al. (2014) published a manuscript in which they argue that plant scientists should become more involved in converting basic knowledge into applications in crops to support food security and agriculture. To date, the improved resolution of many genome-wide technologies and the emerging expertise in canopy imaging, plant phenotyping and field monitoring make it very timely to move from the pathway specifics to important agronomic realizations, thus from pot to plot. The authors plead for a network of protected sites for field trials across the different climates to test improved biotech traits directly in crops.

Tools and Resources

Updates contributed by Stijn Dhondt, Dirk Inzé (VIB, Gent, Belgium), Minami Matsui (RIKEN, Japan), Jan Humplík, Dusan Lazár and Lukás Spíchal (Olomouc, Czech Republic), Jeremy Harbinson (Wageningen University), Justin Borevitz (Australian National University), Xavier Sirault (CSIRO, Canberra), Christine Granier (INRA Montpellier)

Development of novel phenotyping infrastructure and phenotyping pipelines

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 and corn research on growth regulatory networks and mild drought stress. Since this year, the plant phenotyping platforms developed at our department are being commercialized by the machine building company, SMO (www.wiwam.com). The intensive collaboration between SMO and VIB makes the technology available to the plant research community at large.

At the scientific level, we analyzed the leaf and rosette growth response of six *Arabidopsis thaliana* accessions originating from different geographic regions, when exposed to mild drought stress (Clauw et al., 2015). The automated phenotyping platform WIWAM was used to impose stress early during leaf development, when the third leaf emerges from the shoot apical meristem. Analysis of growth related phenotypes showed differences in leaf development between the accessions. In all six accessions, mild drought stress reduced both leaf pavement cell area and number, without affecting the stomatal index. Genome-wide transcriptome analysis (using RNA sequencing) of early developing leaf tissue identified 354 genes differentially expressed under mild drought stress in the six accessions. Our results indicate the existence of a robust response over different genetic backgrounds to mild drought stress in developing leaves. The processes involved in the overall mild drought stress response comprised abscisic acid signaling, proline metabolism and cell wall adjustments. In addition to these known severe drought related responses, 87 genes were found to be specific for the response of young developing leaves to mild drought stress. The analysis of a larger set of natural accessions is currently ongoing.

Furthermore, we developed an *in vitro* growth imaging system (IGIS) to perform time-resolved analysis of rosette growth (Dhondt et al., 2014). In this system, Arabidopsis plants are grown in Petri dishes mounted on a rotating disk, and images of each plate are taken on an hourly basis. Automated image analysis was developed in order to obtain several growth related parameters, such as projected rosette area, rosette relative growth rate, compactness and stockiness, over time. To illustrate the use of the platform and the resulting data, we present the results for the growth response of Col–0 plants subjected to three mild stress conditions. Although the reduction in rosette area was relatively similar at 19 days after stratification, the time-lapse analysis demonstrated that plants react differently to salt, osmotic and oxidative stress. The rosette area was altered at various time points during development, and leaf movement and shape parameters were also affected differently. We also used the IGIS to analyze in detail the growth behavior of mutants with enhanced leaf size. Analysis of several growth-related parameters over time in these mutants revealed several specificities in growth behavior, underlining the high complexity of leaf growth coordination.

Significant efforts towards centrally organized and ontology-driven data management and proper meta-data collection have been realized through the further development of the web application PIPPA (the PSB Interface for Plant Phenotype Analysis). Recent extensions include the support of multiple robotic phenotyping platforms in the department. The integration of new image analysis scripts has been streamlined. Future developments include the realization of a public version of the web interface, which could be used to make phenotyping results available to the community.

The Laboratory of Genetics and Horticulture and Product Physiology group, Wageningen University: The conspicuous technological resources we offer are a high throughput Arabidopsis phenotyping platform based on imaging of chloropyll fluorescence and narrow and broad-band reflectance imaging, smaller scale benchtop imaging systems and a recently built leaf photosynthesis measurement system that can measure gas exchange, chlorophyll fluorescence and light-induced absorbance changes in the far-red (associated with P700 oxidation and therefore giving information about photosystem I) and green (associated with the electrochromic shift and qE type quenching) spectral regions.

The Centre of the Region Haná for Biotechnological and Agricultural Research, Palacky University Olomouc, Czech Republic: Two phenotyping platforms (PlantScreenTM, PSI, Brno, Czech Republic) are operated in the Centre of Region Haná for Biotechnological and Agricultural Research (Palacký University in Olomouc & IEB ASCR & Crop Research Institute) allowing high-throughput integrative analysis of plant growth and physiological status in fully controlled environment. The "XYZ" platform consists of top-view cameras for green area (RGB), chlorophyll fluorescence (PAM FlourCam) and hyperspectral analysis (SWIR). In 2014 a protocol for *in vitro* screening of Arabidopsis growth in culture multiwell plates by RGB camera was developed. The protocol allowing maximum throughput of 480 24-well plates (i.e. 11.520 seedlings) in one run was applied in more than 25 biological screenings (approx. 72 000 individual seedlings). The majority of the experiments represented a part of a chemical biology program focused on screening of chemical libraries for compounds promoting plant growth. A number of experiments was dedicated to studies of effect of heavy metal stress on Arabidopsis growth and studies of mode of action of chemical substances increasing tolerance of the plants in this stress conditions. In this particular application RGB, FluorCam and SWIR sensors were employed for integrative phenotyping.

The second platform allows combining three-view RGB imaging with top-view thermal camera (IR), FluorCam and hyperspectral (NIR) imaging. Plants are transported within the system by conveyor belt allowing also automated weighting and watering. In the system the top-view experiments with Arabidopsis plants have been performed to validate effects of candidate compounds selected in the basic screening by their foliar application to adult plants. In 2014 the main activities were dedicated to studies of effects of various stresses on the crop species. An experimental procedure of integrative high-throughput phenotyping of plant shoots employing automated simultaneous analyses of shoot biomass and photosystem II efficiency to study the cold tolerance of pea (*Pisum sativum L.*) cultivars with throughput of 16 plants per hour was introduced (Humplík et al. 2015) providing a procedure with potential application, not only for selection of cold-sensitive/tolerant varieties of pea, but also for studies of plant cold-response strategies in general. Further experiments were focused on the phenotyping of young cereals (germination, growth and development) and vegetable plants. The recent and future methodological aims of the research are focused on real-time non-invasive and integrative analysis of plant growth in controlled environment followed by further validation of phenotypic traits in field conditions.

INRA LEPSE Montpellier, France: Since 2006, the PHENOPSIS phenotyping platform in INRA was mainly devoted to the phenotyping of *A. thaliana* rosette expansion plasticity from cell to whole rosette, in response to drought stress. It was recently upgraded to increase the diversity of plant traits measured and plants have been exposed to a variety of stresses combining abiotic and biotic challenging situations. Analyzing more traits non-invasively has required the extension of the imaging station with: additional cameras combining both top and lateral acquisition of images to quantify simultaneously leaf expansion and hyponasty (Vasseur et al., 2014), a fluorescence and an infra-red cameras to estimate chlorophyll efficiency (Bresson et al., 2014, Bresson et al., in press) and leaf temperature (Vasseur et al., 2014), respectively.

Combining environmental factors in complex scenarios has required further developments of the watering station, allowing now the use of different nutrient solutions (for instance containing different concentrations of heavy metals; coll. F. Gosti, BPMP Montpellier, France) and modification of the software interface for the use of different types of soil in the same experiment (for instance with or without rhizobacteria; coll. F. Varoquaux, LSTM Montpellier, France; Bresson et al., 2014).

Access to this platform for external users has increased thanks to different sources of fundings (EPPN, ANR, Agropolis-LabIntex): J. Bac-Molenaar (PhD Student, Laboratory of Plant Physiology, Wageningen University, The Netherlands) for Genome Wide Association mapping analyses (Bac-Molenaar et al., in press), C. Vazquez-Rovere for the analysis of the GASA genes and their role in plant response to stresses (INTA, Buenos Aires, Argentine), and W. Rymaszewski for the analysis of natural variation of drought tolerance in Arabidopsis accessions that differ in Annexin levels (PhD Student, Institute of Biochemistry and Biophysics, Warsaw, Poland).

Australian Plant Phenomics Facility: The Australian Plant Phenomics Facility is developing a TraitCapture pipeline. It will dissect complex traits of growth across environments into major genetic components and background variation allowing phenotypic prediction and enabling genomic selection. The software will work in controlled environments on high throughput phenotyping platforms and be extensible to field conditions using remotely operated imaging equipment. TraitCapture has a hardware control module, an image analysis component, multi-trait genome wide association tools, and crop modeling suite.

TraitCapture therefore allows the "capture of traits" throughout development and across environments, from multi-dimensional phenotypes. It is envisioned that TraitCapture will allow breeders to simulate regional variation in trials to pre-select for increased productivity under challenging environments.

IBG2, Forschungszentrum Jülich, Germany: We developed a software package, which provides tools for the quantification of leaf surface properties within natural canopies via 3-D reconstruction from stereo images. Our approach includes a semi-automatic selection process of single leaves and different modes of surface characterization via polygon smoothing or surface model fitting. Based on the resulting surface meshes leaf angle statistics are computed on the whole-leaf level or from local derivations (Müller-Linow et al 2015). These stereo imaging tools can be applied to Arabidopsis as well. We have developed a seed germination and seedlings growth scoring system based on RGB imaging. This system is dedicated to Arabidopsis grown in trays and calculates seedling traits. These traits can be used for identification of seedlings for transplantation. A projector system guides the user through the whole process. A manuscript detailing both hardware and software solutions is in preparation.

Databases and other resources

- Data sharing via PHENOPSISDB has allowed publication of original results by external database users (Schmalenbach et al., 2014).
- The Chloroplast Function Database II is a comprehensive database analyzed by combining genotypic and phenotypic multiparametic analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins. The phenotype and segregation data of Arabidopsis Ds/Spm and T-DNA- tagged mutants of nuclear genes encoding chloroplast proteins includes more than 300 morphological mutants and 48 transmission electron microscopic images of mutant plastid (Fumiyoshi Myouga and Kazuo Shinozaki). (http://rarge.psc.riken.jp/chloroplast).
- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) (http://rarge-v2.psc.riken.jp/phenome/) selected about 4,000 transposon insertion lines which have the Ds transposon in gene coding region, and observed visible phenotypes systematically depending on growth stage. Phenotypic descriptions were classified into eight primary and fifty secondary categories, then all recorded images can be searched by the line number or the phenotype categories.
- RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) is an integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary, with both RIKEN RAPID and CSHL Trapper DB for Ac/Ds transposon tagged lines in Arabidopsis. (Akiyama et al., 2014; Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki). (http://rarge-v2.psc. riken.jp/).
- The RIKENBASE database was 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. (https://database.riken.jp/sw/links/en/cria301u1i/).
- For Genome to Phenome, location information of T-DNA in the genome is available for RIKEN Arabidopsis Activation Tagging lines (Minami Matsui collaboration with NEC Soft co ltd.) (https://database.riken.jp/sw/en/id/ria37i/) (https://database.riken.jp/sw/en/id/cria37u1i/) and around 10,000 Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA Over-eXpressing) lines is available (https://database.riken.jp/sw/links/en/cria301u1i/).
- 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 focuses on rice root development using a root image analysis system (NIAS Agrogenomics Research Center, Dr. Habu, Y). (http://cropgenome.project.affrc.go.jp/kenkyu/koubo/nvr.html)
- At the University of Tokyo, a phenotype analysis program was 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

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evaluation of morphological measurement and named by the software CARTA (clustering-aided rapid training agent) that was developed for auto learning system (Dr. Kutsuna, N. and Hasezawa, S. Univ. Tokyo).

Conferences and Workshops

- The 3rd International Plant Phenotying Symposium "Phenotyping for agriculture sustainability" took place in Feb, 2014 in Chennai, India.
- The European Plant Phenotyping Network organized a Spring School on Plant Phenotyping, Aberystwyth, 9 -13 March, 2015.
- Recent progress in drought tolerance: from genetics to modelling, 8 and 9 June, 2015, Le Corum – Montpellier – France, organized by DROPS and EUCARPIA.
- COST FA 1306 - The quest for tolerant varieties -Phenotyping at plant and cellular level, first general meeting and conference, June 22-24, 2015, IPK Gatersleben, Germany
- Measuring the Photosynthetic Phenome, 7 - 9 July, Wageningen, the Netherlands
- VIB – Ghent University is organizing an EMBO practical course entitled "Insights into plant biological processes through phenotyping" together with University of Louvain and University of Liège from 13 - 19 September 2015.
- European Plant Phenotyping Symposium, 11-12 November, 2015, Barcelona.

Selected Publications

- TraitCapture: genomic and environment modelling of plant phenomic data. (2014) Brown TB, Cheng R, Sirault XR, Rungrat T, Murray KD, Trtilek M, Furbank RT, Badger M, Pogson BJ, Borevitz JO. Current Opinion in Plant Biology. 18:73-9.
- High-resolution time-resolved imaging of *in vitro* Arabidopsis rosette growth. (2014) Dhondt S, Gonzalez N, Blomme J, De Milde L, Van Daele T, Van Akoleyen D, Storme V, Coppens F, T S Beemster G, Inzé D. Plant Journal. (1):172-184.
- Leaf responses to mild drought stress in natural variants of Arabidopsis. Clauw P, Coppens F, De Beuf K, Dhondt S, Van Daele T, Maleux K, Storme V, Clement L, Gonzalez N, Inzé D. (2015) Plant Physiology. (3):800-816.
- Natural genetic variation for acclimation of photosysnthetic light-use efficiency to growth irradiance in *Arabidopsis thaliana*. (2015) van Rooijen R, Aarts, M and Harbinson, J Plant Physiology.
- Multivariate genetic analysis of plant responses to water deficit and high temperature revealed contrasted adaptive strategies. (2014) Vasseur F., Bontpart T., Dauzat M., Granier C. & Vile D. Journal of Experimental Botany. 65 (22) 6457-6469.

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Additional Information

An EU-COST action "The quest for tolerant varieties - Phenotyping at plant and cellular level" was launched in 2014. http://www.cost.eu/COST_Actions/fa/Actions/FA1306. This initiative provides networking opportunities through workshops and dedicated working groups as well as funding for short-term scientific missions.

Proteomics

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

By Joshua Heazlewood (co-chair), Alex Jones (co-chair) with contributions from subcommittee members.

Progress Towards Road Map Goals

A) The subcommittee members maintain and update Arabidopsis proteomic repositories that will eventually contribute to the evolving Arabidopsis Information Portal (AIP). This includes updates to data housed in SUBA, PhosPhAt, MASCP Gator, and AT_CHLORO.

B) The 1001 Proteomes portal was released in 2012 and provides protein level information generated from the natural variation sequencing projects.

C) Members are involved in various programs examining aspects of plant biology that leverage the knowledge obtained through the application of proteomics to Arabidopsis.

D) Subcommittee members maintain extensive resources in the area of protein function in Arabidopsis that is being utilized by the IAIC.

E) Subcommittee members are involved with the initiative on Multi Organism Proteomes (iMOP) as part of the Human Proteome Organization (HUPO) and are active members of the International Plant Proteomics Organization (INPPO).

Future Goals

(A) Maintain and build new resources for Arabidopsis with a focus on proteomics. Examine ways to expand and integrate these resources with data from other species and technologies.

(B) Demonstrate applicability of 1001 proteome data to the research community.

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

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

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

(F) Maintain an active Arabidopsis proteomics subcommittee (http://www.masc-proteomics.org/) with web page re-launch and new initiative.

Tools and Resources

- Pep2Pro - proteo-genomic resource (http://fgcz-pep2pro.uzh.ch/) by Baerenfaller
- ProMEX - mass spectral resource (http://promex.pph.univie.ac.at/promex/) by Wienkoop and Weckwerth
- GelMap - 2-DE proteomic repository (https://gelmap.de/projects-arabidopsis/) by Braun
- APP - targeted proteomics (SRM) tool (http://www.plant-energy.uwa.edu.au/APP/) by Taylor and Millar
- SUBA - subcellular database (http://www.suba.bcs.uwa.edu.au/) by Millar
- PPDB - plant protein database (http://ppdb.tc.cornell.edu/) by van Wijk
- AT_CHLORO - plastid proteomic resource (http://www.grenoble.prabi.fr/at_chloro/) by Rolland
- AraPerox - peroxisome proteomic databse (http://www3.uis.no/AraPeroxV1/) by Reumann
- PhosPhAt - phosphoproteome database (http://phosphat.uni-hohenheim.de/) by Schulze
- P3DB - plant phosphoproteome databse (http://p3db.org/) by Thelen
- RIPP-DB - phosphoproteome database (http://phosphoproteome.psc.database.riken.jp/) by Nakagami
- MASCP Gator - proteomics aggregation portal (http://gator.masc-proteomics.org/) by MASCP
- 1001 Proteomes - non-synonomous SNPs from natural variants (http://1001proteomes.masc-proteomics.org/) by Heazlewood
- MRMaid - MRM design tool (http://elvis.misc.cranfield.ac.uk/mrmaid/) by Jones

Conferences and Workshops

The International Plant Proteomics Organization (INPPO) held its inaugural world congress (September 2014) and was organized by Sabine Lüthje, University of Hamburg (Germany). A number of subcommittee members were on the scientific committee for the congress, including Joshua Heazlewood (The University of Melbourne), Wolfram Weckwerth (University of Vienna) and Stefanie Wienkoop (University of Vienna).

The Human Proteome Organisation (HUPO) has relaunched the initiative Multi-Organism Proteomes (iMOP) during its world congress in Madrid, Spain (October 2014). The initiative appointed Joshua Heazlewood (The University of Melbourne) as the interim plant proteomics representative.

Proteomic Forum 2015 (March 2015) at the Technical University Berlin (Germany) contained several sessions specifically highlighting Plant Proteomics. These sessions were organized and coordinated by Hans-Peter Braun, Leibniz Universität Hannover (Germany).

Selected Publications

- An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. (2015) Van Leene J, Eeckhout D, Cannoot B, De Winne N, Persiau G, Van De Slijke E, Vercruysse L, Dedecker M, Verkest A, Vandepoele K, Martens L, Witters E, Gevaert K, De Jaeger G. Nat Protoc.10: 169-187.

- Meta-Analysis of *Arabidopsis thaliana* Phospho-Proteomics Data Reveals Compartmentalization of Phosphorylation Motifs. (2014) van Wijk KJ, Friso G, Walther D, Schulze WX. Plant Cell. 26: 2367-2389.
- Dissecting the Subcellular Compartmentation of Proteins and Metabolites in Arabidopsis Leaves Using Non-aqueous Fractionation. (2014) Arrivault S, Guenther M, Florian A, Encke B, Feil R, Vosloh D, Lunn JE, Sulpice R, Fernie AR, Stitt M, Schulze WX. Mol Cell Proteomics. 13: 2246-2259.
- Dynamic Proteomics Emphasizes the Importance of Selective mRNA Translation and Protein Turnover during Arabidopsis Seed Germination. (2014) Galland M, Huguet R, Arc E, Cueff G, Job D, Rajjou L. Mol Cell Proteomics. 13: 252-268.
- Comprehensive Cell-specific Protein Analysis in Early and Late Pollen Development from Diploid Microsporocytes to Pollen Tube Growth. (2014) Ischebeck T, Valledor L, Lyon D, Gingl S, Nagler M, Meijon M, Egelhofer V, Weckwerth W. Mol Cell Proteomics. 13: 295-310.

Systems and Synthetic Biology

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

By Siobhan Brady (Chair, sbrady@ucdavis.edu) and Malcolm Bennett (Co-chair, malcolm.bennett@nottingham.ac.uk) with input from Pascal Braun (Member, pbraun@wzw.tum.de)

Progress Towards Road Map Goals

Recent activities:

- Members of the MASC subcommittee contributed to a special issue of Trends in Plant Science containing 5 reviews describing recent efforts to model network to multi scale systems in plants (see Trends in Plant Science Volume 19, Issue 5, Pages 267-338 (May 2014) edition)
- Co-organizing research workshops promoting systems biology research. Recent examples include the systems themed symposium at the last 2 Anuual SEB Meetings (held in Valencia 2013 & Manchester, 2014 – see details below)

Future 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 and knowledge-transfer from Arabidopsis and other plant species to economically important systems.

Conferences and Workshops

Recent research meetings and training events:

- A session on "Breeding - quality and productivity/Synthetic- and systems biology" included at the annual meeting of Plant Biotech Copenhagen, Jan 29-31 2014
- "Modeling plant development from the organ to the whole plant scale", April 9 & 10 2015, Montpellier, France. The aim of this two-day meeting is to illustrate the benefits of a multidisciplinary approach associating plant biologists, physicists, mathematicians and computer scientists to tackle important issues in plant biology.

- Several sessions focusing on Systems Biology, including one on Modelling Cells, at the Society for Experimental Biology's Annual Meeting in Prague from the 29th June - 3rd July, 2015.
- “Computational systems in cell biology : the dynamics of morphogenesis and multi-scale modeling” & “Computational systems biology” themed sessions held July 2014 at Annual SEB Meeting in Manchester
- American Society of Plant Biology Minisymposium, “Transcriptional Networks and Development” held July 14, 2014 at the ASPB Annual Meeting in Portland Oregon. A variety of seminars were presented on transcriptional networks and regulation of leaf, fruit, flower and xylem development in Arabidopsis.
- Gordon Conference on Plant Molecular Biology – “Decision-Making Pathways, Networks, and Models in Plant Biology”. This conference was focused on quantitative biology and the elucidation of information pathways articulated as networks or models, with an emphasis on cross-talk between pathways. It was organized by Steven P. Briggs and Mary Lou Guerinot and held July 20-25, 2014 at the Holderness School in Holderness, New Hampshire, US.
- International Conference on Arabidopsis Research; a session was held on “Modeling, Bioinformatics and Systems Biology” on Tuesday July 29, 2014 in Vancouver British Columbia. Seminars regarding gene regulatory networks, proteomic methodologies, parameter selection for modeling and computational inference methods was presented.
- A session on “Systems Biology and Mass spectrometry” was included at the 1st International Plant Proteomics OrganizationWorld Congress on Plant Proteomics: Methodology to Biology at Hamburg University Aug 31st to Sep 3rd.
- GARNet 2014. A session on “Systems and Synthetic Biology” was held at this meeting titled “The Past, Present and Future of the Genetic Model Revolution with Andrew Millar as the plenary speaker in this session and Siobhan Braybrook. The meeting was held from September 9-10 at the University of Bristol in the United Kingdom.
- EMBO Interdisciplinary Plant Science Conference (21-24 September, 2014, Sainsbury Laboratory, Cambridge, UK) Plant biology is undergoing a major shift in emphasis from the identification and analysis of component parts toward studies of dynamic systems behaviors, with the goal of understanding the relationship between levels of biological organization. This integrative approach is heavily interdisciplinary, involving computational modelling, analysis of the physical properties of tissues, and exploitation of wide species comparisons. Developmental Biology is at the vanguard of this revolution because of its inherently multiscale focus. This EMBO Conference focused on recent progress in achieving an integrated understanding of plant development
- A Plant Synthetic Biology Congress was held at the Heathrow Marriot from October 20-21 in London, UK. A range of different seminars were presented concerning the potential of synthetic biology in plant research, genome and pathway design, natural product biosynthesis, DNA assembly and plant research case studies.
- SynthSys Hands - on Webinar Tutorials on the Arabidopsis Framework Model for plant scientists, 2nd and 5th December 2014, scientifically organized by Andrew Millar and hosted online

Selected Publications

Network scale models

- Quantitative analyses of the plant cytoskeleton reveal underlying organizational principles. (2014) Breuer D, Ivakov A, Sampathkumar A, Hollandt F, Persson S, Nikoloski Z. J R Soc Interface.
- Integration of hormonal signalling networks and mobile microRNAs is required for vascular patterning in Arabidopsis roots. (2014) Muraro D, Mellor N, Pound M, Help H, Lucas M, Chopard J, Byrne H, Godin C, Hodgman C, King JR, Pridmore T, Halariutta Y, Bennett M, Bishopp A PNAS. 111 (2) 857-862.
- An Arabidopsis gene regulatory network for secondary cell wall synthesis. Taylor-Teeples M, Lin L, de Lucas M, Turco G, Toal TW, Gaudinier A, Young NF, Trabucco GM, Veling MT, Lamothe R, Handakumbura PP, Xiong G, Wang C, Corwin J, Tsoukalas A, Zhang L, Ware D, Pauly M, Kliebenstein DJ, Dehesh K, Tagkopoulos I, Breton G, Pruneda-Paz JL, Ahnert SE, Kay SA, Hazen SP, Brady SM. (2014) Nature. Online 12.
- Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. (2014) Webling R, Epple P, Altmann S, He Y, Yang L, Henz SR, McDonald N, Wiley K, Bader KC, Glaber C, Mukhtar MS, Gaigis S, Ghamsari L, Stephens AE, Ecker JR, Vidal M, Jones JDG, Mayer KFX, van Themaat EVL, Weigel D, Schulze-Lefert P, Dangl JL, Panstruga R, Braun P. Cell Host Microbe. 16(3):364-75.
- Arabidopsis ensemble reverse-engineered gene regulatory network discloses interconnected transcription factors in oxidative stress. (2014) Vermeirssen V, De Clercq I., Van Parys T, Van Breusegem F, Van de Peer Y. The Plant Cell. 26, 4656-4679.

