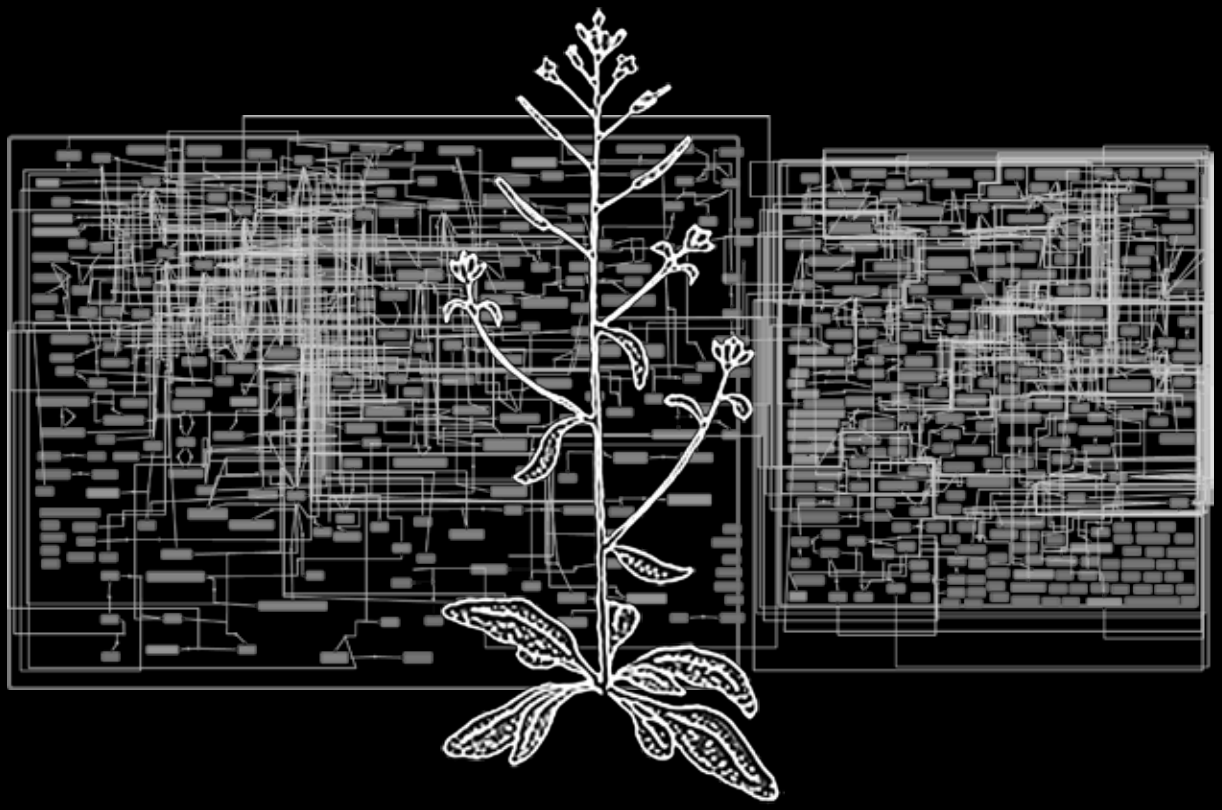
The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2013



Scientific Highlights in 2012 include

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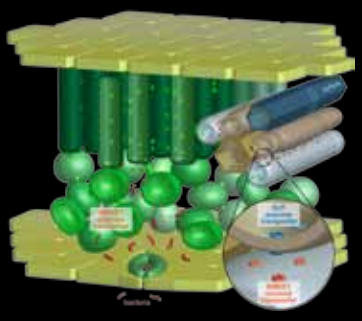

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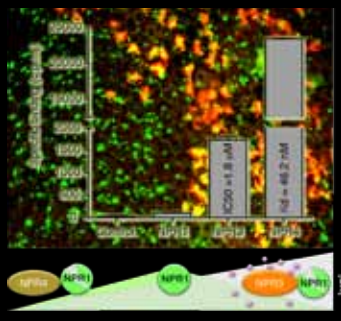
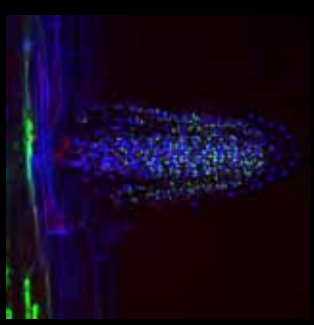


Salicylic Acid Perception



Root Microbiome

The Multinational Arabidosis Steering Committee · June 2013

The Multinational Arabidopsis Steering Committee Report 2013

Annual Report

Wolfram Weckwerth
wolfram.weckwerth@univie.ac.at
MASC Chair

Barry Pogson
barry.pogson@anu.edu.au
MASC Co-chair

Luise H. Brand
luise.brand@uni-tuebingen.de
MASC Coordinator, Executive Secretary