Multi-cellular models

- Systems analysis of auxin transport in the Arabidopsis root apex. (2014) Band L, Wells DM, Fozard JA, Ghetiu T, French AP, Pound MP, Wilson MH, Yu L, Li Wenda, Hijazi H, Oh J, Pearce S, Perez-Amador MA, Yun J, Kramer E, Alonso JM, Godin G, Vernoux T, Hodgman TC, Pridmore TP, Swarup R, King JR, Bennett MJ. Plant Cell. 26 (3) 862-875.
- Plasma membrane H+-ATPase regulation is required for auxin gradient formation preceding phototropic growth. Hohm T, Demarsy E, Quan C, Allenbach-Petrolati L, Vernoux T, Bergmann S & Fankhauser C. (2014) Mol Sys Biol. 10:751.

Mechanical models

- Mathematical modeling of an oscillating gene circuit to unravel the circadian clock network of *Arabidopsis thaliana*. (2013) Bujdoso N, Davis SJ. Front Plant Sci. 4:3.
- Mechanical modelling quantifies the functional importance of outer tissue layers during root elongation and bending. (2014) Dyson R, Vizcay-Barrena G, Band L, Fernandes A, French A, Fozard J, Hodgman CT, Kenobi K, Pridmore T, Stout M, Wells D, Wilson M, Bennett M, Jensen O. New Phytologist.
- Arabidopsis cell expansion is controlled by a photothermal switch. (2014) Johansson H, Jones HJ, Foreman J, Hemsted JR, Stewart K, Grima R, Halliday KJ. Nat Commun. 5:4848.
- An auxin-mediated shift towards growth isotropy promotes organ formation at the shoot apical meristem in Arabidopsis. (2014) Sassi M, Ali O, Boudon F, Cloarec G, Abad U, Cellier C, Milani P, Chen X, Friml J, Vernoux T, Godin C, Hamant O & Traas J. Curr Biol. 24:2335-2342.

Multi-scale models

- Multiscale digital Arabidopsis predicts individual organ and whole-organism growth. (2014) Chew YH, Wenden B, Flis A, Mengin V, Taylor J, Davey CL, Tindal C, Thomas H, Ougham HJ, de Reffye P, Stitt M, Williams M, Muetzefeldt R, Halliday KJ, Millar AJ. PNAS .E4127-E4136.
- Plant development. Integration of growth and patterning during vascular tissue formation in Arabidopsis. (2014) De Rybel B, Adibi M, Breda AS, Wendrich JR, Smit ME, Novák O, Yamaguchi N, Yoshida S, Van Isterdael G, Palovaara J, Nijsse B, Boekschoten MV, Hooiveld G, Beeckman T, Wagner D, Ljung K, Fleck C, Weijers D. Science.

Arabidopsis Community Projects and Resources

A major goal of the Multinational Arabidopsis Steering Committee (MASC) is to coordinate and strengthen international collaboration. The Arabidopsis community is and has always been very open, so today researchers and funding bodies can look back on more than 20 years of strong international collaboration and data sharing. The efforts of the Arabidopsis community have always been guided by decadal plans, which alongside led to the establishment of many Arabidopsis community projects and resources:

- The Arabidopsis genome research project (1990-2001) led to the completion of the Arabidopsis genome. During this decade two out of three stock and resource centers ABRC (Arabidopsis Biological Resource Center, U.S.) and NASC (Nottingham Arabidopsis Stock Center, U.K.) were founded.
- The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project (2002-2011) led to the functional annotation of most of the *Arabidopsis thaliana* genes. Alongside The Arabidopsis Information Resource (TAIR) was founded in 2001 to meet the needs of the growing Arabidopsis research community.
- From Bench to Bountiful Harvests (2012-2021) aims to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, to be able to build a predictive model of an Arabidopsis plant. In order to provide a flexible platform to enable open sharing of the vast amount of data generated by today's omics approaches, the International Arabidopsis Informatics Consortium (IAIC, page 33) founded the Arabidopsis Information Portal in 2013 (Araport, page 35).

Since 2007 Arabidopsis community project and resource directors regularly contributed to the MASC report and present their respective goals, progress and news. General plant projects and resources are included in the MASC report since last year reflecting the growing connections between researchers focussing on different plant species. This year the following projects and resources contributed:

Resource and Stock Centers

- Arabidopsis Biological Resource Center (ABRC) (page 32)
- Nottingham Arabidopsis Stock Center (uNASC) (page 32)
- RIKEN BioResource Center (BRC) (page 32)

Arabidopsis Informatics and Data Sharing Resources

- International Arabidopsis Informatics Consortium (IAIC) (page 33)
- Arabidopsis Information Portal (AIP - now Araport) (page 35)
- The Arabidopsis Information Resource (TAIR) (page 35)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

- Bio-Analytic Resource for Plant Biology (BAR) (page 36)
- BrassiBase (page 37)
- European Plant Phenotyping Network (EPPN) (page 38)

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

Resource and Stock Centers

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

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

The past year has been marked by a record number of individual donations, including new TALEN-generated mutants, CRISPR/Cas9 expression vectors, as well as a number of ORF clones and sets, including a set of TF ORF clones for Y1H analysis (for details please see the ORFeomics Committee report). ABRC will continue soliciting donations of resources and the tools required to generate new resources using new technologies (e.g. TALEN, CRISPR/Cas). We will also continue encouraging donations of DNA clone sets, generated as a result of high-throughput studies, and with a potential to be utilized for novel high-throughput-based discoveries.

Our overall distribution has remained stable at about 80,000 stocks sent in 2014/2015, with over 2,000 stocks sent as part of our education kits. This group of stocks continues to grow in its popularity among teachers, lecturers and other educators. We continue to perform rigorous testing on newly donated and reproduced stocks, as well as on the stocks that users report as problematic. Our latest quality control statistics can be found at http://abrc.osu.edu/quality-control.

Coordination 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 (Araport) is ongoing.

News

We are pleased to announce a release of a number of existing segregating lines from the SALK, SAIL, WISC, and GABI-Kat collections, based on the annotation for 166,439 insertions identified in 100,013 T-DNA insertion lines. These insertions were identified using TDNA-seq, a next-generation sequencing method for capturing T-DNA flanking sequence tags developed in the Ecker laboratory. These newly characterized insertions can be distinguished by the presence of a "seq" after the polymorphism name (i.e. SALKseq, SAILseq, GABIseq, WISCseq). Approximately 120,000 of these insertions are newly discovered and constitute a large set of potential loss-of-function mutants for the community.

Thanks to a new custom-made Seed Aliquoting Machine (SAM) developed in collaboration with Labman Automation, UK, new installments of the confirmed SALK sets will be generated much more efficiently. Funding for this automated system was provided by the NSF MCB grant “Making the ABRC Business Model Possible”.

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

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

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

If you wish to comment on any of our services (or propose new ones) then we invite you to contribute to our biannual survey. This will be assessed and reworked every 6 months by our advisory board (Chaired by Prof. Don Grierson [FRS, OBE]) and can be found on our home page, our twitter feed and directly at http://t.co/U7KRnNLINo. If you have suggestions for additional areas to discuss, please email us. A list of committee members is available through the ‘About NASC’ link on our home page.

Please do 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 constructive complaints ! We will also be presenting in our sponsored session and welcome questions then or at any time throughout the year (including emails to curators@arabidopsis.info).

Ordering statistics at NASC continue to be healthy and high for the seed service with well over 100,000 individual stocks sent this ordering year; and many more as sets. Please see our site for a comprehensive and up-to-date list of new stocks, collections and lines for this year as always.

See you in Paris !

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

By Masatomo Kobayashi (coordinator)

RIKEN BioResource Center (RIKEN BRC) was established in 2001 and provides of plant, animal, human and microorganisms resources including cultured cells and DNA materials to the international research community. Our aim is the promotion of life sciences to contribute food, health and environment problems that are urgent global issues for human being. Since 2002, we join with the National BioResource Project (NBRP) funded by the Japanese Government (http://www.nbrp.jp/index.jsp). The Experimental Plant Division is selected as the Core Facility of Arabidopsis/Cultured plant cells and genes from NBRP, and is responsible for distributing plant resources from RIKEN BRC. Approximately, 830,000 materials are preserved, and they have been distributed to ca. 1,800 laboratories and research groups in 45 countries.

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

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

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

Arabidopsis Informatics and Data Sharing Resources

International Arabidopsis Informatics Consortium (IAIC)

http://www.arabidopsisinformatics.org/

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

The International Arabidopsis Informatics Consortium (IAIC) was initiated by Arabidopsis community members in 2009 and formally established in 2011 following funding from the US National Science Foundation awarded to Blake Meyers (University of Delaware), who serves as the Interim IAIC Director. The purpose of the Consortium is to facilitate a coordinated global Arabidopsis informatics efforts to maintain the continuity of key Arabidopsis resources while simultaneously expanding their breadth and depth. Key aims are to include in the IAIC new technologies, resources, and participants on a global scale and advance plant biology while creating novel opportunities for research and education, and strengthening international collaborations.

Arabidopsis community members have participated in all stages of Consortium development and activities including through leadership from the North American Arabidopsis Steering Committee (NAASC), election of the Scientific Advisory Board by the Multinational Arabidopsis Steering Committee (MASC), and community participation in eight IAIC workshops including several organized specifically for IAIC design and development and several at general plant biology conferences.

Key project goals include to: (1) enable community analysis of key informatics needs and challenges of the Arabidopsis community; (2) develop a public platform via an IAIC web page to coordinate activities and serve as a community resource; (3) facilitate the collaborative effort to establish and fund a new web-based "Arabidopsis Information Portal" for the global plant biology community; (4) facilitate the election of a Scientific Advisory Board (SAB) to guide the new portal; (5) maintain communication with the Arabidopsis community via scientific publications, presentations, and workshops at conferences and seek opportunities to present project updates and solicit input; (6) engage with PIs of portal-funding proposals and the SAB to ensure community engagement and representation; (7) advocate for community interests and convey information for involvement via modules (and other activities and products) produced by community members; (8) liaise with leaders of the major Arabidopsis stock centers to ensure continued collaborations with the new portal; and (9) communicate with funding agencies to convey relevant opportunities to the community.

Past accomplished goals include (1), (2), (3), and (4)- the new portal is called 'Araport' (https://www.araport.org/).

Ongoing efforts are being made with respect to goals (5), (6), (7), (8) and (9). For example, IAIC leadership convenes regular community workshops and communicates and co-operates with portal leaders, the SAB, module developers, the community at-large, and with funders.

Key goals accomplished recently

(1) Joint development of two community workshops at the 25th International Conference on Arabidopsis Research (ICAR) in Canada (July, 2014) including one that focused on IAIC progress and how community members can develop and contribute modules to the Arabidopsis Information Portal (now named 'Araport') and a second, more technical workshop by Araport leaders that focused on users and module developers. In the former, Blake Meyers presented a brief overview of how the IAIC was formed and why, and detailed efforts underway internationally to support development of the Araport portal. Matt Vaughn introduced Araport, its plan for sustainability, recent progress, and planned connections with a broad array of community-generated modules and their associated data. Presentations by Nick Provart, Mayumi Nakano, and Eva Huala highlighted resources that are, or could be, integrated within Araport. The key outreach goal of the workshop was to connect with two types of researchers: (1) those who are developing (or want to develop) tools and resources to integrate into Araport and (2) end-users who want to learn about current and future Araport features and modules that might accelerate and enhance their research. The latter workshop by Araport staff, entitled 'Arabidopsis Information Portal (AIP) Developer and User Workshop', will be described more fully in the Araport/AIP section of the MASC report.

(2) A second recent IAIC accomplishment was joint-sponsorship of a Portal-developer workshop oriented toward Arabidopsis researchers and students, led by Araport PIs last November, 2014, in Austin, Texas, USA. The main goals were to provide instruction on how to make data available via web services and how to contribute web apps to Araport. The first part of the workshop included lectures and tutorials by AIP developers which participants then put to work in the hands-on part of the workshop that focused on developing apps, with assistance of Portal staff. The interactive workshop included group discussion and strategies on how to implement their apps once they return to their home institutions.

Future IAIC goals

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

The proposed collaboration includes several activities:

(a) NAASC-organized community workshop at ICAR 2015 on bioinformatics, computational and quantitative skills and training for 21st Century Plant Biology led by Siobhan Brady (NAASC) and Joanna Friesner (NAASC, IAIC), with participation by Blake Meyers and Nick Provart (NAASC, IAIC). The workshop will incorporate current research using bioinformatic and computational skills and techniques along with presentations and community discussion on emerging training needs.

(b) NAASC and IAIC co-organized Focus Group on "Computational training of biologists for academia and industry in the 21st Century" led by Blake Meyers and Nick Provart, with assistance from Joanna Friesner and Siobhan Brady, including topics such as: What are the bioinformatics and computational skills needed by plant scientists of the 21st century to deal with more complex data sets (predictive, quantitative and theory-driven)? What are the bottlenecks to providing students with the needed skills? What do employers (of various types) need/want from employees; what are marketable skills in this area?

(c) NAASC and IAIC co-authored white paper disseminating the outcomes of the activities described above.

(2) Another future IAIC goal is to incorporate the outcomes from the activities described above into a hands-on workshop prior to ICAR 2017, envisioned to span 4-5 days and encompass both wet-lab and computational and bioinformatic analysis and techniques. Additional NAASC-sponsored activities focused on emerging genomics technologies (tentatively scheduled for 2016) are expected to inform this 2017 activity as well.

Conferences and Workshops

- Plant and Animal Genomes (PAG) meetings: IAIC presentations: January 2014 and 2015: San Diego
- International Conference on Arabidopsis Research (ICAR): IAIC presentations: August 2014 (Canada), July 2015 (Paris)
- Co-sponsor: AIP Developer Workshop: November 2014, Texas.

The Arabidopsis Information Portal (Araport)

www.araport.org

By Chris Town (Principal Investigator)

The Araport project (www.araport.org) is now in its second year; a lot has been accomplished.

After a preview release in April 2014, we made our first full release in early July 2014. The site included ThaleMine, a data warehouse integrating a number of different data types, and JBrowse, a slick data browser that hosts much of the TAIR 10 genome annotation data. We have since augmented both tools with additional data sets. ThaleMine now contains additional annotation data, publications linked to genes and proteins, GO assignments, Affymetrix expression data, eFP pictographs developed by the Bio-Analytic Resource (BAR; Nick Provart, PI), protein interaction data from various sources (aggregated by BAR), co-expression data from ATTED-II and ortholog data sets developed both by Panther and Phytozome. Users can execute queries across all of these data sets, a driver for housing them within a single database. JBrowse now facilitates retrieval of user-selected epigenomic data sets from Epic-CoGe in real time. At a user's request, we have written and deployed a sequence viewer tool called SeqLighter that allows users to highlight various gene features such as start and stop sites, exons and UTRs (similar to TAIR's Seqviewer). We have added additional data tracks including some RNA-seq gene structure predictions and experimental evidence to transcriptional initiation and termination sites.

We also enriched content in the Downloads, Developer Zone, and Science apps sections of Araport. The Community sections offers news, meetings, questions and answers. Users can post their own job openings.

Under the hood, we continue to develop a robust and open portal infrastructure that will facilitate community contributions. This will enable biologists to contribute sophisticated modules with a minimum of programming hassle. We are about to release developer kits for exposing data through web services, for writing Science apps to visualize and integrate data streams, and for testing and deploying apps and services within Araport. Our kits offer partial solutions, easy-to-follow instructions, and best-practices advice.

Looking ahead, we will continue to enrich Araport with both new data sets and new apps that either expose or operate on data. An update to the TAIR10 "Gold Standard" Col-0 annotation using over 100 sets of publically available RNA-seq data is in progress and will likely be released by the time this report is published. Assimilation of stock and phenotype data into our underlying Chado database is well under way and these data types will be available through ThaleMine in the coming months. The project is scheduled for a review by NSF in mid-May, and we are guardedly optimistic that we will be given approval to transition from this prototype phase to a fully funded development phase for a further three years.

Araport receives funding from the NSF (USA) and BBSRC (UK).

News

"Araport: the Arabidopsis Information Portal" was published in the 2015 Nucleic Acids Research Database Issue: Vol. 43, D1003–D1009. doi: 10.1093/nar/gku1200

Conferences and Workshops

On the outreach side, we have made presentations or held workshops at a number of meetings: ASPB (Portland, 2014), ICAR (Vancouver, 2014), PAG (San Diego, 2015), Maize Genetics (St. Charles IL, 2015) as well as at several universities and regional meetings in the Washington DC area.

To train a cadre of developers to learn the inner workings of Araport and empower them to develop their own apps, we hosted a developer workshop at the Texas Advanced Computing Center (TACC) in November 2014. This was attended by 18 programmers and developers from 16 different groups in the North America and Europe and was regarded by everybody as a great success.

We are beginning to work one-on-one with individual sites to help them expose their data and integrate it into Araport. In summer 2015, we will be present and present at ASPB (Minneapolis) and ICAR (Paris).

The Arabidopsis Information Resource (TAIR)

www.arabidopsis.org

By Leonore Reiser (TAIR curator) and Eva Huala (Director)

Since implementing a subscription requirement one year ago, TAIR has successfully transitioned from grant funds to sustainable, long term community-based funding. We are pleased to be able to continue to provide data and services that complement, enhance and support the global Arabidopsis informatics and research effort. With extraordinary support from our subscribers, TAIR continues to serve the community under the umbrella of our new non-profit Phoenix Bioinformatics (www.phoenixbioinformatics.org). Going forward, we will continue to add integrated, expertly curated data to TAIR. Phoenix will also continue to pursue its mission of developing sustainable solutions that can help other databases maintain operational support for the long term. We express our gratitude to those who have subscribed and we thank you for the opportunity to continue to serve the needs of the Arabidopsis research community.

Curation

TAIR continues to be the primary source of manually curated, continuously updated information about Arabidopsis gene function, expression and phenotypes. TAIR curators extract these experimental data from the literature and make them available in a variety of formats including free text gene summaries and computationally accessible Gene Ontology (GO) and Plant Ontology (PO) annotations. Phenotype information is currently captured as a manually composed short summary with details on mutagens, mutation sites, and mutation effects detailed in the allele record. With subscription revenues we have been able to hire new staff and re-invigorate our annotation efforts. In 2014, we added a total of 677 gene symbols, new and updated gene summaries, and new GO and PO annotations to 17,876 genes (including experiment-based annotations from published research articles to 2,936 genes). For the coming year, our priorities are capturing information about previously uncharacterized (aka unknown) genes, and incorporating new information for known genes, including gene expression, allele data, and mutant phenotypes.

Subscriptions and Free Access

To ensure the widest possible access we offer a variety of subscription options including individual monthly/yearly, institutional, consortium and country-level subscriptions. Nearly 12 months since we shifted to user-based funding, researchers from over 27 countries are supporting TAIR through subscriptions. Subscribers as of March 2015 include 1 country (China), 4 academic consortia, over 140 individual institutions (see list here: http://bit.ly/19sY7VR), and approximately 200 individuals. Corporate subscribers include 5 major agricultural companies and 5 smaller companies. We also provide free subscriptions for teachers and students who are using TAIR as part of a class. TAIR is also accessible without charge to researchers from countries with the lowest GDPs. Free access is also available for infrequent users or those who only want to order stocks from the ABRC. Our revamped registration process allows researchers to complete a basic TAIR registration and optionally add ABRC ordering privileges (no cost) or a subscription for full unlimited access. Individuals can subscribe from within their existing accounts or request information about institutional subscriptions.

Data Releases

In accordance with our data sharing policy, TAIR made its first quarterly data release on December 8, 2014. This release file included all Gene Ontology and Plant Ontology annotations, gene symbols/names, links between loci and publications, and updated gene descriptions added to TAIR through 12/31/2013. Additional data releases containing data added to TAIR over one year previously will be made on a quarterly schedule beginning on March 31 2015. Access to the quarterly release files does not require a subscription and we do not impose any restriction on reuse or redistribution on data contained in these year-old data releases. Subscribers have immediate access to all new information in TAIR through the website, which is updated on a weekly basis, and they may also request custom data sets via our helpdesk (curator@arabidopsis.org).

Plant Projects and Resources with Strong Participation of Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR)

http://bar.utoronto.ca

By Nicholas Provart (Director)

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

- 128,000 Single Nucleotide Polymorphisms
- 145 million gene expression measurements (75 million from *A. th.*), plus "expressologs" (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser
- Documented subcellular localizations for 9.3k 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 36,306 documented PPIs (rice interologs also available!)
- 67,275 predicted protein tertiary structures and 700+ experimentally-determined structures

News

All tools mentioned below may be accessed via http://bar.utoronto.ca:

Our Arabidopsis eFP Browser now has an "ordered tab" feature for the various Data Source options in our eFP Browser, so that you can immediately see in which data source your gene of interest is most highly expressed. We've also added a new Developmental Mutants view encompassing expression data from guard cell mutants from the Torii Lab, trichome mutants from the Marks and Grotewold Labs, and root epidermis mutants from the Schiefelbein Lab.

It is now possible to explore ~800 Arabidopsis transcription factor binding specificities (TFBSs; Weirauch et al., 2014, doi: 10.1016/j.cell.2014.08.009) for any promoter set in Arabidopsis using our Cistome tool.

The ~800 TFBSs from Weirauch et al. (2014) and ~48 from the JASPAR database may also be explored in the context of more than 90,000 conserved non-coding sequences across the Brassicaceae from Haudry et al. (2013, doi:10.1038/ng.2684) with our GeneSlider tool.

The BAR's Expressolog framework was expanded to include grape, based on sequence data and an expression atlas by Fasoli et al. (2012, doi: 10.1105/tpc.112.100230).

The BAR contributed an Interactions Viewer "app" to Araport.org. This was developed at a "hack-a-thon" organized by Araport in November 2014. Further modules and apps, such as a molecular structure viewer and a fast RNA-seq/eFP Browser viewer are currently being developed for Araport under a Genome Canada Bioinformatics and Computational Biology grant.

We've added two new views to our Maize eFP Browser for viewing genome-wide gene expression patterns: a developmental atlas from Lewis Lukens lab (Downs et al., 2013, doi: 10.1104/pp.112.213231) and a tassel and ear primordia data set from the Jackson lab (Eveland et al., 2014, doi:10.1101/gr.166397.113).

Conferences and Workshops

The BAR conducted user testing for its new zoomable user interface, ePlant, for exploring Arabidopsis data from the kilometer to nanometer scale in an intuitive manner. Testing was done at ICAR2014 in Vancouver, and is planned for ICAR2015 in Paris. The BAR was also at the plant bioinformatics booth at ASPB in 2014, and will be so again in 2015.

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

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

By Marcus A. Koch (director)

Since the project-phase 1 started in Sept. 2011 we developed BrassiBase into a fully functional knowledge database system. Because of very positive feedback during the first months of the project we decided at the earliest stages of the project to make the first versions of BrassiBase online available as soon as possible. Consequently, we invested more time into the development of those tools asked for from the scientific community. We were able to announce two releases of BrassiBase in 2013 and 2014, respectively. The first release (version 1.1) basically provided the information on taxonomy on genus and tribal level including a large body of literature. The concept and future perspectives were formulated (Koch et al. 2013; BrassiBase: Tools and biological resources to study characters and traits in the *Brassicaceae* – version 1.1. TAXON 61: 1001-1009). The second release (version 1.1.9.) introduced new tools on phylogenetics and cytogenetics (Kiefer M, Schmickl R, German DA, Lysak M, Al-Shehbaz IA, Franzke A, Mummenhoff K, Stamatakis A, Koch MA. 2013. BrassiBase: Introdcution to a novel database on Brassicaceae evolution. PCP 55 (1): e3.

In the current stage of BrassiBase we can offer the following tools:

1. Taxonomy tool: This is the "heart" (backbone) of the database system. Actually the system is based/build on genera and tribes. Because of many recent taxonomic adjustments major efforts were undertaken to solve various taxonomic problems on the genus level (among them important issues concerning Aethionema, Arabidopsis, Noccaea or Thellungiella). Since the beginning of the second project phase (2014-2017) a complete species check-list (appr. 3770 species) is being developed and will be available soon. Consequently the taxonomic backbone of the database will change to this lower taxonomical hierarchy. Actually, the taxonomy tool do not only provides all relevant information (including taxonomy, relevant literature, or descriptions) but provide links to genus/tribal-wide ITS alignments and tribal phylogenies. Forward-searches allow accessing directly other taxonomic databases such as IPNI and TROPICOS.
2. Phylogenetics tool: This tool has implemented species-level information given as various reference alignments (based on thousands of checked ITS sequences according to sequence quality but also because of voucher documentation and phylogenetic-systematic background information given in the various original publications). Actually these alignments are not linked interactively to the database´ taxonomic backbone. This will be done as soon as the complete species check-list is available. The Phylogenetics tool allows quick and reliable identification using a simple ITS-barcode. This tool is working quite well even on the species level. All details are given in Kiefer et al. (2014). This tool will be developed further towards the future "phylogenetic backbone" to place characters and traits with a given phylogeny. Actually it is not intended to replace careful phylogenetic analysis.
3. Cytogenetics tool: This tool provides a first idea of future "data exploration" tools. We reviewed and checked nearly 10,000 chromosome number reports. All primary literature is given and linked to the individual reports. We also developed a concept to define base chromosome numbers and the various types of "polyploids", and both have been incorporated into the database. This means that the user can also distinguish between various types of polyploids and "true" diploids. The data can be searched on the species level (but for the taxonomic backbone the same arguments as for the Phylogenetics tools do apply). In addition we added many hundreds of carefully explored genome size estimates. These data are displayed as major evolutionary trends on the tribal level, but any data can be exported separately in table formats. In summary, this tool provides many important insights into genomes and genome evolution.
4. Material Collection tool: These resources are now online (fully searchable after registration with BrassiBase), and most of the material cultivated in Heidelberg during the last 5 years is now available with the originally proposed full documentation.

We invite and encourage the Arabidopsis community to register with BrassiBase (its free) and help improving the system - either reporting and contributing results and data and/or spotting problems and make suggestions for future improvements.

Conferences and Workshops

At Botany2015 in Edmonton (Canada, 25-29 July 2015) a special session is dedicated to "Recent advances in phylogeny and systematics of *Brassicaceae*". It can be expected that exciting insights into the evolutionary history and genome evolution will be presented, which are also important for our understanding of the genus Arabidopsis.

The next 2-days BrassiBase workshop will be held in Heidelberg in October 2015. More information can be found at: http://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html.

European Plant Phenotyping Network (EPPN)

http://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 analyze 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 access is based on a simple application procedure and includes scientific and logistic support needed to complete the proposed experiment. Within the first project nearly 60 experiments were initiated within the Transnational Access scheme and 39 have been completed so far. 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. Approximately over 800 Arabidopsis lines have been screened in EPPN experiments. A short summary of the completed experiments is available online: http://www.plant-phenotyping-network.eu/eppn/selected_projects. The Transnational Access call permanently open.

News

EPPN facilities are open for Transnational Access

http://www.plant-phenotyping-network.eu/eppn/access

Conferences and Workshops

- EPPN Plant Phenotyping Symposium, Barcelona 11-12. November 2015

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

TOC

Arabidopsis Basic Research and its Impact on Applied Research

Scientific Highlights in 2014/15

Sufficient food supply is one of basic human needs, which ensures stability and progress of human societies. The food supply depends on agriculture, which is facing an ever increasing world population and the effects of climate change. In order to face these challenges governments began to put greater emphasis on plant research. A better understanding of plant processes from the biggest to the smallest parts will help to enhance agriculture and to ensure food supply. But this approach will be successful only, if the support is broad and covers applied as well as basic plant research. It is an investment in future keeping in mind that the time lapse between an original scientific discovery and its biotechnological application is often quite long. Therefore, it can be beneficial in the long term to study model organisms like Arabidopsis or tobacco alongside, which are easier to manipulate and thus, facilitate faster progress in plant biology research.

Basic research with *Arabidopsis thaliana* serves the plant community as great resource since more than 40 years. The plant community has enjoyed the ease of manipulating Arabidopsis to better understand plant biology and the underlying molecular processes. Arabidopsis' 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. Studies in Arabidopsis have greatly benefited from strong international collaborations and these were strengthened in the last two decades by the Arabidopsis genome project and the Arabidopsis functional genomics project both spanning across several countries and continents.

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). During the previous 15 years an impressive number of 42,169 articles referring to Arabidopsis were published in peer-reviewed journals. The reasons for Arabidopsis to be considered as reference plant for dicots are besides its previously listed features also the availability of advanced resources and portals as well as the huge network of Arabidopsis researchers worldwide. The success of Arabidopsis research based on peer-reviewed publication record is massive having increased 10.8-fold between 1994 and 2014, while rice and corn publications increased about 7-fold and 3.5-fold, respectively. Last year 4,337 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.

The constant development of tools and resources that are adapted to the evolving needs of the Arabidopsis community have greatly facilitated a large body of cutting-edge research that allows for rapid advances in plant biology. 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 few major advances in Arabidopsis research, notably, the authors of these publications are from three or more countries, reflecting the cooperation and truly international nature of the Arabidopsis community. Links to many more selected high impact publications can be found in most chapters throughout the MASC report.

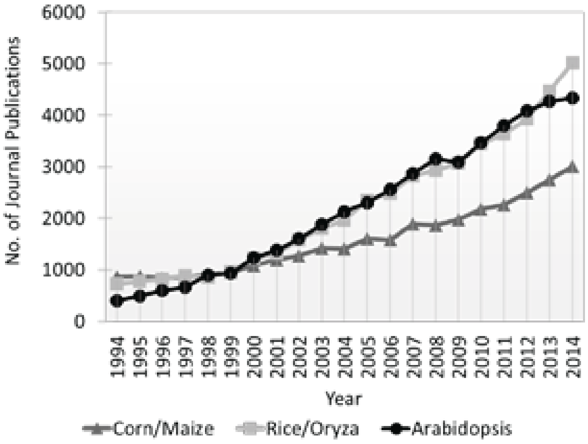

Figure 3. Number of Journal Publications from 1994 until 2014 citing the model organisms Arabidopsis, rice or corn.

Source (2015-05-05): http://www.ncbi.nlm.nih.gov/pubmed query e.g.: Arabidopsis[Title/Abstract] AND ("journal article"[Publication Type] OR "review"[Publication Type]) AND ("2014"[PDAT] : "2014"[PDAT]).

Integration of growth and patterning during vascular tissue formation

By Christian Fleck (Wageningen University, Netherlands) and Dolf Weijers (Wageningen University, Netherlands)

De Rybel B, Adibi M, Breda AS, Wendrich JR, Smit ME, Novák O, Yamaguchi N, Yoshida S, Van Isterdael G, Palovaara J, Nijsse B, Boekschoten MV, Hooiveld G, Beeckman T, Wagner D, Ljung K, Fleck C, Weijers D (2014) Plant development. Integration of growth and patterning during vascular tissue formation in Arabidopsis. Science 345(6197):1255215.

Coordination of cell division and simultaneous pattern formation is central to tissue and organ development, particularly in plants, where rigid walls prevent cell migration. In this paper we have used the establishment of vascular tissue in the early Arabidopsis embryo as a model to study coordination of these events. We had previously shown that root vascular tissues develop from four provascular initial cells. Within these, the auxin-dependent TMO5/LHW transcription complex triggers several rounds of oriented, periclinal cell divisions (De Rybel et al., Dev. Cell 2013). As this cell population grows in number, it is patterned in discrete domains: a central xylem axis and flanking cambial cells. This pattern is laid down during embryogenesis and stably maintained post-embryonically. While growth and pattern formation are both critical for normal development, it was unknown how these processes are regulated and whether the molecular pathways controlling each are distinct or overlapping.

Here, we have identified immediate transcriptional targets of the TMO5/LHW transcription factor dimer. We found that the cytokinin biosynthesis gene LOG4 is activated by the TMO5/LHW transcription complex, and through genetic analysis we show that cytokinin biosynthesis is a critical output of TMO5/LHW function in determining vascular tissue growth during embryogenesis. Auxin and cytokinin were previously shown to regulate vascular tissue patterning. To rationalize the integration of patterning and growth, we developed a computational model that enabled the analysis of regulatory interactions in a growing cellular template of the embryonic vascular tissue. Our simulations suggested that the auxin-cytokinin regulatory network reinforces an early embryonic bias in auxin distribution and tissue geometry and creates a local, non-responding cytokinin source. Genetic and theoretical evidence demonstrated that the cytokinin source, displaying high auxin signaling, organizes the vascular tissue by directing the domain of cytokinin-dependent oriented cell divisions to neighboring cells. Correct pattering is achieved via coupling of two incoherent feed-forward network motifs. One generates a high-auxin domain between two source cells and the other produces sharp boundaries between the high-auxin domain and the neighboring CK response domains. Integration of both motifs results in stable hormonal response zones inside the growing vascular tissue.

In addition to identifying a regulatory network that is sufficient to explain tissue growth and patterning, our work reveals a surprising contribution of initial tissue geometry to vascular patterning. A broader implication is that symmetry breaking, critical for later steps in plant development, might occur during the first embryonic divisions.

How to branch out – Hormonal regulation of axillary buds initiation

By Yuling Jiao (Institute of Genetics and Developmental Biology, CAS, Beijing, China)

Wang Y, Wang J, Shi B, Yu T, Qi J, Meyerowitz EM, Jiao Y (2014) The stem cell niche in leaf axils is established by auxin and cytokinin in Arabidopsis. Plant Cell 26(5):2055-2067.

Wang Q, Kohlen W, Rossmann S, Vernoux T, Theres K (2014) Auxin depletion from the leaf axil conditions competence for axillary meristem formation in Arabidopsis and tomato. Plant Cell 26(5):2068-2079.

Plants differ from most animals in their ability to initiate new cycles of growth and development, which rely on the establishment and activity of branch meristems harboring new stem cell niches. In seed plants, this is achieved by axillary meristems, which are established in the axil as of each leaf base as buds and develop into lateral branches. The activity of axillary buds play vital roles in plant architecture and crop yield. Whereas recent years have witnessed enormous progress the control of bud outgrowth, our knowledge of AM initiation remains rudimentary.

In 2014 two groups of researchers, one from China and USA, and the other from Germany and France, were able to show that two classical phytohormones, auxin and cytokinin, regulate axillary meristem initiation. One group started from imaging of reporters for hormone signaling, followed by genetic analysis, and the other group started from analyzing auxin transport mutants and then imaged auxin distribution. Both groups also manipulated endogenous auxin contents by making transgenic plants. They ended up with the same conclusion that leaf axil auxin minima, presumably serve as a positional cue, are required for axillary meristem initiation. Both auxin efflux and auxin influx play important roles in the establishment of the leaf axil auxin minima. One group also showed the importance of cytokinin in axillary meristem initiation. A cytokinin signaling pulse appears just before axillary meristem initiation. Different from auxin, cytokinin promotes axillary meristem initiation. Genetic analysis suggested that axillary meristem initiation relies on the canonical cytokinin signaling pathway.

Taken together, these studies provide a framework for the study of axillary meristem initiation. Activity of axillary buds has significant roles not only in plant architecture, but also crop yield. These works open up new avenues of research towards understanding shoot branching mechanisms.

TOC

Flower development and MADS transcription factors - dynamics of regulation

By Kerstin Kaufmann (University of Potsdam, Germany) and José-Luis Riechmann (Center for Research in Agricultural Genomics, Barceona, Spain)

Pajoro A, Madrigal P, Muiño JM, Matus JT, Jin J, Mecchia MA, Debernardi JM, Palatnik JF, Balazadeh S, Arif M, Ó'Maoiléidigh DS, Wellmer F, Krajewski P, Riechmann, JL, Angenent GC, Kaufmann K (2014) Dynamics of chromatin accessibility and gene regulation by MADS-domain transcription factors in flower development. Genome Biology 15, R41.

Development of eukaryotic organisms is controlled by transcription factors that trigger specific and global changes in gene expression programs. In plants, MADS-domain transcription factors (TFs) act as master regulators of developmental switches and organ specification. For instance, MADS-domain TFs determine the identities of the different types of floral organs (sepals, petals, stamens, and carpels) via modification of the leaf developmental program. However, whereas it is known that these factors act throughout the developmental process, the mechanisms by which they dynamically regulate the expression of their target genes at different developmental stages are still poorly understood.

In 2014, researchers from The Netherlands, Poland, Argentina, Ireland, Spain and Germany addressed this issue by characterizing the relationship of chromatin accessibility, gene expression, and DNA binding of two MADS-domain proteins at different stages of Arabidopsis flower development, APETALA1 (AP1) and SEPALLATA3 (SEP3). AP1 is an important regulator of floral meristem identity, which plays an additional role as homeotic regulator of sepal and petal identity, whereas SEP3 is a mediator of higher-order MADS protein complex formation that has an important role in the specification of floral organ identities.

Dynamic changes in AP1 and SEP3 DNA binding correlated with changes in gene expression, and many of the target genes could be associated with the developmental stage in which they are transcriptionally controlled. Researchers also observed dynamic changes in chromatin accessibility during flower development. Remarkably, DNA binding of AP1 and SEP3 is largely independent of the accessibility status of their binding regions and it can precede increases in DNA accessibility. These results suggested that APETALA1 and SEPALLATA3 may modulate chromatin accessibility, thereby facilitating access of other transcriptional regulators to their target genes.

The findings by Pajoro et al. indicate that different homeotic factors regulate partly overlapping, yet also distinctive sets of target genes in a partly stage-specific fashion. By combining the information from DNA-binding and gene expression data, researchers were able to propose models of stage-specific regulatory interactions, thereby addressing dynamics of regulatory networks throughout flower development.

In conclusion, this work represented a first step to a better understanding of the dynamics of regulatory networks in plants. Furthermore, MADS-domain TFs may regulate gene expression by alternative strategies, one of which is modulation of chromatin accessibility. Future research needs to reveal which target genes are specifically regulated by a certain homeotic protein complex, and by which exact molecular modes of action different sets of target genes can be modulated in specific ways.

Water provides blueprints for root branching

By José R. Dinneny (Carnegie Institution for Science, Stanford, USA)

Bao Y, Aggarwal P, Robbins NE 2nd, Sturrock CJ, Thompson MC, Tan HQ, Tham C, Duan L, Rodriguez PL, Vernoux T, Mooney SJ, Bennett MJ, Dinneny JR (2014) Plant roots use a patterning mechanism to position lateral root branches toward available water. Proc Natl Acad Sci U S A 111(25):9319-24.

Water is the most limiting resource for plant growth on land and determines the extent to which crops can be successfully cultivated. Water physically connects the soil, root, shoot and atmosphere, and plays important roles from nutrient transport to photosynthesis. Despite the importance of water, our understanding of how plants sense the availability of this vital resource in their environment is far from clear. Plants take up water from soil through their root system and the architecture of the branched root system determines the efficiency at which water is accessed.

Recent work published in PNAS has led to important insight into the role that water availability has in sculpting branching decisions in the root and has led to the discovery of a potentially adaptive response to water termed "hydropatterning". Bao et al. observed that roots contacting a water-conducting surface induce the development of root branches towards the contacted side, while regions contacting air are inhibited from doing so. The ability of the media to induce hydropatterning is directly related to the availability of water and cannot be induced by touch alone. The lab of José Dinneny at Carnegie Institution for Science, Department of Plant Biology showed that such responses were conserved between Arabidopsis and crop plant models such as maize and rice. Water availability generated a bias in root branch patterning very early at the root tip and resulted in a permanent change in the competence of root domains to form branches. These data suggest that intermittent drought may have long-term consequences on the ability of root systems to branch. In collaboration with the groups of Malcolm Bennett and Sasha Mooney at the University of Nottingham, X-ray micro-Computed Tomography (microCT) was used to show that hydropatterning could also be observed in a natural soil context.

Together, this work is of particular significance as it defines the exact physical properties of water that affect important developmental decisions in the root, which ultimately determine architecture and water-uptake efficiency of this organ system. These data also show that roots are able to perceive the spatial distribution of water at an extremely fine scale, which closely matches how such stimuli vary in the soil.

A mechanical feedback maintains pavement cell shape

By Olivier Hamant (INRA-CNRS-UCBL-ENS Lyon, France), Henrik Jönsson (SLCU Cambridge, UK), Elliot Meyerowitz (SLCU Cambridge, UK and Caltech, USA)

Sampathkumar A, Krupinski P, Wightman R, Milani P, Berquand A, Boudaoud A, Hamant O, Jönsson H, Meyerowitz EM (2014) Subcellular and supracellular mechanical stress prescribes cytoskeleton behavior in Arabidopsis cotyledon pavement cells. Elife 16;3:e01967.

One of the defining features of cell identity is shape. For instance, a neuron can be easily distinguished from a lymphocyte just by looking. Although a lot is known of the molecular actors that contribute to shaping cells, the mechanisms through which a cell shape is stably maintained in time are, so far, only hypothetical. Here we investigate whether mechanics may serve as cue to provide such a memory, using the Arabidopsis jigsaw puzzle-shaped pavement cell as a model system.

Pavement cells exhibit a stereotypical cortical microtubule (CMT) pattern during their rapid growth phase: CMTs tend to form parallel arrays between opposing necks, while remaining disorganized in lobes. Using Atomic Force Microscopy, we could detect stiffer wall regions connecting opposite neck domains, matching the underlying CMT pattern. This finding is thus consistent with a scenario in which the CMT pattern in pavement cell determines the pattern of cellulose deposition, which in turn biases the mechanical anisotropy of cell walls, thus stabilizing the jigsaw puzzle shape of these cells. The pavement cell shape memory thus lies at least in part in the mechanical properties of its cell wall.

Is there more to it? In particular, the CMT pattern itself needs to remain stable to have a significant impact on the cell wall. It is well established that plant cells are under high turgor pressure (more than 5 bars) and that this internal pressure generates huge tensions in the cell wall. Now considering the tissue, it is generally accepted that the epidermis itself is under tension, while internal tissues are under compression, in aerial tissues. Using finite element modeling and these assumptions, we calculated the stress patterns in the pavement cell top walls and found that maximal tension strongly aligns in the neck regions, matching the CMT pattern. Using micromechanical perturbations, we observed that CMTs reorient and align along the new stress pattern. This provides another memory layer, in which the cell shape itself prescribes a stress pattern, which in turn stabilizes CMT orientation and cellulose deposition in a feedback loop.

This finding is likely to apply to other cells, and could even be transposed to animal cells, focusing on cortical actin. How this response to stress is regulated is another major outlook of this research. Incidentally, we found that mechanical stress enhances the rate of microtubule severing, which itself promotes the self-organization of CMTs, suggesting that cell shape may also contribute to the rate of the response to mechanical stress.

How to know where to not to grow: the genetic basis for leaf shape diversity

By Miltos Tsiantis (Max Planck Institute for Plant Breeding Research, Cologne, Germany)

Vlad D, Kierzkowski D, Rast MI, Vuolo F, Dello Ioio R, Galinha C, Gan X, Hajheidari M, Hay A, Smith RS, Huijser P, Bailey CD, Tsiantis M (2014) Leaf shape evolution through duplication, regulatory diversification, and loss of a homeobox gene. Science 343(6172):780-3.

This paper demonstrates how comparative analyses between *Arabidopsis thaliana* and its relative *Cardamine hirsuta* can help understand the genetic basis for trait diversification of plant morphology at considerable depth. The authors investigated leaf shape differences between the two species – simple leaves in *A. thaliana* and compound leaves with leaflets in *C. hirsuta*. Through forward genetics in *Cardamine hirsuta* they identified the REDUCED COMPLEXITY (RCO) HD-ZIP class I transcription factor, which promotes leaflet formation in *C. hirsuta*, but was lost in *A. thaliana* resulting in leaf simplification in this species. RCO arose in the *Brassicaceae* through gene duplication of the floral regulator *LATE-MERISTEM IDENTITY* (*LMI1*), which is retained in the whole mustard family. Remarkably, transformation of the *RCO* gene from *C. hirsuta* into *A. thaliana* was sufficient to reverse some of the effects of evolution and make the leaf more complex. This result provides a rare example where presence or absence of a single gene that arose through gene duplication had a key role in generating morphological diversity between related species. By conducting swaps of regulatory and coding sequences the authors showed that diversification of *LMI1* and *RCO* function arose through evolution of a novel expression domain of *RCO* at the leaf base. Thus in this instance regulatory evolution coupled with gene duplication had a major role in generating evolutionary change. The next question the paper addresses is how the RCO protein influences morphogenesis to modify leaf shape. This was done through development of advanced time lapse imaging methods that allowed tracking tissue growth through development. This work revealed that RCO acts locally at the base of leaflets to repress growth, thus facilitating their separation and growing out as distinct units. Phylogenetic analysis coupled with transgenic work demonstrated that this growth repressive potential was already present before the appearance of *RCO* in the *Brassicaceae*, and probably before the split of eudicots from other seed plants. In conclusion, this study provides a nice example of how a combination of developmental genetics, evolutionary biology and advanced imaging can help understand which are the causal genetic changes underlying diversification of plant form and how those are translated to phenotypic differences through the process of morphogenesis.

TOC

Impact on Applied Research and Industry

Within the last 20 years Arabidopsis was established as reference plant for basic and applied research 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 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 Arabidopsis and plant biology in general.

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 patent applications. 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 13,700 utility patents referring to Arabidopsis were published compared to more than 49,900 on rice and 102,800 on maize (Figure 4A). But the success of Arabidopsis as non-agricultural plant is tremendous and increasing, having published 1,684 utility patent in 2014 compared to 23 in 1994 in the U.S. The trend in published applications in Europe was comparable to the U.S. until 2011, when the general situation for especially genetically modified crops became more difficult in Europe and the trend was reversed (Figure 4B). Last year the number of applications in Europe fell to the level of 2009, being 122 applications referring to Arabidopsis, 929 to rice and 1,391 to maize. Interestingly, a decrease in international patent applications was also observed in 2012 and 2013

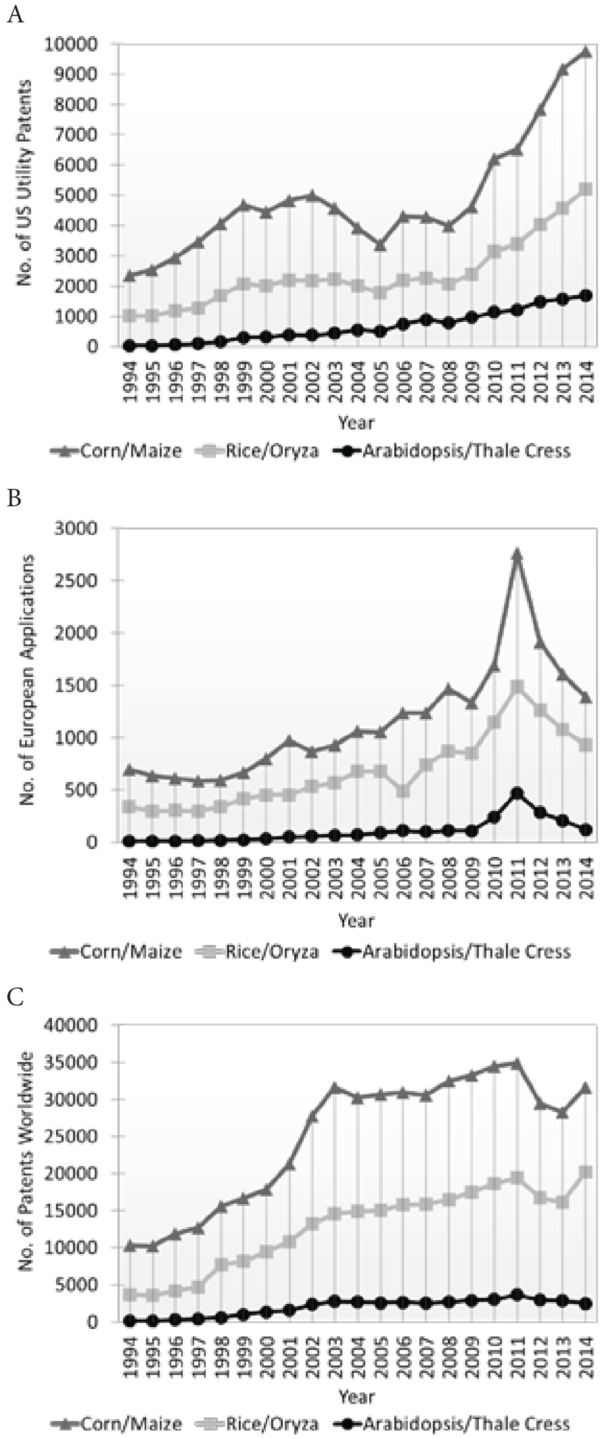

Figure 4. Trends of patents referencing model organisms (maize, oryza, Arabidopsis) from 1994 until 2014; (A) number of utility patents in the United States; (B) number of published applications in Europe; (C) number of patents worldwide, Patent and Cooperation Treaty applications (PCT) according to the World Intellectual Property Organization (WIPO, 187 contracting states).

Searches were performed (2014-05-05): A) http://patft.uspto.gov/netahtml/PTO/search-adv.htm, e.g. query: SPEC/rice OR SPEC/oryza AND ISD/20140101->20141231; B) http://worldwide.espacenet.com/advancedSearch?locale=en_EP, select EP collection, e.g.: Keyword(s) in full text: rice OR oryza, Publication date: 2014; C) http://patentscope.wipo.int/search/en/structuredSearch.jsf, select any field, e.g. English all: rice OR oryza, Publication date: 2014.