Thomas Altmann altmann@ipk-gatersleben.de
Ruth Bastow ruth@garnetcommunity.org.uk
Malcolm Bennet malcolm.bennett@nottingham.ac.uk
Dominique Bergmann Bergmann@stanford.edu
Jim Beynon jim.beynon@warwick.ac.uk
Dario Bonetta dario.bonetta@uoit.ca
Siobhan Brady sbrady@ucdavis.edu
Jelena Brkljacic brkljacic.1@osu.edu
Jorge J. Casal casal@ifeva.edu.ar
Charis Cook charis@garnetcommunity.org.uk
Brian Dilkes bdilkes@purdue.edu
Joe Ecker ecker@salk.edu
Maria E. Eriksson maria.erikson@plantphys.umu.se
Fabio Fiorani f.fiorani@fz-juelich.de
Joanna Friesner jdfriesner@ucdavis.edu
Robert Furbank robert.furbank@csiro.au
Erich Grotewold grotewold.1@osu.edu
Wilhelm Gruissem wgruissem@ethz.ch
Klaus Harter klaus.harter@zmbp.uni-tuebingen.de
Heribert Hirt hirt@evry.inra.fr
Marie-Theres Hauser marie-theres.hauser@boku.ac.at
Joshua Heazlewood jlheazlewood@lbl.gov
Ykä Helariutta yrjo.helariutta@helsinki.fi
Eva Huala huala@acoma.stanford.edu
Alexandra Jones alex.jones@sainsbury-laboratory.ac.uk
Jitendra P. Khurana khuranaj@genomeindia.org
Masatomo Kobayashi kobayasi@rtc.riken.jp
Minami Matsui minami@riken.jp
Sean May sean@arabidopsis.org.uk
Blake Meyers meyers@dbi.udel.edu
Javier Paz-Ares jpazares@cnb.csic.es
J. Chris Pires piresjc@missouri.edu
Nicholas Provart nicholas.provart@utoronto.ca
Kazui Saito ksaito@psc.riken.jp
Ben Scheres b.scheres@uu.nl
Motoaki Seki mseki@psc.riken.jp
Giovanna Serino giovanna.serino@uniroma1.it
Charles Spillane charles.spillane@nuigalway.ie
Ramamurthy Srinivasan srinivasan53@gmail.com
László Szabados szabados@brc.hu
Lieven De Veylder lieven.deveylder@psb.vib-ugent.be
Sacco de Vries sacco.devries@wur.nl
Shaul Yalovsky ShaulY@tauex.tau.ac.il
Weicai Yang wcyang@genetics.ac.cn
Viktor Zarsky viktor@natur.cuni.cz

The Multinational Arabidopsis Steering Committee
June 2013

Imprint

Editor

Luise H. Brand
University of Tuebingen
Auf der Morgenstelle 1
72076 Tübingen
Germany
luise.brand@uni-tuebingen.de

Cover Design

Luise H. Brand, MASC coordinator (University of Tuebingen, Germany)

Cover Images

Metabolic network of *Arabidopsis thaliana* (center) courtesy of Thomas Naegele, University of Vienna, Austria.

Chloroplast biogenesis (bottom left) courtesy of Paul Jarvis, University of Leicester, U.K., graphics: Paula Töpel: Chloroplasts from three different genotypes of *Arabidopsis thaliana*: wild type (center), *ppi1* mutant (bottom) and *sp1 ppi1* mutant (top) (see "Scientific Highlights in 2012" on page 35).

Model of sucrose transport in leaves (bottom, left center) courtesy of Wolf B. Frommer, Carnegie Institution for Science, U.S., artwork: Guido Grossmann (see "Scientific Highlights in 2012" on page 35).

Salicylic acid perception (bottom, right center) courtesy of Xinnian Dong, Duke University, U.S. (see "Scientific Highlights in 2012" on page 36).

The *Arabidopsis thaliana* root microbiome (bottom right) courtesy of Sarah Lebeis, The University of North Carolina at Chapel Hill, U.S.: A fluorescent micrograph capturing the presence of bacteria (shown in green) on the surface of an emerging Arabidopsis lateral root (plant nuclei shown in blue) (see "Scientific Highlights in 2012" on page 36).

For further information please visit

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

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Acknowledgements

We thank the German Science Foundation (DFG) for providing the funds to publish this report.

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

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

NASC, The European Arabidopsis Stock Centre: http://arabidopsis.info/progreports.html

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Foreword to the Report

This is the 2012/2013 annual report of the Multinational Arabidopsis Steering Committee (MASC). In 1990 nine scientists from the United States, Europe, Japan and Australia formed an *ad hoc* committee to promote large-scale studies in *Arabidopsis thaliana*. A report outlining a plan for international cooperation was prepared and the Multinational *Arabidopsis thaliana* Genome Research Project (1990- 2001) was initiated. The aim of this project was to understand at the molecular level the physiology, biochemistry, growth and development of a flowering plant. A significant goal was to determine the complete sequence of the Arabidopsis genome by the year 2000, concurrent with the development of other vital resources and collaborations. The international scientific community agreed to cooperate on several objectives including: the identification and characterization of the structure, function, and regulation of Arabidopsis genes; development of technologies for genome studies; establishment of biological resource centers; development of an informatics program to facilitate exchange of research results; and development of human resources and support of workshops and symposia. Most importantly, the community agreed that multinational cooperation was essential and must involve the free exchange of ideas and information through open communication and interactions. The Multinational Arabidopsis Steering Committee (MASC) was established to implement overall research coordination and was charged with annually reviewing scientific progress and identifying needs and new opportunities for the global Arabidopsis research community. MASC also acts in an advisory capacity to various national funding agencies.

The Multinational *Arabidopsis thaliana* Genome Research Project completed the sequencing of the reference Arabidopsis genome in 2000. The success of this project inspired the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project, an ambitious plan to determine the function of every Arabidopsis gene by the year 2010. Numerous laboratories internationally took part in this project and very large datasets and resources were generated leading to breakthroughs in understanding the fundamental processes underlying plant growth development and responses to the environment. The success of this project is the result of numerous factors, including the ease of manipulation of Arabidopsis, the synergistic development of a powerful set of tools, the ease of access to stocks and other key reagents, the collegiality of the Arabidopsis scientific community and the generous support from various national funded programs. Whilst the function of every Arabidopsis gene has not yet been determined, the progress of studies at the level of the genome, transcriptome, proteome, metabolome and other '-omes' has been unprecedented. Studies originally conducted in Arabidopsis are increasingly resulting in the development of new solutions to global agricultural challenges.

As research continues, new large-scale funding mechanisms need to be in place to continue the promotion of discovery in this reference plant. Equally as important are the needs for strong funding in support of individual research labs doing creative work focused on a smaller scale, and of projects that link basic and applied approaches. Given the increasingly important role that Plant Science will play in the future, new support mechanisms for Arabidopsis resources should be identified. For example following two community workshops to consider how the very large amount of data generated by Arabidopsis researchers can be managed (and funded) in a coordinated manner internationally, the creation of the International Arabidopsis Informatics Consortium (IAIC) funded by a variety of sources was proposed (IAIC, (2010) Plant Cell 22: 2530-2536). In 2011, the IAIC became a reality and more information on the development of this infrastructure can be found on page 10.

Building upon its well-established tradition for international cooperation in 2010 MASC began working on a road map for the next decade. This document entitled "From Bench to Bountiful Harvests" was published in 2012 and aims to inform scientists, funding bodies and decision makers on the future foci of Arabidopsis research (Lavagi et al. (2012) Plant Cell 24:2240-2247). We expect the road map will help all Arabidopsis researchers to continue to provide the underlying knowledge that will be essential to combat the current global challenges we face. This report details progress made over the last year by the international Arabidopsis community including highlights from intensive efforts in basic research and advances in translating basic to applied research. Although the timeframe of translation into applied research can be long, and the outcomes unpredictable, the very rapid increase in publication rate and patent filing in the last 15 years indicates what we might expect in the next decade. This report demonstrates the continued high level of cooperation that exists throughout the global community and the impressive returns that funding agencies gain from supporting Arabidopsis research.

The Multinational Arabidopsis Steering Committee

June 2013

Executive Summary

The increasing demands of a growing, prosperous world for improved agricultural products including food, fiber and fuel, intensifies the need for an extensive understanding of the basic biology and ecology of plants. As the first plant to have its entire genome sequenced, *Arabidopsis thaliana* has become the most important model system for plant biology and a vital resource for the study of other multicellular organisms. Arabidopsis research has increasingly impacted on our understanding of other plants. We expect that the knowledge gained from this reference species will serve to advance understanding of other organisms, particularly crop species. Thus the knowledge generated by Arabidopsis research will translate into new and improved plant products and contribute to agricultural productivity. The transfer of knowledge from Arabidopsis to other systems is accelerating due to the efforts of a vibrant research community and the leveraging of advances and resources made over the last two decades. Arabidopsis has shifted from model to reference organism - the plant in which fundamental principles are established and to which other plants are compared. Arabidopsis is now uniquely poised to address biological questions that range from the molecular to the ecosystem level. Further, the resources currently available and under development will allow rapid experimentation to answer existing and future challenging questions. However, the impact of Arabidopsis research extends far beyond the plant realm; researchers studying other organisms such as humans, flies, worms, fungi, and mice increasingly rely on the extensive collection of Arabidopsis resources and knowledge to inform their own research. Therefore, continued and expanded funding and international collaboration are critical to future success. Maintaining and strengthening ties between researchers in all parts of the world, and between basic and applied scientists, is necessary to create the synergy needed to effectively meet the health and agricultural challenges facing us.

The highly active and enthusiastic Arabidopsis community around the world continues to attract new researchers. According to The Arabidopsis Information Resource (TAIR), 24,453 researchers and 9,586 labs total are registered at TAIR as of 15th March 2013. Of these, the records for 9,731 people and 3,907 labs were updated in the past 5 years. It is interesting to note that the number of people and laboratories updated in the past five years continues to increase, suggesting that the increasing number of researchers and laboratories registered at TAIR represents an increase in active users, not just the gradual accumulation of inactive accounts. Arabidopsis continues to be an ideal training system for future generations of researchers with broadened expertise, for example, through the recent development of systems biology projects, which combine classical 'wet lab' approaches with, advanced computational methods. Resources must continue to be coordinated in order to maximize the efforts of the various labs around the world. It remains as true today as it was eleven years ago at the release of the reference genome, that only sustained collaborations and timely sharing of data, stocks, and other resources will enable the Arabidopsis community to achieve its ambitious goals.

- Community Projects and Resources: Since 2007 several Arabidopsis community projects and resources contributed reports to the annual MASC report to inform the community about their progress, activities and goals. This year the three biological resource centers Arabidopsis Biological Resource Center (ABRC, U.S.), the Nottingham Arabidopsis Stock Centre (NASC; U.K.) and the RIKEN BioResource Center (RIKEN BRC; Japan) submitted reports, as well as the online information resource TAIR and the International Arabidopsis Informatics Consortium (IAIC) (see page 9 ff.). The transfer of TAIR data to the iPlant server is in progress to facilitate the availability after the end of the funding period in August 2013. The IAIC and the Bioinformatics Subcommittee continue to work closely together.