(PCT-WIPO, 187 contracting states, Figure 4C). In 2014 this trend seemed to be reverted again being positive for rice and corn. The general trend of European and International filed applications was constantly positive over the last 20 years for Arabidopsis, rice and corn. Since 1994 a total of 41,945 international patent applications were published referring to Arabidopsis compared to 266,834 on rice and 522,833 on maize. More and more applications take Arabidopsis into account and the number of international patents referring to Arabidopsis increased by 16-fold within 20 years (1994 -151 patents, 2014 - 2,479).

Patents on corn and rice naturally far exceed those citing Arabidopsis, but the translation of Arabidopsis knowledge and technologies to crop species should not be underestimated. A plethora of laboratories around the world study Arabidopsis and crop species in parallel. Arabidopsis is often the first choice 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 a basic understanding of plant processes in order to leverage applied studies with other plant species to finally face the current challenges in agriculture. 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.

On vacation - Improving drought tolerance in petunia

Estrada-Melo AC, Ma C, Reid MS and Jiang C-Z (2015) Overexpression of an ABA biosynthesis gene using a stress-inducible promoter enhances drought resistance in petunia. Horticulture Research 2, 15013.

An important trait for ornamental plants like petunia is to increase drought tolerance or in other words - your balcony plants will survive, even if you forget to water them for one or two weeks. Two research groups from the US recently published their work on transgenic petunia with an increased drought resistance phenotype. The researcher therefore employed a well characterized stress inducible promoter *rd29A* from Arabidopsis to drive expression of a rate-limiting enzyme in abscisic acid (ABA) hormone biosynthesis from tomato called 9-cis-epoxycarotenoid dioxygenase (NCED). Previous studies in Arabidopsis, tomato and tobacco already showed that constitutive over expression of NCED led to ABA accumulation and increased drought resistance. The downside of these studies were the severe phenotypic defects like stunted growth and low germination rates. Expression of the enzyme in leaves only helped to overcome the seed dormancy effect but did not reduce the pleiotropic growth defects.

Estrada-Melo and colleagues decided to use a strong but stress only inducible promoter to drive expression of tomato NCED and were successful. First experiments with three independent petunia transgenic lines revealed that these lines displayed the wild type phenotype including robust germination rates. Next the authors tested the recovery rate of 6 week old plants; after two weeks without watering only 11% of the wild type plants recovered, whereas 94.4% of the *Atrd29A:LeNCED1* survived. In additional experiments the authors could show that the transgenic plants lost 50% less water compared to wild type and only after drought stress the *Le*NCED1 transcript was detectable in leaves. After three days without watering physiological parameters were significant but much more subtle, like CO_2 assimilation rate, leaf conductance, transpiration rate, and stem water potential. The ABA and Proline content, markers for drought resistance were much higher under drought stress in transgenic versus wild type plants.

It can be expected that the transferability of this system to other crop species and experiments under field conditions will be done soon. This work is a great example how powerful biotechnology in plants can be and the more processes we understand the more success we can expect from projects like this.

Sweet sweet sugar beet

Jung B, Ludewig F, Schulz A, Meißner G, Wöstefeld N, Flügge U, Pommerrenig B, Wirsching P, Sauer N, Koch W, Sommer F, Mühlhaus T, Schroda M, Cuin TA, Graus D, Marten I, Hedrich R, Neuhaus HE (2015) Identification of the transporter responsible for sucrose accumulation in sugar beet taproots. Nature Plants 1, 14001.

Sucrose from natural sources like sugar beet and sugar cane is the most important sugar of the world being used for food, consumables and biofuel production. From sugar beet alone one third of the consumed sugar is produced. Sugar beet breeding efforts during the last two centuries led to a 4.5 fold increase of sugar content in the roots of up to 18% fresh weight. The main sucrose storage compartment in the root cells are the vacuoles. Although the transportation route of sucrose from cells in the leaf via the phloem to cells in the root is understood quite well, it remained unknown so far, which transporter(s) are responsible for the transport of sucrose into the vacuoles of sugar beet root cells.

Researchers from Germany and KWS recently identified this missing link by using proteomics of sugar beet tonoplasts. Besides already known subunits of H^+-ATPase amongst the top 50 candidates in two independent experiments was a protein similar to Arabidopsis tonoploast monosaccharide transporter 2 (*At*TMT2). The authors identified four orthologous in *Beta vulgaris* and named these tonoplast sugar transporter family (*BvTST1*, *2.1*, *2.2* and *3*). Subsequent experiments in Arabidopsis verified that the identified protein *Bv*TST2.1 is incorporated in the vacuolar membrane and its transcript level is highly upregulated in the *Beta vulgaris* high yielding variety Belladonna (KWS) compared to a low-sucrose containing variety. To finally proof that *Bv*TST2.1 is capable of transporting sucrose into the vacuole experiments with intact vacuoles from transiently transformed tobacco leaf cells were performed. These patch clamp experiments were done under various pH conditions and it was shown that *Bv*TST2.1 is a specific proton-sucrose antiporter that exports protons from the vacuole while importing sucrose into the vacuole. In contrast the homolog *Bv*TST1 had a low substrate specificity of sucrose compared to glucose. The sucrose import specificity of *Bv*TST2.1 was further verified by failing to complement the Arabidopsis tonoplast glucose transporter mutants *Attst1* phenotype.

The above summarized experiments revealed the first sucrose-specific proton antiporter. The low abundance of sugar tonoplast transporters in Arabidopsis partially explains, why the TST family was not identified before. This example shows that Arabidopsis is a perfect model to test specific hypothesis alongside other model organisms. More research has to be done to find out, if the sugar concentration in sugar beet can be increased even more due to this finding. At the very least these findings will help sugar beet breeders with targeted selection of breeding approaches.

It takes two for resistance against pathogens

Narusaka M, Hatakeyama K, Shirasu K, Narusaka Y (2014) Arabidopsis dual resistance proteins, both RPS4 and RRS1, are required for resistance to bacterial wilt in transgenic Brassica crops. Plant Signaling & Behavior, 9:e29130.

Many known mechanism in plant pathogen defense were discovered first in Arabidopsis. Although many examples exist, where defence related genes from Arabidopsis did not mediate pathogen resistance in other plant species, we still might expect to see more examples in future. This can be concluded from the work by a Japanese research group around Yishihiro Narusaka published in 2014.

Already in 2009 the group discovered that two disease resistance (R) genes of the Toll/interleukin-1 receptor (TIR)-NLR class, called RRS1 and RPS4 funtion together and are required for effector-triggered immunity in Arabdiopsis. In the genome of the Arabidopsis ecotype Wassilewskija on Chromosome 5 RPS4 and RRS1 are arranged head-to-head. Narusaka and colleagues generated two independent constructs of RPS4 and RRS1 and transformed these individually or simultaneously into a relative of Arabidopsis *Brassica rapa* var. *perviridis* (Japanese Mustrard Spinach). The transgenic plants were indistinguishable from wildtype and exhibited no differential expression of a defense-related marker gene. Next they inoculated the roots of *Brassica rapa* with a *Ralstonia solanacearum* cultivar expressing the PopP2 effector, which is recognized by RRS1. Interestingly, the bacterial growth was reduced about 10-fold in transgenic plants carrying both R genes compared to wildtype. Also they saw that 7 to 10 days after inoculation wildtype plants were completely wilted, whereas the transgenic plants with both R genes were vital. Already 4 days after inoculation wilting could be observed in single transformants and wildtype but not in RRS1/RPS4 expressing plants. To show specificity they also inoculated *Brassica rapa* with a *Ralstonia solanacearum* cultivar lacking the PopP2 effector, which resulted in a comparable phenotype in all three transgenic plants and wildtype.

Thus the authors conclude, that Arabidopsis is at the very least a great model to understand plant defense mechanisms but also an excellent tool to identify new ways to engineer Brassica crops. Already six other R gene pairs are assumed to work only together but not alone. It can be expected that there are many more R gene pairs that need to be discovered thus, bearing the potential to be used to enhanced pathogen resistance in crops.

New attempts to engineer plant photosynthesis

Giraldo JP, Landry MP, Faltermeier SM, McNicholas TP, Iverson NM, Boghossian AA, Reuel NF, Hilmer AJ, Sen F, Brew JA, Strano MS (2014) Plant nanobionics approach to augment photosynthesis and biochemical sensing. Nature Materials 13.

In recent years the development of nanomaterials in pure and reasonable amounts became feasible, which today fuels a new applied research field covering the interface between physics, chemistry and biology. The basic idea behind these research approaches is to engineer cellular functions by synthetic materials. A quite promising new nanomaterial are single-walled carbon nanotubes (SWNT). This are nanomolecular tubes consisting of a single layer of carbon atoms. Different kind of SWNTs, like metal and semiconductor tubes with unique characteristics, can be produced.

Last year Giraldo and colleagues published a completely new attempt to engineer and augment plant photosynthesis by using carbon nanotubes. Their principle idea is to transfer nanotubes into the inner membrane of plant chroloplasts in order to widen the absorption spectra of the antennae complexes by the infrared spectrum, to increase electron transportation rate and thus, in the end sugar production. To test this hypothesis they first had to show that the nanotubes are delivered fast and directional into the chloroplast. Giraldo and colleagues demonstrated in chloroplast isolates from spinach that semiconductor nanotubes spontaneously assemble within the chloroplasts, when preincubated with charged molecules like single stranded (ss) DNA or chitosan. This delivery mechanism was so far unknown and seems to be quite robust. To further test this they infiltrated Arabidopsis leaves with a ssDNA coated nanotube solution and could show that the nanotubes co-localize with chloroplasts and these leaves exhibited a unique near-infrared fluorescence spectrum. The life span of the nanotube versus mock infiltrated leaf was comparable, suggesting that there is no negative effect on plant senescence. One of the most interesting results was that the maximum electron transport rate was about 30% increased compared to mock treated leaves.

The final proof that carbon nanotubes might increase photosynthesis efficiency is still lacking because biomass or sugar content was not measured, and of cause environmental risks have to be assessed before engineered plants like these can become available. Nevertheless, the approach opens a new applied research field, where model plants like Arabidopsis can be very useful. The researchers do not only think of higher plants but also they see application of nanotubes in engineering algae and besides engineering of photosynthesis they foresee the use of nanomaterials to develop nanosensors in plants because a variety of substances can be added to the nanotubes.

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Country Reports of the International Arabidopsis Community

Country Highlights

Argentina

- Petrillo et al. (2014) A chloroplast retrograde signal regulates nuclear alternative splicing. Science.
- The 11th International Plant Molecular Biology Congress will be held in Iguazú Falls, at the border of Argentina and Brazil

Austria

- 4 ERA CAPS projects awarded funding in 2014 and 2 new ERC grants awarded funding in 2015
- Chen X et al. (2014) Inhibition of cell expansion by rapid ABP1-mediated auxin effect on microtubules. Nature.

Belgium

- Belgian national research project focusing on how root and shoot influence each other (http://.iuap-mars.be/)
- Vanhaeren H et al. (2014) Combining growth-promoting genes leads to positive epistasis in *Arabidopsis thaliana*. Elife.

Canada

- Genome Canada-funded grant to develop modules for the NSF-funded Arabidopsis Information Portal, (www.Araport.org)
- The Bio-Analytic Resource for Plant Biology (http://bar.utoronto.ca/welcome.htm)

Czech Republic

- Komis G et al. (2014) Dynamics and organization of cortical microtubules as revealed by superresolution structured illumination microscopy. Plant Physiology.
- Kouřil R et al. (2014) Structural characterization of a plant photosystem I and NAD(P)H dehydrogenase supercomplex. The Plant Journal.

Denmark

- Cho SK et al. (2014) COP1 E3 ligase protects HYL1 to retain microRNA biogenesis. Nat Commun.
- Mravec J et al. (2014) Tracking developmentally regulated post-synthetic processing of homogalacturonan and chitin using reciprocal oligosaccharide probes. Development.

Finland

- A phenomics facility is currently being built at the Viikki campus of the University of Helsinki (ready by mid 2015).
- Furuta KM et al. (2014) Arabidopsis NAC45/86 direct sieve element morphogenesis culminating in enucleation. Science.

ICAR 2015 PARIS - FRANCE

France

- The French society of Plant Biology (SFBV) together with members of the Saclay Plant Science LabEx are organizing the 26th ICAR at the Palais des Congrès in Paris, 5th-9th July 2015
- Ariel F et al. (2014) Noncoding transcription by alternative RNA polymerases dynamically regulates an auxin-driven chromatin loop. Molecular Cell.

Germany

- New AFGN website at: http://www.dbg-afgn.de and new mailing list at https://listserv.uni-tuebingen.de/mailman/listinfo/afgn.
- Fuentes I et al. (2014) Horizontal genome transfer as an asexual path to the formation of new species. Nature.

Greece

- Project to translate knowledge gained from Arabidopsis: H2020-MSCA-RISE-2014 “Bioresources For Oliviculture” (BeFOre)
- Kemen AC et al. (2014) Investigation of triterpene synthesis and regulation in oats reveals a role for β-amyrin in determining root epidermal cell patterning. PNAS USA.

TOC

India

- Sethi V et al. (2014) A mitogen-activated protein kinase cascade module, MKK3-MPK6 and MYC2, is involved in blue light-mediated seedling development in Arabidopsis. Plant Cell.
- Singh A et al. (2014) Balanced activity of microRNA166/165 and its target transcripts from the class III homeodomain leucine-zipper family regulates root growth in Arabidopsis thaliana. Plant Cell Rep.

Israel

- The I-Core Plant Adaptation to Changing Environment includes Arabidopsis and crop research, brings together plant biologists and computer scientists
- Two new Arabidopsis research labs were established by young PIs: Eilon Shani, Tel Aviv University and Assaf Mosquna, The Hebrew University of Jerusalem

Italy

- Heidstra R, Sabatini S (2014) Plant and animal stem cells: similar yet different. Nat Rev Mol Cell Biol.
- Researchers will participate with an outreach program on plant development and agro-biodiversity conservation in the EXPO 2015 in Milan

Japan

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

Netherlands

- Mähönen AP et al. (2014) PLETHORA gradient formation mechanism separates auxin responses. Nature.
- De Rybel, B et al. (2014) Integration of growth and patterning during vascular tissue formation in Arabidopsis. Science 345.

New Zealand

- Laing WA et al. (2015) An upstream open reading frame is essential for feedback regulation of ascorbate biosynthesis in Arabidopsis. Plant Cell.
- Brownfield L et al. (2015) Organelles maintain spindle position in plant meiosis. Nature Communication.

South Korea

- 27th ICAR will be hosted by Inhwan Hwang and the local organizing committee in GyeongJu in June 29th-July 3rd, 2016

ICAR 2016 KOREA GyeongJu

- Kim DH et al. (2014). An ankyrin repeat domain of AKR2 drives chloroplast targeting through coincident binding of two chloroplast lipids. Dev Cell.

Spain

- Monte I et al. (2014) Rational design of a ligand-based antagonist of jasmonate perception. Nat Chem Biol.
- ICREA Workshop: From model system to crops, challenges for a new era in Plant Biology was held on 7-8 May 2014 in Barcelona

Sweden

- Swedish Plant Scientists formulate an agenda on 'Plant Biotechnology for a Bio-based Economy'
- Plant Biology Scandinavia 2015, the 26th Congress of the Scandinavian Plant Physiology Society (SPPS) will be held in Stockholm 2015

Switzerland

- SwissPlant Symposium 2015, Leukerbad, Switzerland, 28-30 Jan 2015
- Vermeer JE et al. (2014) A spatial accommodation by neighboring cells is required for organ initiation in Arabidopsis. Science.

United Kingdom

- GARNet, the national network for Arabidopsis and the wider plant science research community, was awarded renewed funding to continue serving the community until 2020.
- UK awarded BBSRC funding to create iPlant UK; high performance computing-based cyberinfrastructure for sharing, storing and analysing 'big' plant science data.

United States

- ICAR 2014 was organized by the North American Arabidopsis Steering Committee in Vancouver, Canada
- NAASC received an NSF grant to fund 'Arabidopsis Research and Training for the 21st Century (ART-21)'
- Araport, the new Arabidopsis Information Portal, launched this past year

Argentina

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

General Activities

Arabidopsis Research Facilities

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

Current Arabidopsis Projects

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

Conferences and Workshops

- The 16th International congress of Photobiology was held in Córdoba, Argentina, 8-12 September 2014, with strong participation of Arabidopsis researchers.
- The 11th International Plant Molecular Biology Congress will be held in Iguazú Falls, at the border of Argentina and Brazil, and organized by a bi-national Argentine-Brazil Committee.

Selected Publications

- Heteromerization of PIP aquaporins affects their intrinsic permeability. Yaneff A, Sigaut L, Marquez M, Alleva K, Pietrasanta LI, Amodeo G. (2014) Proc Natl Acad Sci U S A. 111(1):231-6.
- A chloroplast retrograde signal regulates nuclear alternative splicing. Petrillo E, Godoy Herz MA, Fuchs A, Reifer D, Fuller J, Yanovsky MJ, Simpson C, Brown JW, Barta A, Kalyna M, Kornblihtt AR. (2014) Science. 344(6182):427-30.
- Role for LSM genes in the regulation of circadian rhythms. Perez-Santángelo S, Mancini E, Francey LJ, Schlaen RG, Chernomoretz A, Hogenesch JB, Yanovsky MJ. (2014) Proc Natl Acad Sci U S A. 111(42):15166-71.
- The transcriptional regulator BBX24 impairs DELLA activity to promote shade avoidance in *Arabidopsis thaliana*. Crocco CD, Locascio A, Escudero CM, Alabadí D, Blázquez MA, Botto JF. (2015) Nat Commun. 6:6202.
- The Arabidopsis DNA Polymerase δ Has a Role in the Deposition of Transcriptionally Active Epigenetic Marks, Development and Flowering. Iglesias FM, Bruera NA, Dergan-Dylon S, Marino-Buslje C, Lorenzi H, Mateos JL, Turck F, Coupland G, Cerdán PD. (2015) PLoS Genet. 11(2):e1004975.

Major Funding Sources

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

Austria

Marie-Theres Hauser (marie-theres.hauser@boku.ac.at) University of Natural Resources and Life Sciences, Vienna and with input from the Austrian Arabidopsis community

General Activities

Arabidopsis Research Facilities

University of Natural Resources & Life Science Vienna (BOKU), Department of Applied Genetics & Cell Biology (DAGZ) (www.dagz.boku.ac.at/en/)

Gregor Mendel Institute of Molecular Plant Biology (GMI) (www.gmi.oeaw.ac.at/)

Max F. Perutz Laboratories (MFPL) (www.mfpl.ac.at/)

Plant Sciences Facility, Campus Science Support Facilities GmbH (CSF) (www.csf.ac.at/plants)

Institute of Science and Technology, Austria (IST Austria) (www.ist.ac.at/en/)

University of Salzburg, Division of Plant Physiology (www.uni-salzburg.at/index.php?id=32701&L=1)

Research Groups

- Population Genetics

Magnus Nordborg (www.gmi.oeaw.ac.at/research-groups/magnus-nordborg): genetic basis of adaptation.

- Molecular Biology and Signaling

Andrea Pitzschke (www.uni-salzburg.at/index.php?id=67501&L=1): Stress signaling and Mitogen-Activated Protein Kinases; Andreas Bachmair (www.mfpl.ac.at/mfpl-group/group/bachmair.html): Protein biochemistry, posttranslational modification; Claudia Jonak (www.gmi.oeaw.ac.at/research-groups/claudia-jonak): Stress signal transduction and cellular responses

- Chromosome Biology

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

- Epigenetics

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

- Development

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

- Molecular Genetics & Cell Biology

Marie-Theres Hauser (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-hauser): development, stress; Lindy Abas (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-abas): membrane proteins, hormone transport; Jürgen Kleine Vehn (www.dagz.boku.ac.at/arbeitsgruppen/team-kleine-vehn/): phytohormonal crosstalk, differential growth regulation; Barbara Korbei (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-korbei): Role of TOL proteins in post-Golgi trafficking in *Arabidopsis thaliana*

- Glycobiology

Richard Strasser (www.dagz.boku.ac.at/en/abteilung-fuer-molekulare-zellbiologie-und-glykobiotechnologie/ag-strasser): Function of N-glycans; Doris Lucyshyn (www.dagz.boku.ac.at/en/abteilung-fuer-pflanzengenetik-und-zellbiologie/ag-abas/projekt-lucyshyn): O-GlcNAcylation

- RNA Metabolism

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

- Plant Pathogen Interaction

Youssef Belkhadir (www.gmi.oeaw.ac.at/research-groups/youssef-belkhadir): Plant cell signalling at the interface of growth and defences; Armin Djamei (www.gmi.oeaw.ac.at/research-groups/armin-djamei): Effectomics - exploring the toolbox of plant pathogens; Raimund Tenhaken (www.uni-salzburg.at/index.php?id=32790&L=1): Nucleotide sugars biosynthesis and function

Current Arabidopsis Projects

SFB projects

since 2010 “RNA Regulation of the transcriptome” SFB 43 (www.mfpl.ac.at/rna-biology/focus-regulatory-rna/)

since 2008 "Chromosome Dynamics“ SFB 34 (www.mfpl.ac.at/research/research-networks/chromosome-dynamics.html)

Doctoral programmes financed by the FWF

- since 2012 "Chromosome Dynamics" (www.mfpl.ac.at/training/phd-opportunities/doctoral-program-chromosome-dynamics.html)
- since 2010 "Biomolecular Technology of Proteins - BioToP" (biotop.boku.ac.at/)
- since 2006 "RNA biology" (www.mfpl.ac.at/rna-biology/doctoral-program)
- 2013-2017 "CALIPSO - Calcium and Light Signals in Photosynthetic Organisms" (itn-calipso.univie.ac.at/)
- 2013–2017 "COMREC: Control of Meiotic Recombination: Arabidopsis to Crops" (www.birmingham.ac.uk/comrec)

ERA-CAPS projects

- 2014-2017 "The role of the N-end rule pathway in controlling plant response to the environment (N-vironment)" (www.eracaps.org/joint-calls/era-caps-funded-projects/era-caps-first-call-%E2%80%93-2012/role-n-end-rule-pathway-controlling)
- 2014-2017 "Delineating the crossover control networks in plants (DeCOP)" (www.eracaps.org/joint-calls/era-caps-funded-projects/era-caps-first-call-%E2%80%93-2012/delineating-crossover-control)
- 2014-2017 "Dimorphic fruits, seed and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments (SeedAdapt)" (www.eracaps.org/joint-calls/era-caps-funded-projects/era-caps-first-call-%E2%80%93-2012/dimorphic-fruits-seeds-and-seedlings)
- 2014-2017 "European Plant Embryology Consortium (EURO-PEC)" (www.eracaps.org/joint-calls/era-caps-funded-projects/era-caps-first-call-%E2%80%93-2012/european-plant-embryology-consortium)

European Science Foundation

- 2010 – 2015 "EPICOL – Ecological and evolutionary plant epigenetics" (www.esf.org/coordinating-research/eurocores/completed-programmes/euroeefg/projects/epicol.html)

Commission of the European Communities FP7

- 2011–2015 "Trans-national infrastructure for plant genomic science" (www.transplantdb.eu/)
- 2011–2016 "ERC Advanced Grant: MAXMAP: Developing maximum-resolution genotype-phenotype maps using whole-genome polymorphism data" (cordis.europa.eu/project/rcn/98994_en.html)
- 2014–2019 "ERC Starting Grant: EFFECTOMICS: elucidating the toolbox of plant pathogens" (http://cordis.europa.eu/project/rcn/110437_en.html)
- 2015-2020 "ERC Starting Grant: sRNA-EMB: Small RNA regulation of the body plan in Arabidopsis embryos"
- 2012-2017 "ERC consolidator grant: PSDP: Polarity and subcellular dynamics in plants" (cordis.europa.eu/project/rcn/100844_en.html)
- 2015-2020 "ERC starting grant: AuxinER: Mechanism of Auxin-dependent Signaling in the Endoplasmatic Reticulum" (Project Nr. 639478)

WWTF projects

- 2014-2018 "Quantitative Live Imaging to Determine the Regulatory Impact of Chromatin Dynamics" (wwtf.at/projects/research_projects/details/index.php?PKEY=4148_DE_O&lang=EN)
- 2011-2018 "Plant Cell and Molecular Biology" (www.wwtf.at/projects/research_groups/details/index.php?PKEY=1328_DE_O&lang=EN)

Road Map Related Activities

Arabidopsis Tools and Resources

- GWAPP: A Web Application for Genome-wide Association Mapping in *A. thaliana* (as part of the 1001 Genomes)
- PoolHap: Software for Inferring Haplotype Frequencies from Pooled Samples
- BRAT: Root Phenotyping Pipeline
- CyMATE: Cytosine Methylation Analysis Software
- CSF-ProTech: CRISPR/Cas9 service center (www.csf.ac.at/facilities/protein-technologies)
- CSF-Plant Sciences: Automated, high-throughput phenotyping and environmental simulation (www.csf.ac.at/plants)
- IST Austria: Light sheet (SPIM) microscope for Arabidopsis, Vertical confocal microscope allowing automatic tracking of the root growth
- Andreas Bachmair: Mutants lacking different ubiquitin ligases or SUMO ligases, Protocols for in vitro conjugation of SUMO
- Maria Kalyna: Pipeline for RNA-Sequencing data analysis with focus on alternative splicing in plants

Outreach Activities

- GMI Movie Night: screening of 2 documentaries on plants for the general public
- Long Night of Research
- Uni Salzburg: Stress experiments with pupils
- IST Austria: Open campus day
- Austrian children university (www.kinderuni.at)
- Vienna daughters day (www.toechtertag.at)

Conferences and Workshops

- VBC PhD Symposium 2014 "Complexity of Life - the quality of being complicated" (www.gmi.oeaw.ac.at/events/event-detail/12th-annual-vbc-phd-programme-symposium-complexity-of-life-the-quality-of-being-complicated)
- VBC Summer School: high school students from around the world invited to take part in research at the GMI (www.vbcphdprogramme.at/summer-school)
- GMI Career Day 2014: career tracks for scientist (www.gmi.oeaw.ac.at/events/event-detail/gmi-career-day-2014-sept-16)
- 2014 ATSPB meeting Lunz,(www.atspb.org/)

- Sept. 2015: Plant EMBO meeting, Brno
- Viennese Plant Networkers Meetings, 29.4.2014, 13. 2. 2015 and 27.11.2015

Selected Publications

- A DEK Domain-Containing Protein Modulates Chromatin Structure and Function in Arabidopsis. Waidmann S, Kusenda B, Mayerhofer J, Mechtler K, Jonak C (2014) Plant Cell 26(11): 4328-4344.
- Quantitative Phosphoproteomics of the ATM and ATR dependent DNA damage response in *Arabidopsis thaliana*. Roitinger E, Hofer M, Köcher T; Pichler P, Novatchkova M, Yang J, Schlögelhofer P, Mechtler K (2015) Mol Cell Proteomics 14(3):556-571.
- Arabidopsis PIAL1 and 2 promote SUMO chain formation as E4 type SUMO ligases, and are involved in stress responses and sulfur metabolism. Tomanov K, Zeschmann A, Hermkes R, Eifler K, Ziba I, Grieco M, Novatchkova M, Hofmann K, Hesse H, Bachmair A (2014) Plant Cell 26: 4547-4560.
- Auxin regulates SNARE-dependent vacuolar morphology restricting cell size. Löfke C, Dünser K, Scheuring D, Kleine-Vehn J. (2015) Elife. doi: 10.7554/eLife.05868
- Inhibition of cell expansion by rapid ABP1-mediated auxin effect on microtubules. Chen X, Grandont L, Li H, Hauschild R, Paque S, Abuzeineh A, Rakusová H, Benkova E, Perrot-Rechenmann C, Friml J. (2014) Nature 4;516(7529):90-3.

Major Funding Sources

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

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

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

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

OeAD www.oead.at/projects_cooperations/EN/

Belgium

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

Current Arabidopsis Projects

Belgian Arabidopsis projects are funded by university-, regional- 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 inter- national 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, to Moritz Nowack to study programmed cell death in plant reproduction, and to D. Van Der Straeten to study mitochondrial editing factors.

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

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

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

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

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

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

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

Other developed resources include:

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

Conferences and Workshops

- Plant Organ Growth Symposium, Gent March 2015, http://www.psb.ugent.be/plantorgangrowthsymposium/

Selected Publications

- The Arabidopsis abiotic stress-induced TSPO-related protein reduces cell-surface expression of the aquaporin PIP2;7 through protein-protein interactions and autophagic degradation. Hachez C, Veljanovski V, Reinhardt H, Guillaumot D, Vanhee C, Chaumont F, Batoko H. (2014) Plant Cell. 26(12):4974-90.
- An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. Van Leene J, Eeckhout D, Cannoot B, De Winne N, Persiau G, Van De Slijke E, Vercruysse L, Dedecker M, Verkest A, Vandepoele K, Martens L, Witters E, Gevaert K, De Jaeger G (2015) Nat Protoc. 10(1):169-87.
- Combining linkage and association mapping identifies RECEPTOR-LIKE PROTEIN KINASE1 as an essential Arabidopsis shoot regeneration gene. Motte H, Vercauteren A, Depuydt S, Landschoot S, Geelen D, Werbrouck S, Goormachtig S, Vuylsteke M, Vereecke D (2014) Proc Natl Acad Sci U S A. 111(22):8305-10.
- Combining growth-promoting genes leads to positive epistasis in *Arabidopsis thaliana*. Vanhaeren H, Gonzalez N, Coppens F, De Milde L, Van Daele T, Vermeersch M, Eloy NB, Storme V, Inzé D (2014) Elife. 3:e02252.
- Programmed cell death controlled by ANAC033/SOMBRERO determines root cap organ size in Arabidopsis. Fendrych M, Van Hautegem T, Van Durme M, Olvera-Carrillo Y, Huysmans M, Karimi M, Lippens S, Guérin CJ, Krebs M, Schumacher K, Nowack MK (2014) Curr Biol. 24(9):931-40.

Major Funding Sources

Flanders Institute for Biotechnology (VIB; www.vib.be)

European Union Framework Programs (cordis.europa.eu/)

Belgian Federal Science Policy Office (www.belspo.be)

Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; www.iwt.be)

Research Foundation – Flanders (FWO; http://www.fwo.be/en/index.aspx)

Fonds de la Recherche Scientifique (FNRS, http://www.frs-fnrs.be)

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

Canada

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General Activities

Arabidopsis Research Facilities

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

The Bio-Analytic Resource for Plant Biology (http://bar.utoronto.ca/welcome.htm)

Current Arabidopsis Projects

A Genome Canada-funded grant to Nicholas Provart, Stephen Wright and 8 others to develop modules for the NSF-funded Arabidopsis Information Portal, Araport.org. The first two modules of transcriptomics and protein-protein interactions were released on Araport.org in March 2015. 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. Modules for expressologs/synteny, protein structures, and visualization will be delivered to Araport in the coming year.

Outlook on Arabidopsis Research

Funding for basic Arabidopsis research is largely from the Natural Sciences and Engineering Council of Canada, which funds university, industrial and organizational research. The total NSERC budget has hovered around CAD $1 billion for the past 7 years. In 2014 the Discovery Grants program, which funds basic research, saw an increase of about 5%. In general however, funding for plant research, compared with all other NSERC funded research, has continued to drop since 2009.

Major Funding Sources

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

Genome Canada (http://www.genomecanada.ca/en/)

Czech Republic

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General Activities

Arabidopsis Research Facilities

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

In Brno

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

In Olomouc

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

In České Budějovice

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

In Prague

Institute of Experimental Botany (http://www.ueb.cas.cz/en); Charles University in Prague (http://kfrserver.natur.cuni.cz/english/index.html)

Current Arabidopsis Projects

Arabidopsis research in the Czech republic is funded mostly on the individual grants basis. In 2014 Department of Experimental plant biology at the Charles University was granted a "Center of plant experimental biology, Charles University" project supported by Minsitry of Education. 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

Due to plant research infrastructure development funded by the EU over last several years it is to be expected that Arabidopsis driven reasearch will be very important in the Czech republic - in coming years it will be important, that Czech governement will sustain the momentum brought about by the EU funding. It is expected that in coming years Arabidopsis research in Czech republic will be further stably well supported mostly on the individual projects level.

Road Map Related Activities

Arabidopsis Tools and Resources

BRNO - CEITEC - Central European Institute of Technology, Proteomics Core Facility (http://www.ceitec.eu/ceitec-mu/proteomics-core-facility/z8): The Core Facility is part of Czech National Affiliated Centre of INSTRUCT. All CEITEC core facilities are available to external users (academia and companies). Czech and international researchers from universities and research institutes interested in accessing core facilities can benefit from support of CEITEC – open access project funded by the Ministry of Education, Youth and Sports of the Czech Republic.

Outreach Activities

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

Conferences and Workshops

- International symposium "Auxins and Cytokinins in Plant Development" was held in Prague June 29 - July 4, 2014 (http://www.acpd2014.org/)
- Young scientists meeting "12th PhD student conference of plant experimental biology" was held in Olomouc September 4 - 5, 2014 (http://www.kebr2014.cz/registration.html)
- Young scientists meeting "Trends in natural products research 2014" was held in Olomouc, June 23 - 25, 2014 , 2014 (http://www.tnpr2014.com/)

Selected Publications

- Compromised telomere maintenance in hypomethylated *Arabidopsis thaliana* plants. Ogrocká A, Polanská P, Majerová E, Janeba Z, Fajkus J, Fojtová M. (2014) Nucleic Acids Research 42 (5):2919-2931.
- Telomere repeat binding proteins are functional components of Arabidopsis telomeres and interact with telomerase. Procházková Schrumpfová P, Vychodilová I, Dvořáčková M, Majerská J, Dokládal L, Schořová Š, Fajkus J (2014) The Plant Journal 77(5):770-781.
- Involvement of YODA and mitogen activated protein kinase 6 in Arabidopsis post-embryonic root development through auxin up-regulation and cell division plane orientation. Smékalová V, Luptovčiak I, Komis G, Šamajová O, Ovečka M, Doskočilová A, Takáč T, Vadovič P, Novák O, Pechan T, Ziemann A, Košútová P, Šamaj J (2014) New Phytologist 203(4):1175-1193.
- Dynamics and organization of cortical microtubules as revealed by superresolution structured illumination microscopy. Komis G, Mistrík M, Šamajová O, Doskočilová A, Ovečka M, Illés, Bartek J, Šamaj J (2014) Plant Physiology 165(1):129-148.
- Structural characterization of a plant photosystem I and NAD(P)H dehydrogenase supercomplex. Kouřil R, Strouhal O, Nosek L, Lenobel R, Chamrád I, Boekema EJ, Šebela M, Illík P (2014) The Plant Journal 77(4):568-576.

Major Funding Sources

The major funding agencies for basic research 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 (MSMT CR, http://www.msmt.cz/research-and-development-1)

Targeted or applied research is since recently supported also by the Technology Agency of the Czech Republic (TACR) and Arabidopsis model is accepted as a driver for applications.

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

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

Denmark

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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 initiatíve 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

- COP1 E3 ligase protects HYL1 to retain microRNA biogenesis. Cho SK, Ben Chaabane S, Shah P, Poulsen CP, Yang SW (2014) Nat Commun. 5:5867.
- Tracking developmentally regulated post-synthetic processing of homogalacturonan and chitin using reciprocal oligosaccharide probes. Mravec J, Kračun SK, Rydahl MG, Westereng B, Miart F, Clausen MH, Fangel JU, Daugaard M, Van Cutsem P, De Fine Licht HH, Höfte H, Malinovsky FG, Domozych DS, Willats WG (2014) Development 141(24):4841-50.
- Receptor kinase-mediated control of primary active proton pumping at the plasma membrane. Fuglsang AT, Kristensen A, Cuin TA, Schulze WX, Persson J, Thuesen KH, Ytting CK, Oehlenschlæger CB, Mahmood K, Sondergaard TE, Shabala S, Palmgren MG (2014) Plant J. 80(6):951-64.
- A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in *Arabidopsis thaliana*. Lindemose S, Jensen MK, Van de Velde J, O'Shea C, Heyndrickx KS, Workman CT, Vandepoele K, Skriver K, De Masi F (2014) Nucleic Acids Res. 42(12):7681-93.
- Arabidopsis accelerated cell death 11, ACD11, is a ceramide-1-phosphate transfer protein and intermediary regulator of phytoceramide levels. Simanshu DK, Zhai X, Munch D, Hofius D, Markham JE, Bielawski J, Bielawska A, Malinina L, Molotkovsky JG, Mundy JW, Patel DJ, Brown RE (2014) Cell Rep. 6(2):388-99.

Finland

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General Activities

Arabidopsis Research Facilities

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

Research at the University of Helsinki focuses plant stress responses and plant development. Research projects address the role of reactive oxygen species (ROS) as signaling molecules in plants, the role of transcription factors in the stress response, receptor and receptor-like kinase signaling, plant stem cell maintenance, root development, plant-pathogen interactions as well as the role of the proteasome in the regulation of flowering. Groups in Helsinki are also exploiting the natural variation of *Arabidopsis thaliana* to identify new regulators of stress tolerance.

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

The Centre of Excellence (CoE) "Molecular Biology of Primary Producers" (2014-2019) funded by the Academy of Finland has started officially in January 2014 and brings together groups from Turku and Helsinki in order to combine expertise on plant development, stress signaling and photosynthesis. While the CoE uses several plant species and also cyanobacteria much of the research is carried out in Arabidopsis.

Current Arabidopsis Projects

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

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

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

Outlook on Arabidopsis Research

Research on Arabidopsis or using Arabidopsis as a tool continues to be a major factor in Finnish plant science. Efforts include translation of knowledge from Arabidopsis towards tree research.

At the University of Helsinki doctoral training was re-organized in 2014. The previous national doctoral education programme in plant sciences (FDPPS and before that FGSPB) became a local University of Helsinki programme - the Doctoral Programme in Plant Sciences. All the national collaboration remains with the Universities of Turku, Eastern Finland and Oulu, along with that of LuKe, but the students are now all registered at the University of Helsinki. As many research groups at the University of Helsinki use Arabidopsis as their model species there is a heavy emphasis on Arabidopsis research in the Doctoral Programme in Plant Sciences.

Road Map Related Activities

Arabidopsis Tools and Resources

A phenomics facility is currently being built at the Viikki campus of the University of Helsinki (ready by mid 2015). This high throughput facility is part of a National Plant Phenotyping Infrastructure that also includes a high precision unit at the University of Eastern Finland. The Viikki facility will accommodate tools for morphological and physiological analysis of Arabidopsis by imaging (fluorescence and thermal).

Outreach Activities

Plant scientists from the University of Helsinki organized a 2014 event (yearly since 2012) to introduce the public to modern plant science. The day included lectures but also hands on experiments with plants.

Conferences and Workshops

- First SPPS Early Career PI meeting. Naantali Spa, Naantali, Finland. November 25-26, 2014

Selected Publications

- Arabidopsis NAC45/86 direct sieve element morphogenesis culminating in enucleation. Furuta KM, Yadav SR, Lehesranta S, Belevich I, Miyashima S, Heo J, Vaten A, Lindgren O, De Rybel B, Van Isterdael G, Somervuo P, Lichtenberger R, Rocha R, ThitamadeeS., Tähtiharju S, Auvinen P, Beeckman T, Jokitalo E, Helariutta Y (2014) Science 345 (6199): 933-937
- PLETHORA gradient formation mechanism separates auxin responses. Mähönen A P., ten Tusscher K, Siligato R, Smetana O, Diaz-Trivino S, Salojärvi J T, Wachsman G, Prasad K, Heidstra R, Scheres B (2014) Nature 515 (7525): 125-129

- Transcriptomics and Functional Genomics of ROS-Induced Cell Death Regulation by RADICAL-INDUCED CELL DEATH1. Brosche M, Blomster T, Salojärvi J, Cui F, Sipari N, Leppälä J, Lamminmäki A, Tomai G, Narayanasamy S, Reddy RA, Keinänen MJ, Overmyer K, Kangasjärvi J (2014) PLoS Genetics 10(2): e1004112
- Protein phosphatase 2A (PP2A) regulatory subunit B'γ interacts with cytoplasmic ACONITASE 3 and modulates the abundance of AOX1A and AOX1D in *Arabidopsis thaliana*. Konert G, Trotta A, Kouvonen P, Rahikainen M, Durian G, Blokhina O, Fagerstedt K, Muth D, Corthals GL, Kangasjärvi S (2015) New Phytologist 205(3): 1250-1263
- GRIM REAPER peptide binds to receptor kinase PRK5 to trigger cell death in Arabidopsis. Wrzaczek M, Vainonen JP, Stael S, Tsiatsiani L, Help-Rinta-Rahko H, Gauthier A, Kaufholdt D, Bollhoner B, Lamminmäki A, Staes A, Gevaert K, Tuominen H, Van Breusegem F, Helariutta Y, Kangasjärvi J (2015) EMBO Journal 31(1): 55-66

Major Funding Sources

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

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

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

France

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General Activities

Current Arabidopsis Projects

Important restructuration of plant research laboratories are in progress in the South-West of Paris. In the context of the Excellence initiative of Paris-Saclay, the Institute of Plant Sciences Paris-Saclay (IPS2, Paris-Saclay) was created to strengthen research and teaching potential in plant sciences, to improve synergies and create a higher visibility of Plant Sciences at the national and international levels. The creation of IPS2 involves the Institute of Plant Biology (IBP, Orsay), the Research Unit of Plant Genomics (URGV, Evry) and part of the Institute of Plant Sciences (ISV, Gif sur Yvette); these three well-known but geographically dispersed plant research structures were dissolved in December 2014. The IPS2 is supported by 5 institutions: The universities of Paris-Sud, Evry Val d'Essonne and Paris-Diderot, the CNRS and the INRA.

The novel IPS2 Institute is part of the laboratory of Excellence Saclay Plant Sciences, LabEx SPS, together with the Institute Jean-Pierre Bourgin (IJPB, Versailles) and few labs originated from ISV and who joined the newly created Institute for integrative biology of the Cell (I2BC, Gif sur Yvette).

Outlook on Arabidopsis Research

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

The french national research agency, ANR (http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency/), provides funding for project-based research. In 2014, novel rules and a two-step evaluation procedure were developed by the ANR. Main work programme takes up the nine challenges identified in the "France Europe 2020" national strategic agenda largely based on "Horizon 2020" European framework programme.

The corresponding generic call for proposals favors collaborative research projects and in biology is very much centered on human health and well-being. In this context, funding of fundamental research projects outside of this major societal challenge is more and more difficult. Arabidopsis projects are directly impacted.

In 2014, only 3 fundamental Arabidopsis projects were selected in the generic call on "life, health and well-being". This low score was partially compensated by funding of plant projets (rarely using Arabidopsis as a model) in other categories as efficient ressource management and adaptation to climate change, clean, secure and efficient energy and mainly food security and demographic challenges. Similar generic call is reconducted in 2015 which could be shortly detrimental to our research field, specifically on Arabidopsis.

Road Map Related Activities

Arabidopsis Tools and Resources

The *Arabidopsis thaliana* Stock Centre at INRA Versailles continously 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). this plateform will move in 2015 to the novel research plant institute IPS2 at Paris-Saclay University.

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 to750 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, http://www.gisbiotechnologiesvertes.com/en/presentation-du-gis-bv) was created following the "Genoplante" network (http://www.genoplante.com). The GIS BV is build on a large public-private partnership community, which gathers public research institutes (including work performed on model plants as Arabidopsis), seed companies, technical institutes, sector representatives, and competitive clusters.

Conferences and Workshops

- ICAR 2015 will take place in Paris from 5th to 9th of July (http://www.arabidopsisconference2015.org). The meeting is organized by the French Society of Plant Biologists (SFBV, http://sfbv.snv.jussieu.fr/) with the help of the Saclay Plant Sciences Laboratory network of excellence (SPS LabEx, http://www6.inra.fr/saclay-plant-sciences).

Selected Publications

- In 2014, researchers of french teams published 649 publications refering to *Arabidopsis thaliana* in the title, the keywords or the abstract. Among these articles, 35 were published in high ranked journals with IF > 10.
- Noncoding transcription by alternative RNA polymerases dynamically regulates an auxin-driven chromatin loop. Ariel F, Jegu T, Latrasse D, Romero-Barrios N, Christ A, Benhamed M, Crespi M (2014) Molecular cell 55: 383-396
- Mapping the epigenetic basis of complex traits. Cortijo S, Wardenaar R, Colome-Tatche M, Gilly A, Etcheverry M, Labadie K, Caillieux E, Hospital F, Aury JM, Wincker P, Roudier F, Jansen RC, Colot V, Johannes F (2014) Science 343: 1145-1148
- Dominance hierarchy arising from the evolution of a complex small RNA regulatory network. Durand E, Meheust R, Soucaze M, Goubet PM, Gallina S, Poux C, Fobis-Loisy I, Guillon E, Gaude T, Sarazin A, Figeac M, Prat E, Marande W, Berges H, Vekemans X, Billiard S, Castric V (2014) Science 346: 1200-1205
- Structural basis for oligomerization of auxin transcriptional regulators. Nanao MH, Vinos-Poyo T, Brunoud G, Thévenon E, Mazzoleni M, Mast D, Lainé S, Wang S, Hagen G, Li H, Guilfoyle TJ, Parcy F, Vernoux T, Dumas R. (2014) Nat Commun. 5:3617.
- A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. Sayou C, Monniaux M, Nanao MH, Moyroud E, Brockington SF, Thevenon E, Chahtane H, Warthmann N, Melkonian M, Zhang Y, Wong GK, Weigel D, Parcy F, Dumas R (2014) Science 343: 645-648

Major Funding Sources

ANR, generic call or international calls (http://www.agence-nationale-recherche.fr/en/funding-opportunities/)

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

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

TOC

Germany

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General Activities

Arabidopsis Research Facilities

Arabidopsis research in Germany is very broad and projects cover all aspects of Arabidopsis research. 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 working group under the umbrella of the German Botanical Society (DBG) and the new AFGN website is online at: http://www.dbg-afgn.de. A new mailing list was initiated to facilitate a direct information exchange between Arabidopsis researchers; subscription at https://listserv.uni-tuebingen.de/mailman/listinfo/afgn.

Current Arabidopsis Projects

Funding of basic Arabidopsis research is and will be provided by the DFG via several funding instruments (see examples below). Since 2013 the DFG funds the MASC/AFGN coordinator until end of 2015 by a grant awarded to Klaus Harter. Besides the DFG several other funding instruments exist, e.g currently 7 projects are funded by the European Research Council (http://erc.europa.eu/projects-and-results/erc-funded-projects/Arabidopsis?f[0]=sm_field_cordis_project_hi_count%3AGermany&retain-filters=1).

Individual Funding

Currently a total number of 175 individual projects referring to Arabidopsis are funded by the DFG: 7 by the Emmy Noether Program, 2 by the Heisenberg Program, 9 by the Postdoctoral Fellowships and 159 by individual research grants.

Priority Programs

Arabidopsis researchers are involved in 8 priority programs, out of these 4 are in the subject of Plant Science:

- 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 1395 (since 2010) Information and Communication Theory in Molecular Biology
- SPP 1212 (2007-2014) Microbial reprogramming of plant cell development (http://www.plant-micro.de/)

Collaborative Research Centers

Arabidopsis researchers are involved in 16 collaborative research centers, out of these three 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 924 (since 2011) Molecular Mechanisms Regulating Yield and Yield Stability in Plants (http://sfb924.wzw.tum.de/index.php?id=3)
- SFB 648 (since 2005) Molecular mechanisms of information processing in plants (http://www.sfb648.uni-halle.de/)

Research Training Groups

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

Research Units

- FOR 2092 (since 2014) Biogenesis of thylakoid membranes: Spatiotemporal organization of photosynthetic protein complex assembly (http://www.uni-kl.de/for2092/start/)
- FOR 1061 (since 2008) Dynamic storage functions of plant vacuoles during cold and osmotic stress (http://www.uni-kl.de/for1061/)

Road Map Related Activities

Arabidopsis Tools and Resources

- Arabidopsis Functional Genomics Network (www.dbg-afgn.de)
- 1001 genomes platform (http://1001genomes.org/)
- German Plant Phenotyping Network (DPPN, http://www.dppn.de/en)
- The Arabidopsis Protein Phosphorylation Site Database (PhosPhAt, http://phosphat.uni-hohenheim.de/)
- GABI Primary Database (GabiPD, http://www.gabipd.org/)
- The Plant Transcription Factor Database (http://plntfdb.bio.uni-potsdam.de/v3.0/)

Outreach Activities

Projects that use knowledge gained from Arabidopsis for translational research are funded by the BMBF (see http://www.pflanzenforschung.de), some examples:

- PLANT-KBBE IV (2014-2017): Nematode susceptibility targets for a durable resistance
- PLANT-KBBE IV (2014-2017): Control of the abiotic stress response in plants by DELLA proteins and chemicals
- Plant biotechnology (2011-2014): Sugar beet (*Beta vulgaris*) - Manipulation of tap root metabolism and photosynthate allocation by increasing sink and source capacities
- International plant biotechnology (2011-2015): New generation techniques for genetic engineering of cultivated plants

A public panel discussion was held during the TNAM 2014: Green Biotechnology– opportunity or risk?