MASC Subcommittees

The MASC Subcommittees promote international cooperation in a number of areas of functional genomics research:

- Bioinformatics: Two major International Arabidopsis Informatics Consortium (IAIC) community meetings were held at the 2012 ICAR in Vienna (Austria) and PAG Conference 2013 (San Diego). Further progress towards developing a new "Arabidopsis Information Portal" (AIP) was made, a grant application to develop the AIP was submitted to U.S. NSF and the preparation of a detailed project plan is in progress (see page 13).
- ORFeomics: The ORF and cDNA clones table was updated again to keep track of the progress made towards clones for all annotated Arabidopsis protein coding genes (see page 14).
- Metabolomics: The subcommittee's webpage has recently been launched (www.masc-metabolomics.org). The MASCM (Multinational Arabidopsis Steering Committee Metabolomics) gator portal is under development. The web interface will provide a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases in a way comparable to that offered by the MASCP (MASC Proteomics) gator portal (http://gator.masc-proteomics.org/). Four joint US and

Japanese research teams have been awarded funding ($12 million) to develop new environmentally-friendly techniques to increase the production of renewable biofuel and reduce pesticide use based on cutting-edge metabolomics research (see page 16).

- Natural Variation and Comparative Genomics: The Arabidopsis 1001 genome project released 816 genomes until April, 2013. The relationships among the crop Brassicas are beginning to be elucidated and ongoing studies for multi-locus nuclear phylogenies for the *Brassicaceae* are in progress. Following three 2011 genome sequences publications, 2012 has been a year to make progress on dozens of other genomes in the Brassicales. Brassibase has been created, which is an online-accessible knowledge and database system for *Brassicaceae* taxonomy, systematics and evolution. The subcommittee has also made progress regarding their specific goals towards the 2020 road map (see page 17).
- Phenomics: In 2012 the plant phenotyping community has continued to respond towards alleviating the 'phenomics bottleneck' by increasing the capacity and throughput of existing infrastructure and by establishing new, non-invasive methodologies based on a growing number of imaging modes characterized by a various level of automation of both plant cultivation and imaging routines, and data analysis pipelines (see page 20). Phenomics co-chair Ulrich Schurr stepped down and was followed by Fabio Fiorani in 2012.
- Proteomics: The past year has seen the subcommittee develop approaches to support the objectives of the Arabidopsis road map (see page 25). This has included the development of a proteomics portal (1001 Proteomes) to enable exploitation of natural variation sequence data by Arabidopsis proteomic researchers. A proteomics workshop was held in July 2012 at ICAR (Vienna, Austria). Proteomics co-chair Wolfram Weckwerth stepped down and was followed by Alexandra Jones in 2012.
- Systems Biology: Two Systems Biology sessions were held at ICAR 2012 in Vienna, Austria; one was a workshop co-organized by Siobhan Brady and Wolfgang Busch and related specifically to root development. Several members of the MASC subcommittee contributed to a special issue of Plant Cell containing 4 reviews describing recent efforts to model network to multi scale systems in plants. The aims of the subcommittee according to the road map were stated and include the establishment of a subcommittee website for efficient exchange of information and dissemination of activities to be launched in 2013 (see page 27). The new co-chairs of the Systems Biology subcommittee Malcolm Bennett and Siobhan Brady succeeded Rodrigo Gutierrez and Andrew Millar.

Analysis and Recommendations

Progress especially towards the short term goals of the road map published in 2012 has been made. The results of the design workshop of the Arabidopsis Information Portal (AIP) held end of 2011, were published in Plant Cell in 2012. The proposal for funding to develop the AIP was submitted to the U.S. NSF and a detailed implementation plan was requested. The Arabidopsis community is encouraged to approach the goals of the road map (see page 29 ff.). MASC short term recommendations for 2013 are:

- Development of the Arabidopsis Informatics Portal and communicating the status to the plant science community
- Translating the fundamental understanding of processes such as flowering, stress physiology, developmental processes etc. into applied systems, especially crop plants and breeding studies, for example development of strategies for common conferences and symposia
- Intensification of the analysis of natural genetic variation in *Arabidopsis thaliana*
- Development of *in silico* models of Arabidopsis from molecular to organismic level

Arabidopsis Basic Research and its Impact on Applied Research

- Scientific Highlights in 2012: The past year continued to be strong for Arabidopsis publications. 4,086 Arabidopsis peer-reviewed research papers were published in 2012, a more than 10-fold rate increase over 1994 (when 402 peer-reviewed papers were published; Fig. 1, page 33). This report includes summaries of just a few research highlights in the past year (see page 33 ff.) including:
  - Development of a nano sensor to assay in vivo auxin distributio
  - Insights into egg cell –sperm cell communication
  - Discovery of new class of DNA-double strand break small RNAs (diRNAs)
  - Discovery of the transporters mediating sucrose export close to the site of phloem loading
  - Insights into chloroplast biogenesis
  - Discovery of two salicylic acid receptors
  - Publication of the *Arabidopsis thaliana* root bacterial microbiome
  - Insights into Casparian strip formation
- Impact of Arabidopsis Research on Applied Research and Industry: The knowledge gained from studies in Arabidopsis serves to advance our understanding of other plant species, partic-ularly crop species, and thus translate into new or improved plant products and increased agricultural productivity. Importantly, basic research in Arabidopsis provides the foundation for applied studies. The filing of patents is one measure of potential commercial activity and while many patents worldwide acknowledge research on Arabidopsis, a widely-held

myth is that few of these discoveries are ever turned into useful products. US utility patents referencing Arabidopsis patents continue to increase: in 2012 there were 1,489 utility patents referencing Arabidopsis compared to 23 in 1994, an almost 65-fold increase (see Fig. 2, page 38). In the same timeframe, a 25- and a 26-fold increase have been recorded for European and world's published applications (i.e. patents) referencing Arabidopsis (see Fig. 2, page 38). It has been estimated to take up to 12 years or more to navigate the commercialization pipeline from initial discoveries to agricultural products. This report highlights a few examples of discoveries that demonstrate how basic research in Arabidopsis can be translated into real-world applications. Each study vitally depended on Arabidopsis data and resources (see page 38 ff.):

- Increasing stress tolerance with a chemical PARP inhibitor
- Overexpression of *At*BBX32 increases grain yield in soybean
- Bacterial phosphite-specific oxidoreductase expressed in plants reduces application of phosphate fertilizers and herbizides
- Whole-genome analyses to predict performance of hybrid maize
- Mutation in Early Flowering 3 (ELF3) in legumes is linked to variants cultivated in regions with short growing seasons

Country Highlights

Researchers working on Arabidopsis are still highly encouraged to get involved in MASC activities for example by representing their country in MASC. The activity of MASC country representatives constitutes an important hub to further strengthen the national and international network of Arabidopsis and the wider plant community. Last year 22 countries have been involved in MASC activities and 18 contributed to the MASC report 2013 (see page 42 ff.).

Progress and Activities of MASC

In 2012, Wolfram Weckwerth (University of Vienna, Austria) succeeded Mark Estelle (UC San Diego, U.S.) to become MASC chair and Barry Pogson (Australian National University, Canberra, Australia) became co-chair. Barry Pogson will become the new MASC chair when Wolfram Weckwerth steps down following the annual International Conference on Arabidopsis Research (ICAR) in June, 2013.

To help monitor the progress and advances of the Arabidopsis community and ICAR, an abstract submission process has been developed and has been in place since 2006. The system is hosted at The Arabidopsis Information Resource (TAIR) website. Thanks to this submission process it is possible to associate abstracts within TAIR to the genes listed, effectively monitoring the progress towards understanding the function of all Arabidopsis genes (Table 1). For the 2012 ICAR in Vienna, 602 abstracts were submitted and the abstract upload to TAIR is in progress.

Google Analytics were employed beginning June, 2007 to track the usage of MASC web pages at TAIR which are maintained by the MASC coordinator. The community regularly visits the MASC pages: in the one year period between May 13, 2012 and May 13, 2013, 48 different MASC pages were viewed 4,811 times. The top-viewed page (1,157 views) contains information on the projects funded through the U.S. NSF 2010 project (www.arabidopsis.org/portals/masc/projects.jsp). Other frequently viewed pages include the NAASC page (www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp), the International Arabidopsis Informatics Consortium (IAIC) page (www.arabidopsis.org/portals/masc/projects.jsp) and the coordinator's journal (www.arabidopsis.org/portals/masc/journal.jsp), which received 527, 466 and 296 views respectively over the last year. Since 2011 a separate IAIC website exists (http://www.arabidopsisinformatics.org/).

MASC subcommittees, proposed in 2002, were established to help track the progress and advances made by the international Arabidopsis community. In the past some committees were discontinued according to the evolving needs of the community. The minimum requirements for a subcommittee to be considered active include submission of an annual report and input at MASC annual meetings. A discussion regarding the reorganization of inactive subcommittees took place at the 20th ICAR, held in 2009 in Edinburgh. It was decided that the MASC chair should confirm leadership of the existing subcommittees and that, if necessary, new subcommittee chairs should be found. A 3-year minimum term for each subcommittee chair was also instituted to provide continuity. Similarly, it was decided that the new chair should confirm the interest of subcommittee members and that co-chairs could help promote activity of the subcommittee. No new subcommittees have been formed over the last year and this report includes reports from all 7 current subcommittees: Bioinformatics, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics and Systems Biology (see page 13 ff.). The Phenomics co-chair Ulrich Schurr stepped down and was followed by Fabio Fiorani, as well as the Proteomics co-chair Wolfram Weckwerth, who was followed by Alexandra Jones in 2012. The new co-chairs of the Systems Biology subcommittee Malcolm Bennett and Siobhan Brady succeeded Rodrigo Gutierrez and Andrew Millar. Members of every subcommittee were involved in the session and workshop program of the ICAR 2012 in Vienna, for example the Bioinformatics and Proteomics subcommittee organized workshops.

A full-time MASC coordinator position, established in 2002, has been previously supported by the NSF (U.S.) for 6 years, by the DFG (Germany) for one year and BBSRC (U.K.) for three years. The current coordinator's position filled by Luise Brand is based in Germany again and will be supported by DFG (Germany) from 2013-2015. MASC web pages are hosted at TAIR (http://www.arabidopsis.org/portals/masc/index.jsp). The MASC Coordinator provides help and coordination to MASC, and the larger Arabidopsis functional genomics research community. Duties include (1) serving as the executive secretary of MASC, (2) providing assistance to local representatives in the organization of the annual International Conference on Arabidopsis Research (ICAR), including help with sponsorship, (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, and databases and stock centers, and (5) maintaining and

Table 1. Number of abstracts submitted to ICAR from 2007 – 2012. (n.a.: not available; *: loci that were previously not associated to literature in TAIR)

Year	Total no. of abstracts	No. of abstracts with AGI codes	Total no. of distinct AGI codes	No. of new AGI codes*
2007	776	369	1,722	535
2008	628	336	3,060	926
2009	646	645	1,634	25
2010	922	391	7,54	7
2011	611	141	386	5
2012	602	n.a.	n.a.	n.a.

updating the functional genomics MASC website together with TAIR to inform the global research community about various opportunities, collaborations, large-scale activities and research progress.