The Fascination of Plants Day will be held at 12 institutions in Germany on March 18th 2015 (http://www.plantday12.eu/germany.htm)

Conferences and Workshops

- Tri-National Arabidopsis Meeting (TNAM) biannual conference, hosted by colleagues from Germany, Austria and Switzerland:

  10th TNAM, 14-16 September 2016, Vienna

  9th TNAM, 24-26 September 2014, Heidelberg (www.tnam2014.org).
- Deutsche Botanikertagung

  2015, 30th August - 3rd September, Munich (http://botanikertagung2015.de/)

  2014, 30th September - 4th October, Tübingen
- Tagung Molekularbiologie der Pflanzen (http://pflanzen-molekularbiologie.de/):

  29. Tagung, 23-26 February 2016, Dabringhausen

  28. Tagung, 24-27 February 2015, Dabringhausen

  27. Tagung, 25-28 February 2014, Dabringhausen
- Symposium on Plant-Environment Interactions, 4-6 May 2015, Heidelberg (http://www.cos.uni-heidelberg.de/plant-environment-interactions/Program.html)
- 2nd Summer Academy in Plant Molecular Biology, 13-15 July 2015, Freudenstadt (http://www.summer-academy-pmb.com/)
- 36th New Phytologist Symposium: Cell biology at the plant-microbe interface 29 November- 1 December 2015, Munich, Germany (https://www.newphytologist.org/symposiums/view/38)
- 12th International Conference of the European Chitin Society, 30 August - September 2 2015, Münster
- 9th International Workshop on Sulfur Metabolism in Plants: Molecular Physiology and Ecophysiology of Sulfur, 14-17 April 2014, Freiburg

Selected Publications

German researchers contributed to 546 publications referring to Arabidopsis in the previous year (search at http://www.ncbi.nlm.nih.gov/pubmed: "arabidopsis"[All Fields]) AND "Germany"[Affiliation] AND "2014/05/01"[PDAT] : "2015/04/30"[PDAT]).

- Species-wide genetic incompatibility analysis identifies immune genes as hot spots of deleterious epistasis. Chae E, Bomblies K, Kim ST, Karelina D, Zaidem M, Ossowski S, Martín-Pizarro C, Laitinen RA, Rowan BA, Tenenboim H, Lechner S, Demar M, Habring-Müller A, Lanz C, Rätsch G, Weigel D (2014) Cell 159(6):1341-51.
- Going beyond nutrition: regulation of potassium homoeostasis as a common denominator of plant adaptive responses to environment. Anschütz U, Becker D, Shabala S (2014) J Plant Physiol 71(9):670-87.
- Horizontal genome transfer as an asexual path to the formation of new species. Fuentes I, Stegemann S, Golczyk H, Karcher D, Bock R (2014) Nature 511(7508):232-5.
- Stomatal Guard Cells Co-opted an Ancient ABA-Dependent Desiccation Survival System to Regulate Stomatal Closure. Lind C, Dreyer I, López-Sanjurjo EJ, von Meyer K, Ishizaki K, Kohchi T, Lang D, Zhao Y, Kreuzer I, Al-Rasheid KA, Ronne H, Reski R, Zhu JK, Geiger D, Hedrich R (2015) Curr Biol 25(7):928-35.
- The C2-domain protein QUIRKY and the receptor-like kinase STRUBBELIG localize to plasmodesmata and mediate tissue morphogenesis in *Arabidopsis thaliana*. Vaddepalli P, Herrmann A, Fulton L, Oelschner M, Hillmer S, Stratil TF, Fastner A, Hammes UZ, Ott T, Robinson DG, Schneitz K (2014) Development 141(21):4139-48.

Major Funding Sources

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

Greece

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General Activities

Arabidopsis Research Facilities

Arabidopsis has been widely used as a model species to gain knowledge for translational research in agronomically important crops of Greece including olives, tomato, grapes, peach etc. 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 defense mechanisms in Arabidopsis, HSP90 as a modulator for plant development, signal transduction in plant development epigenetic mechanisms and plant development and regulation, 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 trascriptomics and proteomics, advanced bio-imaging equipment, protein crystallography platform and instruments used for deep analysis of primary and secondary metabolites.

The Members of the Plant Molecular Biology & Biotechnology Consortium are:

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Outlook on Arabidopsis Research

While funding in research activities is highly reduced there are still possibilities to support infrastructure through the establishment of a network between academic and research institutes.

Road Map Related Activities

Arabidopsis Tools and Resources

Arabidopsis resources with high impact and emerging technologies for research infrastructure:

- National Roadmap for Research Infrastructures (2014): “Integrated Greek Infrastructure for Biomedical Research” (INTEGRA-Biomed)
- National Roadmap for Research Infrastructures (2014): “Synthetic Biology: from omics technologies to genomic engineering” (OMIC-ENGINE)

Outreach Activities

Projects that use knowledge gained from Arabidopsis for translational research:

- H2020-MSCA-RISE-2014 "Bioresources For Oliviculture" (BeFOre)

Conferences and Workshops

- 36th Hellenic Society for Biological Science (EEBE) meeting. Ioannina, Greece
- 65th Hellenic Society of Biochemistry and Molecular Biology (HSBMB) Conference. Thessaloniki, Greece

Selected Publications

- Evolution and significance of the Lon gene family in Arabidopsis organelle biogenesis and energy metabolism. Rigas S, Daras G, Tsitsekian D, Alatzas A, Hatzopoulos P (2014) Front Plant Sci. 5 (145).
- Cortical microtubule patterning in roots of *Arabidopsis thaliana* primary cell wall mutants reveals the bidirectional interplay with cell expansion. Panteris E, Adamakis ID, Daras G, Rigas S (2014) Plant Signal Behav. 9 (4): pii: e28737.
- Alternative transcription initiation and the AUG context configuration control dual-organellar targeting and functional competence of Arabidopsis Lon1 protease. Daras G, Rigas S, Tsitsekian D, Zur H, Tuller T, Hatzopoulos P (2014) Mol Plant. 7 (6): 989-1005.

- Investigation of triterpene synthesis and regulation in oats reveals a role for β-amyrin in determining root epidermal cell patterning. Kemen AC, Honkanen S, Melton R, Findley K, Mugford S, Hayashia K, Haralampidis K, Rosser S, Osbourn A. (2014) Proc Natl Acad Sci USA 111: 8679-8684.
- Transcriptional regulation and functional involvement of the Arabidopsis pescadillo ortholog AtPES in root development. Zografidis A, Kapolas G, Podia V, Beri D, Papadopoulou KK, Milioni D, Haralampidis K. (2014) Plant Science 229: 53-65.

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)

Research Committee of Aristotle University of Thessaloniki (http://www.rc.auth.gr/)

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

India

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General Activities

Arabidopsis Research Facilities

There were only a few groups working exclusively on Arabidopsis in India until recently; many more groups were using Arabidopsis for gene function validation for heterologous genes. However, in recent years many more labs using Arabidopsis as a system have got nucleated due to establishment of new research institutes in India by the Government of India. Some of the areas of research using Arabidopsis as a model system include i) Light regulation of plant development; ii) Hormone and sugar signalling; iii) Abiotic and biotic stress response pathways; iv) Identification of gene regulatory elements by insertional mutagenesis; v) Regulation of patterning and regeneration, vi) Stem cell niches in roots and shoots, vii) Epigenetic memory in plants. Major research centres working on Arabidopsis in India include CCMB, Hyderabad; IISc, Bangalore; University of Delhi South Campus; NIPGR, New Delhi; NRCPB, New Delhi; JNU, New Delhi; IHBT, Palampur; IISER, Thiruvanathapuram; IISER, Mohali; IISER, Bhopal; IIT, Roorke.

All these Institutes/Universities receive funding for Arabidopsis research from the Government agencies based on competitive grants.

Current Arabidopsis Projects

Only those projects that have been approved in the past one year are listed below; the ongoing projects were listed in last year's report. In addition, there are many in-house funded projects supported by the Institutes.

Prof. Sudip Chattopadhyay (NIT, Durgapur)

- Investigation of the interconnecting roles of ZBF1/MYC2 and HY5 in Arabidopsis seedling development and disease defense. Funded by Department of Biotechnology, Govt. of India (2014-2017).

Dr. Girdhar Pandey (University of Delhi South Campus)

- Enhancement of starch accumulation and grain filling by dual specificty protein phosphatase AtDSP in Arabidopsis and OsPP42 in rice. Funded by Department of Biotechnology (DBT), Govt. of India (2014-2017).
- Investigation of alternate salt and osmotic stress signaling pathway in Arabidopsis mediated by calcineurin B-Like associated protein kinase 21. Funded by Department of Science & Technology (DST), Govt. of India (2014-2017).

Outlook on Arabidopsis Research

Since there were only a few labs exclusively working on Arabidopsis in the recent past, funding was somewhat limited. However, with the influx of young faculty in the newly created institutes by the Government of India, they have been able to set up interesting programs, attracting good funding in the process. Future for Arabidopsis research in India looks to be promising.

Road Map Related Activities

Arabidopsis Tools and Resources

Professor Chattopadhyay's laboratory at NIT, Durgapur, in collaboration with Dr. Mukesh Jain's laboratory (at NIPGR, New Delhi) has carried out genome wide ChIP-ChIP studies. They have provided evidence that the binding of GBF1 to the DNA (at genome-wide level) is modulated by bZIP transcription factors, HY5 and HYH, that heterodimerize with it (Ram et al. 2014. Molecular Plant 7: 448-51).

Dr. Ram Kishore Yadav's laboratory has contributed to generating a high-resolution gene expression map of Arabidopsis shoot apical meristem stem cell niche. (Yadav et al. 2014. Development 41(13): 2735-44).

Dr. Y. Sreenivasulu's laboratory at IHBT, Palampur, has developed many insertion lines in Arabidopsis with the aim to isolate promoters specific to reproductive tissues. (Pratibha et al. 2013. Gene 524(1): 22-7)

Outreach Activities

There has been constant exchange of ideas of the researchers working on Arabidopsis with those involved in agricultural research or working in agri-industry. Even the government funding agencies that have the mandate to promote (product oriented) translational research do also encourage the use of Arabidopsis for gene function validation. There is also an effort to develop international linkages for research using Arabidopsis as a system but it is more on one-to-one basis and is successful largely in cases where a young researcher in India had worked in the past in the same lab overseas. In most cases where international linkages are developed through Government agencies, thrust is on crop plants like rice, wheat and mustard.

Conferences and Workshops

An Arabidopsis workshop was organized on October 9-10, 2014 at CCMB, Hyderabad. The purpose of this workshop was to familiarize the Indian Arabidopsis research community about the research activities being carried out in India and also for the young researchers to get to know each other. This turned out to be quite successful and it is aimed to organize such workshops every year at different institutes, by rotation. This will help popularize Arabidopsis among young graduates and in developing research linkages.

Many different conferences and workshops have been held in India in the past year where Arabidopsis research was discussed. Two more major Symposia are scheduled to be held in 2015. One National Symposium is being organized by the Indian Society of Plant Biochemistry and Biotechnology, New Delhi, from August 9-11, 2015. An International Symposium will also be held at JNU Convention Centre, New Delhi, from December 11-15, 2015; this is being jointly organized by the Indian Society of Plant Physiologists, JNU and NIPGR, New Delhi, where a large number of foreign delegates are expected to participate.

Selected Publications

- A mitogen-activated protein kinase cascade module, MKK3-MPK6 and MYC2, is involved in blue light-mediated seedling development in Arabidopsis. Sethi V, Raghuram B, Sinha AK Chattopadhyay S (2014) Plant Cell 26(8): 3343–57.
- A high-resolution gene expression map of the Arabidopsis shoot meristem stem cell niche. Yadav RK, Tavakkoli M, Xie M, Girke T, Reddy GV (2014) Development 41(13): 2735-44.
- Glucose control of root growth direction in *Arabidopsis thaliana*. Singh M, Gupta A, Laxmi A (2014) J Exp Bot 65(12):2981-93.
- Balanced activity of microRNA166/165 and its target transcripts from the class III homeodomain leucine-zipper family regulates root growth in *Arabidopsis thaliana*. Singh A, Singh S, Panigrahi KC, Reski R, Sarkar AK (2014) Plant Cell Rep 33(6): 945-53.
- PLETHORA Genes Control Regeneration by a Two-Step Mechanism. Kareem A, Durgaprasad K, Sugimoto K, Du Y, Pulianmackal AJ, Trivedi ZB, Abhayadev PV, Pinon V, Meyerowitz EM, Scheres B, Prasad K. (2015) Curr Biol Curr Biol 25(8):1017-30.

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 2014-2015

In India, the focus of research on Arabidopsis is to i) understand how light, hormones and sugars interact to regulate plant development; ii) identify transcription factors and components involved in regulating embryogenesis and pattern formation; iii) identify novel regulators of plant defense; iv) identify novel promoters and regulatory sequences by insertional mutatgenesis; v) unravel the transcription factor gene network and its regulation in the shoot and root apical meristem development; vi) mechanism of inheritance of epigenetic memory in plants. Many labs are also using Arabidopsis for gene function validation by using heterologous genes (from rice and wheat) and its mutants in orthologous genes.

Dr. Sudip Chattopadhyay's lab has done pioneering work on light signalling in Arabidopsis; in the past years, his group has identified many Z-box binding transcription factors involved in blue light signaling. Mitogen-activated protein kinase have also been ascribed roles in plant hormone signalling but, until recently, its role in light signaling was virtually unknown. His group has now shown that MPK6 physically interacts with and phosphorylates MYC2, a bHLH transcription factor modulated by blue light, and is phosphorylated by MKK3. MYC2 in turn binds to the upstream promoter region of MPK6 and regulates its expression, displaying a feedback regulation, in blue light signalling. These studies have elucidated the role of novel components in regulating photomorphogenesis. Dr. Ashverya Laxmi, at NIPGR, New Delhi, has been working on the downstram componets involved in light, hormone and sugar signalling. Sugars affect all phases of plant life cycle. Recent studies by her group have provided significant evidences of interactions between glucose and phytohormone response pathways especially auxin, cytokinin and brassinosteroids in controlling various plant growth and development features especially root and hypocotyl directional growth. Work is presently underway to unravel the molecular basis of glucose-hormone interaction in controlling plant development.

Another group interested in plant signalling is nucleated at University of Delhi South Campus. Dr. Girdhar Pandey's laboratory is working on the coding and decoding of mineral nutrient deficiency and abiotic stress signals by studying several signaling components such as phospholipases (PLA, PLC, and PLD), calcium sensors such as calcineurin B-like (CBL) and CBL-interacting protein kinases (CIPK), phosphatases (mainly PP2C and DSP), transcription factors (AP2-domain containing or ERF, WRKY), transporters and channels proteins (K+, Ca2+ and NO3- channels/transporters) in Arabidopsis.

Studies in the laboratory of Dr. Kalika Prasad, at IISER, Thiruvanathapuram, focus on deeper understanding of intermediate developmental phases during regeneration after inductive cues and mechanisms underlying acquisition of pluripotency and completion of organ regeneration. Recently, his group has uncovered a two-step mechanism of regeneration in Arabidopsis. he is keen to understand the role of stem cell regulators in this process. Two other groups are also addressing the stem cell niches in the root and shoot. The laboartory of Dr. Ram Yadav at IISER, Mohali, has recently released a high-resolution gene expression map of Arabidopsis shoot apical meristem stem cell niche. He intends to investigate the transcription factor gene network in the shoot apical meristem. Interest in the laboratory of Dr. Ananda Sarkar is to understand the cross-talk between small RNA classes and protein coding genes in root development. Molecular genetics and functional genomics approaches are being used to uncover the role of tasiRNA and miRNAs. He has recently shown that the miR166/165 and target HD-ZIPIII genes regulate root growth.

Dr. Y. Sreenivasulsu, at IHBT, Palampur, has generated populations of GUS/GFP-tagged Arabidopsis to identify and isolate novel, reproductive tissue specific plant promoters. A detailed characterization of these lines has lead to the identification of a cryptic anther specific bidirectional promoter and another embryosac specific bidirectional promoter. These promoters will be helpful for the manipulation of micro- and mega-gametogenesis during seed development.

To gain insights into plant's defense responses, Dr. Jagreet Kaur at UDSC, New Delhi, is using the *Arabidopsis thaliana* /Alternaria brassicae pathosystem as a tool. Her group has evaluated the available natural accessions of Arabidopsis and accessions with contrasting responses to the pathogen challenge are being used to identify genes imparting resistance/susceptibility to A. brassicae. Additionally, various known Arabidopsis mutants, impaired in innate immune responses, are being evaluated for their response to Alternaria infection. On a related theme, the laboratory of Dr. Ashis Nandi at JNU is concentrating on salicylic acid (SA) signaling and systemic acquired resistance (SAR). Through reverse genetics and over-expression analysis they have identified an AP2 family transcription factor, APD1, that regulates SA biosynthesis. Using SAR deficient mutants it has beeen shown that histone demethylase activity is required for SAR induced memory formation. Dr. Mukesh Lodha at CCMB, Hyderabad, is addressing one of the important questions in the field of epigenetics, i.e. the mechanism of inheritance of epigenetic memory. He has devised a fluorescence microscopy based assay to ask the question whether histone modifications themselves, the enzymes involved in writing and maintaining histone modifications or histone chaperons, are the carrier of epigenetic memory during cell division.

Israel

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General Activities

Arabidopsis Research Facilities

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

Areas of research include plant physiology, biochemistry, development and genomics. Two new Arabidopsis research labs were established by young PIs:

- Eilon Shani, Tel Aviv University (postdoctoral training: the lab of Mark Estelle, UCSD, US).
- Assaf Mosquna, The Hebrew University of Jerusalem (postdoctoral training: the lab of Sean Cutler, UC Riverside, US).

Current Arabidopsis Projects

The Israeli Centers of Research Excellence (I-CORE) program is aimed at fundamentally strengthening the long term positioning of Israel's academic research, promote national and international research collaborations, and to assist in the recruitment of new excellent researchers, by the gradual establishment of "Centers of Excellence" – leading research centers specializing in innovative and ground breaking research in a range of fields (http://www.icore-plants.tau.ac.il/); effective funding until 2021.

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

1. Deciphering the genetic and epigenetic factors affecting short- and long-term (trans-generational) phenotypic plasticity and adaptation to environmental changes.
2. Elucidating the mechanisms underlying the interactions of the environment with intrinsic developmental programs, and the role of phytohormones in stress responses.
3. Elucidating the key factors regulating plant metabolism and catabolism under stress with focus on the switch-points driving cell death versus cell vitality.
4. Dynamics of cell structures (cell wall, membranes, organelles, and protein complexes) and their role in stress responses.
5. Laying a foundation for a computational perspective of plant behavior under a changing environment, and predictions of selected genetic and environmental perturbations that will bring the plant to a desired metabolic or functional state.

Road Map Related Activities

Outreach Activities

- Plant Biotechnology – Achievements and Horizons, 23rd October 2014 at Tel Aviv University

Conferences and Workshops

- The 7th Federation of all the Israel Societies for Experimental Biology (FISEB), Feb 10-13, 2014, Eilat (with dedicated plant sessions).
- CRISPR/CAS9 workshop, Nov 19, 2014, Weizmann Institute of Science, Rehovot.
- The annual meeting of the Israel Society of Plant Sciences, Feb 24, 2015, Weizmann Institute of Science, Rehovot.

Selected Publications

- About 60 research articles employing Arabidopsis were published since the beginning of 2014 and until March 2015.

Major Funding Sources

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

Italy

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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 genetic material are continuously exchanged among laboratories. Arabidopsis genomic, transcriptomics and proteomics workstations have been implemented in several Italian Institutions. Informal multi-institutional collaborations are also common, and new networks and collaborations have recently emerged.

Current Arabidopsis Projects

The Italian Ministry of Education, University and Research (MIUR, http://hubmiur.pubblica.istruzione.it/web/ricerca/home) has continued to fund several Arabidopsis Initiatives in 2014, listed below:

- 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 analyses.
- A project aiming at using "omics" technologies and phentypical analyses to evaluate the toxicity in *Arabidopsis thaliana* of small Cadmium nanoparticles called cadmium sulphide quantum dots (CdS QDs) to N. Marmiroli (University of Parma).
- A project on "Intracellular channels and pores: structural and functional studies provide new rules for engineering artificial channels" to A. Carpaneto (CNR, Genova).
- A FIRB (http://firb.miur.it/) grant for young scientists to R. Dello Ioio/P. Costantino (Futuro in Ricerca) on the development of the root cortex.

Other funding comes from the EU: ERC grants (http://erc.europa.eu) have been awarded S. Sabatini/P. Costantino (on the Hormonal control of Arabidopsis root growth) and F. Cervone/G. deLorenzo, while M. Kater/L. Colombo received funding from a Marie Curie International Research Staff exchange Scheme on "Evolutionary Conservation of Regulatory Network Controlling Flower Development.

A collaboration funded by the Italian Ministry of Foreign Affairs is continuing between the Italian laboratories of M. Cardarelli/G. Serino/P. Costantino (CNR/Sapienza University) and the Japanese laboratories of T. Tsuge/M. Matsui (Kyoto Univ./Riken) . The goal is to find common regulatory networks controlling stamen and hypocotyl growth in Arabidopsis. G. Serino/P. Costantino are members of the COST Action BM1307 and N. Marmiroli was a member of a recently completed COST Action on mineral nutrition in plants (FA0905).

Other Funding sources include private Foundations such as CARIPLO to M. Kater/L. Colombo, Cenci-Bolognetti (to F. Cervone/G. de Lorenzo, S. Sabatini/P. Costantino and P. Vittorioso/P. Costantino), and the Italian Ministry of Agriculture (to F. Cervone/G. de Lorenzo).

Outlook on Arabidopsis Research

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 and 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 and hypocotyl development. Other research areas that will be continued in the next years involve the hormonal control of stamen development and the characterization of ncRNA pathways active in the floral meristem. Emerging 'genome editing' techniques will be set up to study complex gene families putatively involved in flower development. Phytochelatins and heavy metal tolerance in Arabidopsis and tobacco plant are also been investigated.

We expect that for the next years Arabidopsis research in Italy will receive little or no financial support from National Agencies. A similar trend is apparent at the EU levels, suggesting that research focused on Arabidopsis should be translated into applications for improving crop productivity and phyto-remediation technologies.

Funding has been and will be sought through the participation to proposals for collaborative projects in the Eranet ERA-CAPS 2014 call, the ERC program, as well as the Horizon 2020 program.

Road Map Related Activities

Arabidopsis Tools and Resources

- The group of S. Sabatini/P. Costantino has developed a new mathematical model to describe the cytokinin auxin antagonistic interaction. The group of R. Dello Ioio/P. Costantino has started a comparative study of the development of Arabidopsis and Cardamine root to understand the molecular differences underlying anatomical differences.
- N.Marmiroli's group has identified biomarkers to monitor CdS QDs response in Arabidopsis. Microarray data for transcriptomics in wt and mutants during exposure to CdS QDs are also available at N. Marmiroli's lab.
- M. Galbiati/C. Tonelli has developed chimeric promoters for the spatio-temporal control of gene expression in guard cells.
- The group of M.M. Altamura has optimized epifluorescence and histological techniques, including in situ hybridization and immuno-localization, coupled with electron transmission and biochemical analyses.
- A novel heterologous system for the functional characterization of animal intracellular channels and transporters has been developed by A. Carpaneto's group.
- 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 Organisation) on may 2014.

S. Sabatini/P. Costantino, M. Kater/L. Colombo and M.M. Altamura will participate to the EXPO 2015 in Milan with an outreach program on plant development and agro-biodiversity conservation.

Conferences and Workshops

- The research team of N. Marmiroli has organized has organized a workshop focused on nanomaterials (1st PARMA NANODAY).
- Selected Publications
- Plant and animal stem cells: similar yet different. Heidstra R, Sabatini S (2014) Nat Rev Mol Cell Biol. 15(5):301-12.
- Negative feedback regulation of auxin signaling by ATHB8/ACL5-BUD2 transcription module. Baima S, Forte V, Possenti M, Peñalosa A, Leoni G, Salvi S, Felici B, Ruberti I, Morelli G (2014) Mol Plant 27:1006-1025.
- Gene coexpression patterns during early development of the native Arabidopsis reproductive meristem: novel candidate developmental regulators and patterns of functional redundancy. Mantegazza O, Gregis V, Chiara M, Selva C, Leo G, Horner DS and MM Kater (2014) The Plant Journal 79:861–877.
- The DOF protein DAG1 and the DELLA protein GAI cooperate in negatively regulating AtGA3ox1 gene. Boccaccini A, Santopolo S, Capauto D, Minutello E, Lorrai R, Serino G, Costantino P, Vittorioso P (2014) Mol Plant 7: 1486-1489.
- The Arabidopsis NUCLEUS- AND PHRAGMOPLAST-LOCALIZED KINASE1-Related Protein Kinases Are Required for Elicitor-Induced Oxidative Burst and Immunity. Savatin DV, Bisceglia NG, Marti L, Fabbri C, Cervone F, De Lorenzo G (2014) Plant Physiol. 165:1188-1202.