Since 2007 several Arabidopsis community projects and resources contributed reports to the annual MASC report to inform the community about their progress, activities and goals. This year the three biological resource centers Arabidopsis Biological Resource Center (ABRC, U.S.), the Nottingham Arabidopsis Stock Centre (NASC; U.K.) and the RIKEN BioResource Center (RIKEN BRC; Japan) submitted reports, as well as the online information resource TAIR and the International Arabidopsis Informatics Consortium (IAIC) (see page 9 ff.). TAIR director Eva Huala gives an update on the progress of the transfer of TAIR data to the iPlant server, which is well underway. TAIR website usage continues to grow which again underpins the effort of the community to apply for new funding succeeding the end of TAIR funding in August 2013. The design of the new Arabidopsis Information Portal was outlined in a workshop held in 2011 with major contributions from the Bioinformatics Subcommittee and the International Arabidopsis Informatics Consortium (IAIC) (http://www.arabidopsisinformatics.org/). In 2012 the design of the Arabdiopsis Information Portal (AIP) was published in Plant Cell (Baerenfaller, 2012) (see page 10).

Researchers working on Arabidopsis are highly encouraged to get involved in MASC activities by representing their country in MASC. The activity of MASC country representatives constitutes an important hub to further strengthen the national and international network of Arabidopsis and the wider plant community. Country representatives are members of MASC, they usually attend the annual MASC meeting held during the ICAR and contribute to the annual MASC report by submitting country reports. Last year 22 countries have been involved in MASC and 18 contributed to the MASC report 2013 (see page 42 ff.). In 2012 László Szabados agreed to represent Hungary, Shaul Yalovsky succeeded Danny Chamovitz to represent Israel, Dario Bonetta suceeded Bill Crosby and Malcolm Campbell to represent Canda, Lieven De Veylder succeeded Pierre Hilson to represent Belgium and Wolfram Weckwerth joined Marie-Theres Hauser instead of Ortrun Mittelsten-Scheid to represent Austria.

Baerenfaller K, Bastow R, Beynon J, Brady S et al. (2012) Taking the Next Step: Building an Arabidopsis Information Portal. Plant Cell 24:2248-2256

Arabidopsis Community Projects and Resources

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

By Erich Grotewold (ABRC director) and Jelena Brkljacic (ABRC associate director)

The ABRC collects, preserves, reproduces and distributes diverse seed and other stocks of *Arabidopsis thaliana* and related species for research and education. The Center reached a record high distribution in 2012, with over 110,000 samples sent for all resources combined. Seed stock holdings include insertion lines covering 28,929 genes, out of which 24,894 are protein-coding; the 11,000+ TILLING lines; 2,404 distinct natural accessions, some of which are genetically fingerprinted and some sequenced by the 1001 Genomes Project; 31 recombinant inbred populations; a set of near-isogenic lines; RNAi lines; transgenic lines; 50+ accessions of the genus Brassica; and approximately 70 accessions of other closely related species. DNA resources at ABRC include full-length ORF and cDNA clones for almost 17,000 genes, BACs covering the entire genome, BACs of nine related species, the AGRIKOLA GST entry clones, various sets of expression clones and 12,466 amiRNA clones.

ABRC released a number of new types of resources in the past year. These include cell suspension cultures PSB-L and PSB-D, suitable for cell cycle studies. A new protein chip containing 10,000 Arabidopsis proteins (ATPROTEINCHIP_2) was also made available in this period. The fourth installment of the confirmed SALK set representing 3,263 new loci was released at the end of 2012.

Functional genomics resources remain one of the Center's highest priorities. 47,203 confirmed lines, received from the SALK Institute, represent 26,596 loci. 42,191 lines have been made available and are ready for distribution. We also received a large number of GABI-Kat lines through the European Arabidopsis Stock Center (NASC). Both collections continue to be highly ordered. The new License Agreement with Life Technologies allows us to receive and distribute Gateway destination and other vectors in addition to Entry and Expression clones. This agreement enabled the distribution of pANIC and mbSUS vectors, which remain in high demand.

The Center continues to be heavily involved in education and training. Five "Greening the Classroom" education kits have been developed at the ABRC, along with the accompanying handouts, videos, data collection/analysis sheets and example results. These materials, as well as the kits contributed by various researchers and educators, were made available through a separate ABRC outreach website at http://abrcoutreach.osu.edu. The funding comes from the

ASPB Education Foundation TRAINED grant. The demand for education resources has increased significantly since their initial release in 2011 and has reached 1,500 stocks sent in 2012 to 10 different countries and 20 US states.

ABRC has started automating large parts of the operation as part of the NSF grant "Making the ABRC Business Model Possible". We expect that the efficiency of seed dispensing of large sets will be increased 5-6 times with the automated seed dispensing system in place. The design of this piece of custom-made equipment is ongoing and its installation is expected at the end of 2013.

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

By Eva Huala (TAIR director)

Progress on Capturing Function of Arabidopsis Genes

We continue to add gene function annotations from community submissions and direct literature curation. Between November 2011 and December 2012 we added 70,117 new Gene Ontology annotations describing gene function or subcellular localization, from sources including high throughput experiments, community submissions and in-house literature curation. A total of 20,139 out of 27,416 Arabidopsis protein-coding genes currently have at least one function annotation in TAIR and 11,268 have at least one function or subcellular localization annotation based on a direct experiment.