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):

EU (http://ec.europa.eu/research/participants/portal/desktop/en/home.html)

Istituto Pasteur fondazione Cenci Bolognetti (www.istitutopasteur.it/)

CARIPLO Foundation (www.fondazionecariplo.it)

Japan

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

General Activities

Arabidopsis Research Facilities

KAZUSA DNA RESEARCH INSTITUTE

The Kazusa Metabolomics Database (KOMICS) web portal to databases, tools and other information was developed through plant metabolomics studies of Dr. Daisuke Shibata, including integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, co-expressed gene search tools and regulatory network research. (http://www.kazusa.or.jp/komics/en/) in Kazusa DNA Research Institute (http://www.kazusa.or.jp/e/).

RIKEN BRC

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The Experimental Plant Division (Masatomo Kobayashi) collects, preserves and distributes Arabidopsis resources developed in Japan. The project is funded by the Japanese government through the National BioResource Project (NBRP, http://www.nbrp.jp/index.jsp). Not only Arabidopsis seeds (mutants, transgenic lines, and 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. Distribution of full-length cDNA clones of model plants such as *Brachypodium distachyon*, *Physcomitrella patens*, *Populus nigra* and *Thellungiella halophila* are also available for the international research community.

RIKEN Center for Sustainable Resource Science (CSRS)

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

CSRS was established in 2013 to conduct basic research and also seek out, identify, and work to find solutions for critical scientific, technical and social issues, with special focus on Green Innovation, as well as sustainable production of energy and resources. CSRS integrates plant scientists, chemists and chemical biologists, and also chemists and plant biologists focusing on applied research from the Biomass Engineering Program (BMEP) and the Drug Discovery Platforms Cooperation Division.

- Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi, Tetsuya Sakurai). CSRS established the Arabidopsis metabolomics platform (http://prime.psc.riken.jp/), consisting of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics.
- Hormonome platform and RIKEN Plant Hormone Research Network: (Hitoshi Sakakibara, Mitsunori Seo). CSRS established a highly sensitive high-throughput phytohormone quantification platform consisting of mass spectrometry-based technology. The platform is conducting a wide range of collaboration researches. (http://hormones.psc.riken.jp/)
- Transcriptome platform using next generation sequencers. RIKEN ACCC and IMS (Motoaki Seki, K. Mochida, Minami Matsui, Takaho Endo, Tetsuro Toyoda, Piero Carninci, Kazuo Shinozaki)
- Proteome platform: CSRS (Hirofumi Nakagami, Ken Shirasu) and Keio University (Yasushi Ishihama, Naoyuki Sugiyama) developed high- through-put shotgun phosphoproteomics tool for plants and phosphorylation site databases (https://database.riken.jp/sw/links/en/ria102i; http://pepbase.iab.keio.ac.jp).
- Phenome platform RIKEN Activation tagging lines Database and Full-length-cDNA- overexpressing (FOX) Arabidopsis lines (M. Matsui) (https://database.riken.jp/sw/links/en/cria301u1i/), Rice FOX Arabidopsis line Database (http://ricefox.psc. riken.jp/), RIKEN Arabidopsis Genome Encyclopedia II (RARGE II) integrated phenotype database of Arabidopsis mutant traits using controlled vocabulary (Takashi Kuromori, T. Sakurai, K. Shinozaki) (http://rarge-v2.psc.riken.jp/).
- The Chloroplast Function Database II (Fumiyoshi Myouga, K. Shinozaki) is a comprehensive database analyzed by combining genotypic and phenotypic multiparametic analysis of Arabidopsis tagged-lines for nuclear-encoded chloroplast proteins (http://rarge.psc.riken.jp/chloroplast/).
- Analysis of small Open Reading Frame (Kousuke Hanada, M. Matsui, M. Seki) They identified ~8,000 sORFs with high coding potential in intergenic regions of the Arabidopsis genome.
- MassBank (Masanori Arita, Takaaki Nishioka, K. Saito) Public repository of mass spectral data for sharing spectra among research communities. The data is useful for chemical identification and structure elucidation of metabolites detected by mass spectrometers (http://www.massbank.jp/en/about.html).
- High-throughput genome-wide biochemical analysis using wheat germ cell-free-based protein array technology. The method developed by Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) and RIKEN (M. Seki and K. Shinozaki) is useful for substrate protein, interacting protein and chemical compound screening.

- Biomass Engineering Research Division (www.riken.jp/bmep/english/index.html). The program focuses on interdisciplinary innovation for plant biomass production and renewable chemical materials and bioplastics. Besides Arabidopsis, the program uses Brachypodium as a model of grass biomass.

World Premier International Research Center (WPI) Institute of Transformative Bio-Molecules (ITbM)

ITbM of Nagoya University is one of the institutes of the MEXT WPI program (http://www.itbm.nagoya-u.ac.jp/). ITbM is the first WPI institute studying plant science. The ambitious full-scale collaboration between synthetic chemists, plant and animal biologists, and theoreticians is led by Director Kenichiro Itami, Vice-director Tetsuya Higashiyama and others.

Current Arabidopsis Projects

- Multidimensional Exploration of Logics of Plant Development (MEXT) (2013-2017) (http://logics.plantdev.biol.s.u-tokyo.ac.jp/en/index.html)
- Core Research for Evolutional Science and Technology (JST-CREST) (http://www.jst.go.jp/kisoken/crest/en/research_area/ongoing/areah23-2.html)
- JST-ALCA (http://www.jst.go.jp/alca/en/index.html)
- 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 K. Saito (RIKEN). Research led by Oliver Fiehn (Univ. of California at Davis) and M. Arita (NIG)
- ERATO Higashiyama Live-Holonics Project (2010-2015) (http://www.liveholonics.com/en/) headed by T. Higashiyama, Nagoya University. This project studies intercellular signaling in multicellular organisms with complete control of cells and molecules under microscope by developing new technologies for live-cell analysis.
- Japan Advanced Plant Science Research Network started in 2011. This program’s nine centers of excellence in universities and research institutes support plant researches for green innovation.
- NC-CARP (a program in GRENE; Green Network of Excellence) (nc-carp.org/index) The program “Network of Centers of Carbon Dioxide Resource Studies in Plants: NC-CARP (organizer: Hiroo Fukuda)”.
- DREB project supported by MAFF; Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat.
- SATREPS project supported by JST-JICA; Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant soybean. This project is now applying for next stage funding.
- East Asia Science and Innovation Area Joint Research Program (e-ASIA), JST-NSTDA (Thailand)-MOST (Vietnam) on “Biomass and Plant Science”. Research led by M. Seki (RIKEN CSRS). Ham Huy Le (Institute of Agricultural Genetics) and Jarunya Narangajavana (Mahidol University).

Road Map Related Activities

Arabidopsis Tools and Resources

KAZUSA DNA RESEARCH INSTITUTE

- Kazusa Metabolomics Database portal KOMICS (http://www.kazusa.or.jp/komics/)
- The KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (http://kpv.kazusa.or.jp/)
- MassBase: a plant metabolome database (http://webs2.kazusa.or.jp/massbase/)
- KomicMarket (http://webs2.kazusa.or.jp/komicmarket)
- MS-MS Fragment Viewer (http://webs2.kazusa.or.jp/msmsfragmentviewer/)
- KAGIANA co-expressed gene search tool (http://pmnedo.kazusa.or.jp/kagiana/index.html)
- CoP co-expressed gene search tool (http://webs2.kazusa.or.jp/kagiana/cop0911/)
- RnR regulatory network research (http://webs2.kazusa.or.jp/kagiana/rnr/).
- MFSearcher (http://webs2.kazusa.or.jp/mfsearcher/)

RIKEN BRC

- Resources from RIKEN BRC (http://epd.brc.riken.jp/en/)

RIKEN CSRS

- Arabidopsis metabolomics platform (http://prime.psc.riken.jp/) publicly available platform resources:
- MeKO (Metabolomic characterization of knock-out mutants of Arabidopsis) (http://prime.psc.riken.jp/meko/)
- 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)
- ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (http://spectra.psc.riken.jp/);

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- PRIMeLink (http://spectra.psc.riken.jp/menta.cgi/primelink/index) integrates 3 above databases (AtMetExpress, MS2T and ReSpect) to provide a bi-directional searchable function from the gene or metabolite perspective.
- Standard Spectrum Search (http://prime.psc.riken.jp/?action=standard_index);
- Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index);
- Drop Met (http://prime.psc.riken.p/?action=drop_index);
- SpinAssign (Annotation of metabolites by NMR from 13C-HSQC peaks) (http://prime.psc.riken.jp/?action=nmr_search)
- Plant Hormone Research Network (http:// hormones.psc.riken.jp/)
- The Chloroplast Function Database II (http://rarge.psc.riken.jp/chloroplast/)
- Arabidopsis Activation Tagging Line Database (https://database.riken.jp/sw/en/RIKEN_Activation_tagging_line/cria37u1i/)
- Arabidopsis Genome Encyclopedia (RARGE) (http://rarge-v2.psc.riken.jp/)
- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) (http://rarge-v2.psc.riken.jp/phenome/)
- Plant Phosphoproteome Database (RIPP-DB) (https://database.riken.jp/sw/links/en/ria102i/)

Major Funding Sources

RIKEN is supported by MEXT.

Kazusa projects are supported by Chiba-Prefecture.

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

CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)

ALCA (Advanced Low Carbon Technology Research and Development Program) (http://www.jst.go.jp/alca/en/index.html)

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

“Impulsing Paradigm Change through Disruptive Technologies” (ImPACT) (http://www.jst.go.jp/impact/en/outline.html)

MEXT “Cross-ministerial Strategic Innovation Promotion Program” (SIP) in 2014. (http://www.mext.go.jp/english/topics/1345957.htm)

Netherlands

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General Activities

Arabidopsis Research Facilities

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

Utrecht University: Sugar sensing networks and phase transitions (Smeekens), Flooding stress and light avoidance (Voesenek), Plant-Microbe interactions (Pieterse).

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

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

Current Arabidopsis Projects

- NWO-VIDI grant: Unravelling the molecular and cellular basis of vascular tissue formation
- NWO Chemical Sciences ECHO grant: Clathrin-mediated endocytosis in plant salt stress responses: unravelling the biochemical basis
- Learning-from-Nature (STW) consortium
- NWO-NSFC Plant Development consortium
- Participation in 3ERA-CAPS grants
- > 20 individual grants.

Outlook on Arabidopsis Research

Funding possibilities may increasingly rely on comparative and evolutionary research among Arabidopsis accessions, relatives of Arabidopsis or non-relative wild plants and crops. This is basic and not 'translational' research, because in 'translational' research the aim is to translate/copy knowledge to another species. More challenging is to identify conserved or diverged mechanisms and mode of actions from our core of knowledge in Arabidopsis.

Road Map Related Activities

Arabidopsis Tools and Resources

- A mathematical modeling approach to describe dynamics of Arabidopsis RSA. http://www.plantphysiol.org/content/166/3/1387
- ChIP-seq both experimental methods and bioinformatics tools for the analysis of these data. (Kaufmann et al 2010, Nat. Protocols. 5, - 457 - 472) .

- Proteomics-based identification of low-abundance transcription factor complexes in native plant tissues. (Smaczniak et al. 2012. Nature protocols 7 (12), 2144-2158)

Outreach Activities

The Top Sector policy of the Ministry of Economic Affairs with collaborative projects between breeding companies and Academia supports projects on flowering time regulation in Arabidopsis and Brassica species.

Conferences and Workshops

- Experimental Plant Science Annual Meeting Lunteren
- Lorentz Workshop on Quantitative Biology of Auxin Transport (Leiden)
- Green Life Sciences seminar series (Amsterdam)

Selected Publications

- Capturing Arabidopsis root architecture dynamics with root-fit reveals diversity in responses to salinity. Julkowska MM., Hoefsloot HCJ, Mol S. Feron R, de Boer G-J, Haring MA, Testerink C (2014) Plant Physiology 166, 1387-1402.
- PLETHORA gradient formation mechanism separates auxin responses. Mähönen AP, ten Tusscher K, Siligato R, Smetana O, Díaz-Triviño S, Salojärvi J, Wachsman G, Prasad K, Heidstra R, Scheres B. (2014) Nature. 515:125-129.
- Integration of growth and patterning during vascular tissue formation in Arabidopsis. De Rybel, B, Adibi M, Breda AS, Wendrich JR, Smit ME, Novák O, Yamaguchi N, Yoshida S, Van Isterdael G, Palovaara J, Nijsse B, Boekschoten MV, Hooiveld G, Beeckman T, Wagner D, Ljung K, Fleck C, Weijers D (2014) Science 345.
- Genetic control of plant development by overriding a geometric division rule. Yoshida S, Barbier de Reuille P, Lane B, Bassel GW, Prusinkiewicz P, Smith RS, Weijers D (2014) Dev Cell. Apr 14;29(1):75-87. doi: 10.1016/j.devcel.2014.02.002.
- Structural basis for DNA binding by the auxin-dependent ARF transcription factors. Boer R, Freire-Rios A, van den Berg W, Saaki T, Manfield I, Kepinski S, de Vries SC, Solano R, Weijers D, Coll M (2014) Cell 156, 577-589.

Major Funding Sources

European Research Council & Dutch Science organization

New Zealand

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

General Activities

Arabidopsis Research Facilities

Agriculture and horticulture play major roles in the New Zealand economy, with major crops including rye, clover and other forage crops for diary cattle and fruits such as apple and kiwifruit. In this context, Arabidopsis is largely used as an easily manipulated model for the identification and testing of gene function, with information translated into other species. However, within New Zealand universities there is also strong basic research that uses Arabidopsis.

Research using Arabidopsis in New Zealand is conducted in universities and Government-owned Crown Research Institutes (CRIs). Universities with recently published work involving Arabidopsis include the University of Auckland (School of Biological Sciences; Plant Molecular Science), the University of Canterbury (Biological Sciences), Massey University (Institute of Fundamental Science; Institute of Agriculture & Environment) and the University of Otago (Department of Biochemistry). The major Crown Research Institutes using Arabidopsis in research programs are AgResearch and Plant and Food Research. Research in the universities and the Crown Research Institutes is often linked, with several researches having joint appointments in two facilities.

Current Arabidopsis Projects

Major themes of research in New Zealand involving Arabidopsis:

- Flowering time. Investigating how external cues such as day length, light quality and cold regulate flowering by the University of Auckland, the University of Otago and Plant and Food Research.
- Plant Growth and Development. Investigating the molecular control of various aspects of plant development such as plant reproduction, organ size, the cytoskeleton, senescence and hormone signaling by the University of Auckland, the University of Canterbury, Massey University, the University of Otago and AgResearch.
- Stress and Disease response. Ranging from basic research into the function of R genes and stress responses in Arabidopsis to translation into crop plants by the University of Auckland, Massey University and Plant and Food Research.
- Colour and nutrition. Characterization of the molecular pathways controlling the production of pigments and nutritional compounds in plants by the University of Auckland, the University of Otago and Plant and Food Research.

Outlook on Arabidopsis Research

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

Road Map Related Activities

Outreach Activities

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

Conferences and Workshops

- Queenstown Plant Molecular Biology Meeting, August 24-25 2014, Queenstown, New Zealand.
- ComBio incorporating the annual meeting of the New Zealand Society of Plant Biologists and a Plant Cell Biology conference stream. September 27-October 1 2015, Melbourne, Australia.

Selected Publications

- An upstream open reading frame is essential for feedback regulation of ascorbate biosynthesis in Arabidopsis. Laing WA, Martínez-Sánchez M, Wright MA, Bulley SM, Brewster D, Dare AP, Rassam M, Wang D, Storey R, Macknight RC, Hellens RP (2015) Plant Cell tpc.114.133777.
- The Nuclear Immune Receptor RPS4 Is Required for RRS1SLH1-Dependent Constitutive Defense Activation in *Arabidopsis thaliana*. Sohn KH, Segonzac C, Rallapalli G, Sarris PF, Woo JY, Williams SJ, Newman TE, Paek KH, Kobe B, Jones JDG (2014) PLoS Genet 10(10): e1004655.
- Organelles maintain spindle position in plant meiosis. Brownfield L, Yi J, Jiang H, Minina EA, Twell D, Köhler C (2015) Nature Communication 6:6492.
- Overexpression of Medicago SVP genes causes floral defects and delayed flowering in Arabidopsis but only affects floral development in Medicago. Jaudal M, Monash J, Zhang L, Wen J, Mysore KS, Macknight R, Putterill J (2014) Journal of Experimental Botany, 65(2):429-442.
- The genetic architecture of constitutive and induced trichome density in two new recombinant inbred line populations of *Arabidopsis thaliana*: phenotypic plasticity, epistasis, and bidirectional leaf damage response. Bloomer RH, Lloyd AM, Symonds VV (2014) BMC Plant Biology 14:119.

Major Funding Sources

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

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

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South Korea

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General Activities

Arabidopsis Research Facilities

- Multi-photon system
- Multi-omic approaches for systems study on plant senescence
- Proteomics facility
- Phenome analysis facility

Current Arabidopsis Projects

- Protein distribution systems in plant cells
- Circadian clock regulation of environmental stress adaptation in Arabidopsis
- Global Laboratory Research Program focusing on 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 (~6M $/yr for 10 years by Institute of Basic Research)
- Photosynthesis related project (~ 1.0 $/yr for 5 years)

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. However, it is still ok to use Arabidopsis as a model plant with aim of application in crop plants. In addition, a major funding for the basic research is given to the newly established organization, the Institute of Basic Research. In this institute, the research funding is distributed to its center with a small number of scientists. Thus, it is likely that the basic research, in particular plant science using Arabidopsis, in university will suffer in the near future.

Road Map Related Activities

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.

In Korea, a great effort is given to generate new funding for basic research in plants with the help of KRIBB. In addition, there has been a great emphasis on application of basic knowledge from Arabidopsis research to improving crop plants or to the molecular farming.

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
- East Asian Plant Cell Biology Workshop
- 27th International Conference on Arabidopsis research, Gyeongju, South Korea: June 29th-July 3rd 2016

The 27th
International Conference on
Arabidopsis Research

29 June ~ 03 July 2016,

Gyeongju Hwabaek
International Convention
Center, KOREA

Selected Publications

- A secreted peptide acts on BIN2-mediated phosphorylation of ARFs to potentiate auxin response during lateral root development. Cho H, Ryu H, Rho S, Hill K, Smith S, Audenaert D, Park J, Han S, Beeckman T, Bennett MJ, Hwang D, De Smet I, Hwang I. (2014) Nat Cell Biol. 16:66-76.
- Auxin-callose-mediated plasmodesmal gating is essential for tropic auxin gradient formation and signaling. Han X, Hyun TK, Zhang M, Kumar R, Koh EJ, Kang BH, Lucas WJ, Kim JY. (2014) Dev Cell. 28:132-146.
- Arabidopsis ABCG14 is essential for the root-to-shoot translocation of cytokinin. Ko D, Kang J, Kiba T, Park J, Kojima M, Do J, Kim KY, Kwon M, Endler A, Song WY, Martinoia E, Sakakibara H, Lee Y. (2014) Proc Natl Acad Sci U S A. 111:7150-7155.

- Phytochrome-interacting transcription factors PIF4 and PIF5 induce leaf senescence in Arabidopsis. Sakuraba Y, Jeong J, Kang MY, Kim J, Paek NC, Choi G. (2014) Nat Commun. 5:4636.
- An ankyrin repeat domain of AKR2 drives chloroplast targeting through coincident binding of two chloroplast lipids. Kim DH, Park MJ, Gwon GH, Silkov A, Xu ZY, Yang EC, Song S, Song K, Kim Y, Yoon HS, Honig B, Cho W, Cho Y, Hwang I (2014) Dev Cell. 30:598-609.

Major Funding Sources

The Next-Generation BioGreen Program (SSAC, PJ008109)

The cooperative research program (PJ007850) supported by RDA

Global Research Lab program

Woojangchoon project by RDA

Spain

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Conferences and Workshops

- The `ICREA Workshop: From model system to crops, challenges for a new era in Plant Biology' was held on 7-8 May 2014 in Barcelona.

Selected Publications

- Control of vacuolar dynamics and regulation of stomatal aperture by tonoplast potassium uptake. Andrés Z, Pérez-Hormaeche J, Leidi EO, Schlücking K, Steinhorst L, McLachlan DH, Schumacher K, Hetherington AM, Kudla J, Cubero B, Pardo JM (2014) Proc Natl Acad Sci USA 111: E1806-E1814.
- BR-dependent phosphorylation modulates PIF4 transcriptional activity and shapes diurnal hypocotyl growth. Bernardo-García S, de Lucas M, Martínez C, Espinosa-Ruiz A, Davière JM, Prat S (2014) Genes Dev 28: 1681-1694.
- DNA-binding specificities of plant transcription factors and their potential to define target genes. Franco-Zorrilla JM, López-Vidriero I, Carrasco JL, Godoy M, Vera P, Solano R (2014) Proc Natl Acad Sci USA 111: 2367-2372.
- Rational design of a ligand-based antagonist of jasmonate perception. Monte I, Hamberg M, Chini A, Gimenez-Ibanez S, García-Casado G, Porzel A, Pazos F, Boter M, Solano R (2014) Nat Chem Biol 10: 671-676.
- ELF3-PIF4 interaction regulates plant growth independently of the evening complex. Nieto C, López-Salmerón V, Davière JM, Prat S (2015) Curr Biol 25: 187-193.
- PX1 is a phosphate-dependent inhibitor of Phosphate Starvation Response 1 in Arabidopsis. Puga MI, Mateos I, Charukesi R, Wang Z, Franco-Zorrilla JM, De Lorenzo L, Irigoyen ML, Masiero S, Bustos R, Rodríguez J, Leyva A, Rubio V, Sommer H, Paz-Ares J (2014) S Proc Natl Acad Sci USA 111: 14947-14952.
- Natural variation in arsenate tolerance identifies an arsenate reductase in *Arabidopsis thaliana*. Sánchez-Bermejo E, Castrillo G, Del Llano B, Navarro C, Zarco-Fernández S, Martinez-Herrera DJ, Leo-Del Puerto Y, Muñoz R, Cámara C, Paz-Ares J, Alonso-Blanco C, Leyva A (2014) Nat Commun 5: 4617.

Major Funding Sources

About 80 grants from the Ministry of Economy and Competitiveness of Spain fund Arabidopsis research projects at individual laboratories.

Sweden

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General Activities

Arabidopsis Research Facilities

The Arabidopsis community comprise a few hundred researchers and is spread between more than ten universities in Sweden, engaged in vast areas of research from cell biology to ecological research. Arabidopsis constitutes a first choice model species to address basic questions of plant growth and development, photosynthesis and stress related topics. There is a strong focus on aspects of developmental biology, abiotic and biotic stress, plant growth regulators and photosynthesis.

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 http://www.upsc.se/, comprising Departments at Umeå University and SUAS in Umeå

Current Arabidopsis Projects

Large projects recently awarded in development/systems biology; ShapeSystems - Systems Biology of Plant Cell Shape, funded by The Knut and Alice Wallenberg foundation,lead by Prof. Marcus Grebe.

Understanding the environmental regulation of the annual growth cycle in trees- funded by The Knut and Alice Wallenberg foundation, lead by Prof. Rishi Bhalerao

In addition, there are several vast projects in the area of plant forest biotechnology and genomics (http://www.upsc.se/research/large-projects/) using Arabidopsis as an important model species.

Outlook on Arabidopsis Research

An agenda for 'Plant Biotechnology for a Bio-based Economy' has been formulated, with a vison for (i) research programs in plant breeding funded by governmental funding bodies, (ii) a technology neutral legislation for bio-safety, (iii) increased support for innovations and means for stimulating recruitment within plant sciences. The agenda also expand on ways to interact with the industry and stakeholders, informed by such interactions with industry and other parties. The report is found at the Swedish Agency for Innovation Systems (VINNOVA; http://www.vinnova.se), diarienummer 2013-02678). Grant holder/contact Dr. Jens Sundström, The Swedish University for Agricultural Sciences, Uppsala.

The larger funding bodies regularly advertise or are likely to advertise calls that will support Arabidopsis research in the coming years. However, there is a strong steering towards more applied research, and many grant calls emphasize the need for 'products' for the stakeholders. Hence, more funding is projected to support plant research projects in the area of Agriculture and of Forest Biotechnology with emphasis, for instance, on fiber and energy related research. Still, research for example by Liebsch et al., (see selected publications) show that Arabidopsis is a valid,and an important model plant system also for understanding of wood development.

Road Map Related Activities

Arabidopsis Tools and Resources

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

Conferences and Workshops

- 2014, Symposium in Plant Epigenetics in Development and Disease, 23 May, The Swedish University of Agricultural sciences, Biocenter, Uppsala
- 2014, Biocontrol of Plant Diseases: "From the field to the laboratory and back again", 15-18 June, Uppsala
- 2014, Lignin 2014 Conference, 24-28 Augusti, Umeå
- 2014, Swedish Developmental Biology Organization (SWEDBO) 2-3 October, Umeå
- 2015, The Umeå renewable energy meeting held yearly, most recently 25-27 March, UPSC, Umeå
- 2015, Plant Biology Scandinavia 2015, 26th Congress of the Scandinavian Plant Physiology Society (SPPS), 9-13 August, Stockholm; http://spps2015.org/

TOC

Selected Publications

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

- Natural CMT2 Variation Is Associated With Genome-Wide Methylation Changes and Temperature Seasonality. (2014) Shen X, De Jonge J4, Forsberg SKG, Pettersson ME, Sheng Z, Hennig L, Carlborg Ö. PLoS Genetics 12 (12):e1004842.
- PIRIN2 stabilizes cysteine protease XCP2 and increases susceptibility to the vascular pathogen *Ralstonia solanacearum* in Arabidopsis. (2014) Zhang B, Tremousaygue D, Denanc N, van Esse HP, Hörger AC, Dabos P, Goffner D, Thomma BPHJ, van der Hoorn RAL, Tuominen H. Plant Journal 79 (6):1009-19.
- Arabidopsis AIP1-2 restricted by WER-mediated patterning modulates planar polarity. (2014) Kiefer CS, Claes AR, Nzayisenga JC, Pietra S, Stanislas T, Huser A, Ikeda Y, Grebe, M. Development 142(1):151-61.
- Class I KNOX transcription factors promote differentiation of cambial derivatives into xylem fibers in the Arabidopsis hypocotyl. (2014) Liebsch D, Sunaryo W, Holmlund M, Norberg M, Zhang J, Hall HC, Helizon H, Jin X, Helariutta Y, Nilsson O, Polle A, Fischer U. Development 141 (22):4311-19.
- QTL mapping of freezing tolerance: links to fitness and adaptive trade-offs. Oakley CG, Agren J, Atchison RA, Schemske DW (2014) Molecular Ecology 23(17):4304-15.

Major Funding Sources

The Swedish Research Council (VR; http://www.vr.se)

The Swedish Foundation for Strategic Research (http://www.stratresearch.se)

The Swedish Agency for Innovation Systems (VINNOVA; http://www.vinnova.se)

The Royal Academy of Science (http://www.kva.se)

The Royal Academy of Agriculture and Forestry (http://www.ksla.se)

The Swedish Research Council Formas (http://www.formas.se)

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

Carl Tryggers Foundation for Scientific Research (http://www.carltryggersstiftelse.se/)

The Kempe Foundations (http://www.kempe.com)

Switzerland

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General Activities

Arabidopsis Research Facilities

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

  It is composed of Zurich-Basel Plant Science Center (competence center linking and supporting the plant science research community of the University of Zurich, ETH Zurich and the University of Basel, http://www.plantsciences.uzh.ch/index.html), Arc lémanique plant science, and BeNeFri network.
- Functional Genomics Center Zurich (e.g. genome sequencing of *Arabidopsis halleri*)
- Genetic Diversity Center (e.g. genome-wide polymorphisms of *Arabidopsis halleri*)

Current Arabidopsis Projects

Plant research projects and researchers are listed at the website of Swiss Plant Science Web.

https://swissplantscienceweb.ch/research/research-portfolios/, https://swissplantscienceweb.ch/research/researchers/

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

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

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

Human Frontier Science Program

TAKANO Junpei and Geldner Niko, Molecular dissection of Casparian strip function in nutrient homeostasis in higher plants, Young Investigator Award, 2011-2014

SHIMIZU Kentaro, Sese Jun, Hay Angela, Network merging analysis of duplicate genome function in recently hybridized species, Young Investigator Award, 2011-2014

Outlook on Arabidopsis Research

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

Road Map Related Activities

Arabidopsis Tools and Resources

- Further development of Genevestigator database (Zimmerman et al. 2014)
- Bioinformatic workflow for polyploid genomic analysis (HomeoRoq) applied for Arabidopsis kamchatica (Akama et al. 2014)
- The genome assembly of Arabidopsis halleri subsp. gemmifera and A. lyrata subsp. petraea (Akama et al. 2014)
- Swiss-Prot database contributes to TAIR database

Outreach Activities

- Agora outreach program of Plant Science Center
- Gen Suisse program (http://www.gensuisse.ch/) for high school students in French, "Agriculture from the Garden of Eden to GMOs" by Prof. Christian Fankhauser
- Continuing Education Program in Plant Sciences for Secondary School Teachers http://www.plantsciences.uzh.ch/outreach/atschool.html

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

  Plant Ecophysiology, Feel the puls of the plants (WS II, 2011 - 2014)

  Plant Phylogeny: Light on the Evolution of the Green Organisms (WS III, 2013 - 2014)

  Plant Molecular Biology II: Angewandte evolutionsforschung mit Gemüse aus dem Supermarkt (2), Evolution du Broccoli (Development in 2014 / first time offered in Dec 2014) (WS V)
- PSC Discovery Program for Youth (Swiss National Science Foundation) (2015-)

Conferences and Workshops

- SwissPlant Symposium 2015, Leukerbad, Switzerland, 28-30 Jan 2015
- PSC Summer school
- 2014, Sept. 7 – 12 and Oct. 10, Green Revolution Reloaded: Emerging Technologies for Sustainable Agriculture, Zurich-Basel Plant Science Center
- Frontiers in Plant Sciences Courses Series: Between 2012 and 2014 the PSC received funding for a series of workshops at the frontiers in plant sciences by the SUK "Interuniversity Program" through University of Zurich, ETH Zurich and University of Basel. These workshops are dedicated to applications: i.e. concepts but also tools in these advanced areas:
- 2014: Metabolic fluxes applied to agricultural systems (George Ratcliffe and Nick Kruger, University of Oxford)
- 2014: Insights in RNA biology (HS14)

Selected Publications

- A spatial accommodation by neighboring cells is required for organ initiation in Arabidopsis. Vermeer JE, von Wangenheim D, Barberon M, Lee Y, Stelzer EH, Maizel A, Geldner N (2014) Science 343(6167):178-83.
- ExpressionData - A public resource of high quality curated datasets representing gene expression across anatomy, development and experimental conditions. Zimmermann P, Bleuler S, Laule O, Martin F, Ivanov NV, Campanoni P, Oishi K, Lugon-Moulin N, Wyss M, Hruz T, Gruissem W (2014) BioData Min 7:18.
- Genome-wide quantification of homeolog expression ratio revealed nonstochastic gene regulation in synthetic allopolyploid Arabidopsis. Akama S, Shimizu-Inatsugi R, Shimizu KK, Sese J (2014)Nucleic Acids Res 42(6):e46.

- A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. International Wheat Genome Sequencing Consortium (IWGSC). Mayer KF, Rogers J, Doležel J, Pozniak C, Eversole K, Feuillet C, Gill B, Friebe B, Lukaszewski AJ, Sourdille P et al. (2014) Science 345(6194):1251788.
- Molecular genetic framework for protophloem formation. Rodriguez-Villalon A, Gujas B, Kang YH, Breda AS, Cattaneo P, Depuydt S, Hardtke CS (2014) Proc Natl Acad Sci U S A 111(31):11551-6.

Major Funding Sources

Swiss National Science Foundation

European Research Council (ERC)

SystemsX.ch

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

Syngenta (Plant Science Center - Syngenta Fellowship).

Human Frontier Science Project (see above)

Research and Innovation Staff Exchange (RISE) of European Commission

United Kingdom

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General Activities

Arabidopsis Research Facilities

The main UK funding body for plant science, the Biotechnology and Biological Sciences Research Council (BBSRC; http://www.bbsrc.ac.uk/) continues to be supportive of Arabidopsis research. One of two international facilities, the UK's University of Nottingham Arabidopsis Stock Centre (uNASC; http://arabidopsis.info/) has recently been awarded funding to continue and maintain its germplasm distribution services. Over 300 research groups in Universities and Research Institutes in the UK utilise 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 Centre at the Institute of Biological, Environmental and Rural Sciences (IBERS) at Aberystwyth University. The University of Nottingham has recently opened the state-of-the-art Hounsfield Plant Phenotyping facility campus, and the University of Bristol also has a brand-new £56 million Life Sciences building with extensive facilities for Arabidopsis and plant science research.

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

Current Arabidopsis Projects

Arabidopsis research is largely project-focused, with work based in individual laboratories, multi-institutional collaborations or national Centres and Institutes. OpenPlant (www.openplant.org/), a consortium based in Norwich and Cambridge, is one of three synthetic biology multi-disciplinary research centres announced in 2014 by the UK funding councils BBSRC, EPSRC and TSB will develop open tools and resources.

In the UK, there are currently more than 100 active BBSRC-funded research projects using Arabidopsis, with a combined value of over £54 million. Several large grants have recently been awarded to Arabidopsis researchers in the UK including:

- £1.35 million to Enrico Coen (John Innes Centre) "Organising tissue cell polarity and growth in plants". BBSRC: http://gtr.rcuk.ac.uk/project/5F333C47-FB9E-4264-88F9-67C018D63D3B.

- £1.12 million to Xiaoqi Feng (John Innes Centre) "Epigenetic regulation of sexual lineage development in plants". BBSRC: http://gtr.rcuk.ac.uk/project/DEA800FA-EA77-42E3-AD27-52E6C0CB74FF.
- £800k to Gordon Simpson (University of Dundee) "The Arabidopsis Epitranscriptome" (BBSRC: http://www.bbsrc.ac.uk/pa/grants/AwardDetails.aspx?FundingReference=BB/M010066/1)
- £638k to Sean May (University of Nottingham) to continue and maintain operations for uNASC's germplasm distribution centre.

The Universities of Warwick, Nottingham and Liverpool, and The Genome Analysis Centre, have been awarded BBSRC capital funding to create iPlant UK – a UK-based node of the cyberinfrastructure resources developed by the iPlant Collaborative in the US. The award also provides funds to convert existing software tools for plant data analysis from their current formats to formats that can be shared via the open access iPlant environment. Complementing the work of iPlant UK, and the Sainsbury Laboratories as mentioned above, a new EPSRC and BBSRC-funded Synthetic Biology Centre at the University of Warwick carries out research on four themes, one of which is plant synthetic biology. This also has a significant component of Arabidopsis research.

Outlook on Arabidopsis Research

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

BBSRC is leading the cross-council and cross-government Global Food Security programme. In 2013, plans for a UK Strategy for Agricultural Technologies were announced with £60 million available for research development and £90 million for Centres for Agricultural Innovation – calls for proposals to apply for these funds are now emerging. In October, the Government's Business Secretary also announced funding of £125 million for bioscience Doctoral Training Centres, focusing on training the next generation of food and agricultural scientists.

Road Map Related Activities

Arabidopsis Tools and Resources

- The Arabidopsis Information Portal: Krishnakumar et al, 2014.
  In 2013, BBSRC awarded funds to a group led by Gos Micklem (University of Cambridge) to work with NSF-funded colleagues at the J Craig Ventor Institute, Texas Advanced Computing Centre, and the Carnegie Institution for Science to develop the Arabidopsis Information Portal. This project is now well under way.
- CandiSNP: Etherington et al, 2014.
  A user-friendly web application developed by scientists at The Sainsbury Laboratory Norwich and the Genome Analysis Centre to map mutations in plant genomes.
- Using monoclonal antibodies to label living root hairs: a novel tool for studying cell wall microarchitecture and dynamics in Arabidopsis: Larson et al, 2014.
  Working with US colleagues, Emily Larson from the University of Glasgow was involved in the development of a new protocol for live-cell imaging of Arabidopsis roots with monoclonal antibodies that bind to specific cell wall polymers.
- Using 2k + 2 bubble searches to find single nucleotide polymorphisms in k-mer graphs: Younsi and Maclean, 2014.
  Younsi and MacLean from The Sainsbury Laboratory describe how they used sequence data from 16 *Arabidopsis thaliana* ecotypes to test and validate an algorithm capable of accurately detecting single nucleotide polymorphisms from de Bruijn graphs.
- Cell type-specific transcriptome analysis in the early *Arabidopsis thaliana* embryo: Slane et al, 2014.
  Ive De Smet from the University of Nottingham worked with a German–Belgian team to describe the use of fluorescence-activated nuclear sorting (FANS) to conduct cell type-specific transcriptome analysis in the early Arabidopsis embryo.
- Sample preparation for phosphoproteomic analysis of circadian time series in *Arabidopsis thaliana*: Krahmer et al, 2014.
  A useful review from the SysSynth team at the University of Edinburgh, which discusses methods used in phosphoproteomics.

Outreach Activities

GARNet, the national network for the UK Arabidopsis and wider plant science research community, applied for and was awarded renewed BBSRC funding until 2020. This will allow GARNet to continue serving the community by organising workshops, training and helping to develop community resources. GARNet published a Journal of Experimental Botany paper on 'Data mining with iPlant', describing the benefits of iPlant's cyberinfrastructure for plant scientists in terms of 'big data' storage, sharing and pipeline analysis. GARNet also continues to support the UK Plant Sciences Federation (UKPSF) to establish working groups to implement the recommendations highlighted in its 2013 report, UK Plant Science: Current Status and Future Challenges. GARNet also publishes a twice-yearly newsletter for the UK Arabidopsis community.

British plant scientists took part in outreach events around the country culminating in the public Great British Bioscience festival in London in November. Exhibits included a giant 'super plant' to demonstrate how plant scientists are helping to solve problems such as climate change (Aberystwyth University), an exhibit on engineering plants to produce fish oils (Rothamsted Research/University of Stirling), hands-on activities to show how plants can be used as natural factories (John Innes Centre), and a Lego model of the new Hounsfield Plant Phenotyping facility.

Conferences and Workshops

- GARNet ran two oversubscribed Software Carpentry workshops in 2014, demonstrating the demand for first-principles training in computer programming within the plant science community. The GARNet conference 'Arabidopsis: The Ongoing Green Revolution' was held in September 2014 and attended by almost 100 members of the UK Arabidopsis community. With OpenPlant, GARNet is planning a Synthetic Biology workshop at The Sainsbury Laboratory in September 2015.
- The Society for Experimental Biology's annual conference was held in Manchester in the UK in June 2014.
- IBERS held a Spring School on Plant Phenotyping in March 2015, and The Sainsbury Laboratory is holding a Plant–Microbe Interactions Summer School in August 2015. The UKPSF's annual conference will take place at Harper Adams University in April 2015.

Selected Publications

- Antagonistic roles for H3K36me3 and H3K27me3 in the cold-induced epigenetic switch at Arabidopsis FLC. Yang H, Howard M, Dean C (2014) Current Biology 24(15):1793-1797.
- Arabidopsis NAC45/86 direct sieve element morphogenesis culminating in enucleation. Furuta KM, Yadav SR, Lehesranta S, Belevich I, Miyashima S, Heo JO, Vatén A, Lindgren O, De Rybel B, Van Isterdael G, Somervuo P, Lichtenberger R, Rocha R, Thitamadee S, Tähtiharju S, Auvinen P, Beeckman T, Jokitalo E, Helariutta Y (2014) Science 345(6199):933-937.
- An Arabidopsis gene regulatory network for secondary cell wall synthesis. Taylor-Teeples M, Lin L, de Lucas M, Turco G, Toal TW, Gaudinier A, Young NF, Trabucco GM, Veling MT, Lamothe R, Handakumbura PP, Xiong G, Wang C, Corwin J, Tsoukalas A, Zhang L, Ware D, Pauly M, Kliebenstein DJ, Dehesh K, Tagkopoulos I, Breton G, Pruneda-Paz JL, Ahnert SE, Kay SA, Hazen SP, Brady SM (2014) Nature 517:571-575.
- ELF3 controls thermoresponsive growth in Arabidopsis. Box MS, Huang E, Domijan M, Jaeger KE, Khattak AK, Yoo SJ, Sedivy EL, Jones DM, Hearn TJ, Webb AA, Grant A, Locke JC, Wigge PA (2014) Current Biology 25(2):194-199.
- Two linked pairs of Arabidopsis TNL resistance genes independently confer recognition of bacterial effector AvrRps4. Saucet SB, Ma Y, Sarris PF, Furzer OJ, Sohn KH, Jones JD (2015) Nature Communications 6:6338.

Major Funding Sources

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

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

European Research Council
http://ec.europa.eu/research/era/index_en.htm

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

Natural Environment Research Council
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General Activities

Arabidopsis Research Facilities

There are a large number of US institutions, companies, and facilities that conduct Arabidopsis research.

The Arabidopsis Biological Resource Center (ABRC) collects, preserves, reproduces and distributes diverse seed and other stocks of *Arabidopsis thaliana* and related species. Resources are donated by, and delivered to, researchers from around the world. More than 100,000 samples are shipped annually to 60 countries. ABRC partners with NASC, the European Stock Centre (UK) and RIKEN BioResourceCenter (Japan) to provide valuable Arabidopsis resources to the global community. See the 'Resources' section for more details.

Current Arabidopsis Projects

There are a large number of US Arabidopsis projects that include many partners and encompass a vast array of topics. Just two examples are:

1. Araport is an open-access online community resource for Arabidopsis research which enables biologists to navigate from the *Arabidopsis thaliana* Col-0 reference genome sequence to its associated annotations including gene structure, gene expression, protein function, and interaction networks. See Resources section for more information.
2. IAIC: the International Arabidopsis Information Consortium was established to facilitate a coordinated global Arabidopsis informatics effort to maintain the continuity of key Arabidopsis resources while simultaneously expanding their breadth and depth. See Resources section for more information.

Outlook on Arabidopsis Research

NAASC recommends comprehensive reassessment of training needs for 21st century plant biology. Knowledge gained in Arabidopsis informs our understanding of the genetic basis of plant processes and crop traits, yet the complexity of datasets is only increasing. The challenge for all plant biologists is to study and understand this complexity, which will require a larger focus on quantitative systems and computational approaches. 21st century plant biology will require new education and research training that includes strong integration of wet-lab, computational, quantitative, and bioinformatic approaches. Successful 21st century biologists will need to be comfortable with networks containing genes and their products as well as high-throughput, quantitative and dynamic modeling techniques. Collaborative efforts that maximize the skills of a diverse group of people will fundamentally underpin this integrated approach. A key goal is for contemporary Arabidopsis researchers to be skilled with emerging technologies and approaches where using Arabidopsis as a model organism will provide fundamental discoveries and enable translational research in crop species. NAASC was recently awarded an NSF grant that will enable discussions and information gathering on training needs for 21st century plant biology. Additionally, NAASC will hold a workshop at ICAR 2015 entitled 'Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology".

Road Map Related Activities

Outreach Activities

- ICAR 2015 - NAASC will send about 20 US scientists to the 26th ICAR including via travel scholarships to early-career scientists and groups under-represented in US science.
- NAASC members will organize/co-organize three ICAR 2015 workshops:

  'Bioinformatics, Quantitative Techniques and Computational Skills: Current Research and Future Training Needs for 21st Century Plant Biology' (Siobhan Brady and Joanna Friesner): This workshop will combine wet-lab and computational research threads by featuring presentations from early-career scientists that utilize quantitative or computational techniques and approaches. Presenters will focus some time on what they see as the relevant quantitative, computational, and technological needs for their research program, and for training upcoming students and postdocs. The workshop will also include introductions of several plant biology bioinformatics resources and training initiatives and conclude with an interactive discussion about training needs for 21st century plant biology.

  'Epigenomics' (Doris Wagner, NAASC and François Roudier): This workshop will promote epigenomic and epigenetic research in plants and in particular will highlight novel approaches, tools and resources in this field and their relevance for plant epigenetics. Research talks will focus on histone dynamics, comparative epigenomics and higher order chromatin structure.

  'Novel Tools and Techniques - New frontiers in single cell biology' (Nick Provart, NAASC, and Luise Brand): A key recommendation of the 2012 'Roadmap' produced by the Multinational Arabidopsis Steering Committee is to foster understanding of plant development from the single cell to the whole plant and to plant populations.

This workshop will introduce MASC, have a brainstorming session, and include talks about novel tools and techniques that focus on single cell applications and nanobiology.

- ICAR 2014, organized by NAASC/US, included outreach to industry and applied research.
- IAIC- the International Arabidopsis Informatics Consortium is a US-led international effort to coordinate global Arabidopsis informatics efforts.
- NAASC newsletter contribution: See page 5: http://newsletter.aspb.org/2014/marapr14.pdf

Conferences and Workshops

ICAR 2014

NAASC organized the 25th International Conference on Arabidopsis Research (ICAR) in Vancouver, Canada, July 28 - August 1, 2014. 625 attendees from 34 countries participated in 37 scientific and educational sessions including nearly 200 oral and over 400 poster presentations. In recognition of the significance of the 25th gathering, NAASC asked the Arabidopsis Keynote speakers to provide an assessment of the past, present and future of Arabidopsis research and to address (1) How Arabidopsis research has impacted their field; (2) The history of relevant research in their field; (3) How continued focus on a deeply developed model will contribute to answering remaining key problems in biology; and (4) How such knowledge will impact food security and crop production in a changing climate. NAASC designed the conference program to showcase research by scientists new to ICAR as well as early-career researchers. Several additional novel approaches included concurrent session overviews; an emphasis on talks from submitted abstracts; a new Synthetic Biology plenary session; career development workshops for early-career researchers and under-represented groups in US science; and 'oral poster' presentations. Based on an anonymous online survey (50+% response rate) the 25th ICAR was well-received: 85% of respondents rated the meeting as 'good' or 'excellent'; the program's focus on early-career researchers was met with enthusiasm; and when respondents were asked to rank speakers on a scale of 1-5, where 1= poor, and 5=excellent, ratings were 4.4 (Keynote), 4.3 (Invited), 3.72 (Overview), and 3.58 (Speakers from Abstracts.) We received useful input for future ICARs that we shared with ICAR 2015 and 2016 organizers and will consider for the next NAASC-organized conference, expected to be ICAR 2017.

Additional workshops

- At ICAR 2014 current and former NAASC members organized the workshop 'International Arabidopsis Informatics Consortium: Community Research and Resources, including the Arabidopsis Information Portal and Modules'.
- The NSF-supported IAIC award to Blake Meyers provided joint-sponsorship of an Araport developer workshop oriented toward Arabidopsis researchers and students last November (Austin, Texas, USA.) See the IAIC report for more information.

Selected Publications

There are many US Arabidopsis publications and it would be impossible to select only 5; therefore here we list just one, contributed by several NAASC members on diversity in science and new training workshops at ICAR 2014: See page 5 at http://newsletter.aspb.org/2014/marapr14.pdf.

Major Funding Sources

US Arabidopsis Research is primarily supported by the National Science Foundation (NSF):
http://www.nsf.gov/

US Department of Agriculture (USDA):
http://www.usda.gov/
US Department of Energy (DOE): http://energy.gov/
National Institutes of Health (NIH):
http://www.nih.gov/

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

North American Arabidopsis Steering Committee (NAASC)

North American Arabidopsis Steering Committee (NAASC) members are elected by the community to provide North American representation to MASC and serve 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) ICAR fundraising, (2) serving on advisory committees and boards, (3) acting as leaders and participants for community-related initiatives and (4) acting as liaison between researchers, funders, and other community resources.

1. The eight NAASC members serve four-year terms with two rotating off annually. Nick Provart (University of Toronto) and Jose Alonso (North Carolina State University), conclude their terms in fall 2015 after the next election. Continuing members are Siobhan Brady (University of California, Davis), Keiko Torii (University of Washington), Erich Grotewold (Ohio State University/ABRC), Sarah Assmann (Pennsylvania State University), Doris Wagner (University of Pennsylvania) and Rick Vierstra (University of Wisconsin, Madison).

2. ICAR 2014 funding included awards secured by Keiko Torii, whose NSF award funded 32 participants, and Siobhan Brady, whose USDA award funded 13 participants.
3. Committee service: Jose Alonso and Nick Provart were ICAR 2014 conference co-chairs. Jose Alonso, Nick Provart, and Siobhan Brady serve on the ABRC advisory committee. Nick Provart and Erich Grotewold are members of the IAIC Steering Committee. Siobhan Brady and Sarah Assmann serve on an American Society of Plant Biologists (ASPB) 'Events and Meetings' advisory board and Sarah Assmann is a member of the ASPB Board of Trustees.
4. Joanna Friesner, NAASC Coordinator, supports NAASC including as lead conference organizer for North American ICARs and assisting with NAASC-led community initiatives such as the International Arabidopsis Informatics Consortium.

Notable Awards and Honors for US Researchers Using Arabidopsis

- Elected to the US National Academy of Sciences (NAS), April 2014: R. Scott Poethig (former NAASC), Ken Keegstra, Ed Buckler
- Elected as Fellows of the American Association for the Advancement of Science (AAAS), November 2014: Christoph Benning, Andrew Bent, Eric Mjolness, Stanley Roux
- ASPB 2014: Stephen Hales Prize: Mike Thomashow; Early Career Award: Jing-Ke Weng; Lawrence Bogorad Award for Excellence in Plant Biology Research: Thomas Guilfoyle.
- Genetics Society of America: Thomas Hunt Morgan Medal: Fred Ausubel; Genetics Society of America Medal: Steve Henikoff

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