Data Access after August 2013

We have been working to ensure that Arabidopsis data housed at TAIR will remain accessible after the official end of the TAIR funding period on August 31 2013. We are in the process of migrating TAIR software to servers at the Texas Advanced Computing Center (TACC) with support from iPlant Collaborative staff. This step will reduce the long-term cost of hosting and maintenance and allow TAIR to remain accessible for an additional couple of years. As of March 15 most TAIR software has been installed at TACC and is currently undergoing testing, with completion expected within 4-6 weeks. The TAIR interface will continue to be available at the same URL (http://arabidopsis.org) after the migration is complete, but the URL will direct traffic to the TAIR software running on the TACC servers.

Data Updates after August 2013

We will continue to update TAIR data to the extent that our funding permits after August 2013. TAIR staff will continue to add experimentally derived gene function data from new research articles and community submissions with funding from NIH (via the Gene Ontology Consortium) and from the TAIR sponsorship program (http://arabidopsis.org/doc/about/tair_sponsors/413). Some limited updates to other types of data will be carried out as time permits. We are also working with IAIC on plans to incorporate essential data from TAIR into the proposed new Arabidopsis Information Portal.

Community Data Submission

We continue to strongly encourage submission of Arabidopsis gene function information from authors using our online submission tool (available from the TAIR Submit menu as 'Online Submission for Authors and Others'). We will also continue to accept submissions of updated gene structures and other types of data. If our resources don't allow some types of data to be incorporated into the database we can provide access to them in the form of ftp files.

TAIR Usage

As of March 15, 2013 there were 24,453 registered TAIR users and 9,586 labs registered at TAIR. Of these, the records for 9,731 people and 3,907 labs were updated in the past 5 years. Website usage for TAIR continues to grow with an average of 50,744 unique visitors to the site, 168,692 visits and 3.8 million page views each month in 2012.

TAIR Impact

A Google Scholar search on March 15, 2013 for "arabidopsis.org" OR "arabidopsis information resource" OR "TAIR database" shows that TAIR has been mentioned in the full text of about 10,500 articles. In addition, articles describing TAIR resources have been directly cited in 1,060 publications, based on an analysis using Thompson Reuters Web of Knowledge.

The International Arabidopsis Informatics Consortium (IAIC) www.arabidopsisinformatics.org

By Blake Meyers (University of Delaware) and Joanna Friesner (NAASC)

In the past year, the focus of the IAIC has been to facilitate progress on the effort to secure funding for a new Arabidopsis Information Portal (AIP). The intent is to produce a novel, integrated, distributive, international framework with which to address the informatics needs of the Arabidopsis community now and in the future, while providing a smooth transition from the current TAIR-based central database structure to this stable, sustainable, long-term structure. IAIC leaders and others from the North American and Multinational Arabidopsis Steering Committees facilitated the formation of an expert team to develop a funding proposal to establish the AIP. Chris Town of the J. Craig Venter Institute and Matt Vaughn of the iPlant Collaborative emerged as leaders in the proposal effort, along with colleagues Konstantinos Krampis (JCVI), and Gos Micklem (University of Cambridge). In close consultation with the IAIC and other community leaders, Town et al. submitted a proposal to the United States National Science Foundation (NSF) in September 2012. Prior to the proposal's submission, community input on

AIP design was gathered via a 'Design Workshop'. The goals of the December 2011, Design Workshop were to develop both the user functionalities and the technical requirements for an AIP. The workshop included wet-lab plant biologists, computer programmers, and cyberinfrastructure experts. In short, their mission was to consider how to build the AIP, how to fund it, how to involve the broader community, and how to develop an effective action plan to implement workshop recommendations.

Key Points

1. Once implemented AIP will provide a long-term replacement resource for current TAIR users.
2. The AIP will provide access to, consolidate and maintain current the increasingly large and diverse data sets generated by and relevant to research on Arabidopsis and other plant species.
3. Where appropriate, the AIP project expects to make use of the existing iPlant infrastructure and code base.
4. The AIP will proactively seek out, aggregate, integrate and present data.
5. TAIR staff will assist in migrating the TAIR 'legacy data' into the AIP (data are already being moved to iPlant.)
6. A Scientific Advisory Board (SAB) was elected by the community to provide oversight and direction for the AIP, once it is implemented.
7. Stock center integration is included in a proposal by Sean May that is under review at the UK BBSRC.

Current AIP Status

The AIP PIs have been asked by NSF to develop a detailed "Project Execution Plan" in anticipation of a reverse site visit in late April or early May 2013.

Status of TAIR transfer to Texas Advanced Computing Center (iPlant Collaborative). As of March 15 2013, most TAIR software has been installed at TACC. The TAIR interface will continue to be available at the same URL (http://arabidopsis.org) after the migration is complete, but the URL will direct traffic to the TAIR software running on TACC servers. See TAIR and United States sections of this report for additional information.

Website, Recent Activities, and Governance

- The IAIC Website (http://www.arabidopsisinformatics.org/) contains information on the Subcommittee, the SAB, relevant publications, and IAIC events including community workshops, which serve to engage the community, provide updates, and facilitate dialog.
- Community activities in the past year include a platform talk by Blake Meyers in the ICAR 2012 'MASC Roadmap' concurrent session (Vienna) and an IAIC workshop at the Plant and Animal Genome meeting, 2013 (San Diego). Upcoming is a community workshop at ICAR 2013 (Sydney).
- The inaugural SAB was appointed in February, 2012 following solicitation of community nominations and recommendations by MASC. Current SAB members include: Gloria Coruzzi (New York University, USA), Kazuki Saito (RIKEN, Japan), Magnus Nordborg (GMI, Austria), Mark Estelle, Committee Chair (UC San Diego, USA), Mark Forster (Syngenta, UK), Paul Kersey (EBI, UK), and Xuemei Chen (UC Riverside, USA).
- Subcommittee members will conclude their formal service at the 2013 ICAR. Interim Director Blake Meyers will continue to actively work on this effort through the end of the funding period.
- IAIC activities are supported by an award from the US National Science Foundation to Interim Director Blake Meyers; Award #1062348.

The Nottingham Arabidopsis Stock Centre (NASC) www.arabidopsis.org.uk

By Sean May (NASC director)

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

We have two items of very positive news about NASC Stock Centre longevity and stability: Thanks first to the BBSRC who have funded the NASC seed service for a further 5 year period (2012- 2017); and also to the University of Nottingham, who have generated a new post of NASC Operations Manager as one outcome from the major 2012 UoN Review of NASC. Marcos Castellanos-Uribe, known to many of you will now be working together with the Director to ensure continuity and stability over the next few years of proposed change across resource provision for the Arabidopsis community.

Ordering statistics at NASC continue to be healthy and high for the seed service and we have released several new stocks, collections and lines this year. Please see our site for a comprehensive list. Some stocks that you are likely to see presented at ICAR-Sydney include the GABI-DUPLO double mutants from Bolle, Weisshaar and Leister; the MADS box reporter lines from Berner, Heijmans and Agenent; and the TRANSPLANTA inducible transcription factor lines from Jose Leon in Valencia.

Since ICAR 2012, Vienna, we have refreshed and expanded our existing portfolio of Web Services in anticipation of the new proposed distributed AIP database model that has been driven by the IAIC. As a part of this we have applied for UK funding to become the germplasm and array modules for the IAIC network. It is possible that we may know the funding outcome by ICAR-Sydney but in any case we welcome any potential users/ partners to go ahead and learn about our currently available set at: http://arabidopsis.info/

bioinformatics/webservices or simply discover them through your favourite aggregator. One of the most significant changes this year will be the development of NASC-RESTful services to complement our existing NASC-SOAPlab2 services.

In chip news, we anticipate several ICAR talks integrating results from the AraGene-1-1-ST whole transcriptome chip. It is now our most popular [cheapest and best content] Arabidopsis chip (http://arabidopsis.info/StockInfo?NASC_id=N797864). Some users have found R/Bioconductor analysis on this chip more challenging than for ATH1 because of the multi-exon structure of the probesets; so we have added some basic tips to our site on analysis using oligo() and netaffx() [Partek and Genespring users already have support for this chip from their vendor]. See you in Sydney.

The RIKEN BioResource Center (RIKEN BRC) www.brc.riken.jp/lab/epd/Eng

By Masatomo Kobayashi (RIKEN BRC Coordinator)

The third term of National BioResource Project started in last April. RIKEN BioResource Center (RIKEN BRC) continues to be the core center for Arabidopsis as well as mice, microbes, cells and DNA materials. Experimental Plant Division (plant@brc.riken.jp) collects, preserves and distributes seed stocks of Arabidopsis that include transposon-tagged lines (RATM line, 17,671 lines; insertion site information available; 3,119 homozygous lines also available), activation-tagged (T-DNA) lines (for phenotype screening; 36,650), FOX lines (Arabidopsis plants that overexpress Arabidopsis or rice full-length cDNA; for phenotype screening; 17,739), natural accessions (SASSC stock) and individual mutants and transgenic lines generated in Japan. In addition, the Division distributes DNA resources such as full-length cDNA clones of Arabidopsis (RAFL clone; 251,382), *Physcomitrella patens* (149,363), poplar (23,100), cassava (19,968), tobacco (3,068), *Thellungiella halophila* (19,429), *Brassica rapa* (9,903) and *Striga hermonthica* (35,198). We also preserve and distribute plant cultured cell lines which include Tobacco BY-2 and Arabidopsis T87 cells. We shipped cell lines not only to domestic institutions and universities but also to those in abroad. Total number of plant materials in the Division is 664,151, and 1,651 laboratories around the world have received our materials.

In 2012, RIKEN BRC revised the catalogue for transposon-tagged lines using TAIR 10 genome annotation. Additional information obtained by RIKEN BRC is now available for users.

Catalogue for the full-length cDNA clones of *Brachypodium distachyon*, a monocot plant for laboratory works, is under preparation. Distribution will start within this year.

RIKEN BRC has joined the Asian Network of Research Resource Centers (ANRRC). Last year, 4th ANRRC meeting was held in Korea during October 17-19, 2012. The 5th meeting, which will be held in Japan in this autumn, will be organized by RIKEN BRC and National Institute of Genetics.

Reports of the MASC Subcommittees

Bioinformatics

By Nicholas Provart (Chair) with contributions from subcommittee members and the wider Arabidopsis community. 20 March 2013.

Several new Arabidopsis bioinformatics tools and large data sets were published or released in 2012.

Big Data and Tools for Mapping, Genotyping, and Phenotyping

For better understanding the segregation of phenotypic traits in hybrids, the Weigel lab generated a large data set looking at the recombination landscape in 7045 F2 plants with 237 informative markers for a total of 1.6 million data points (Salome, 2012). The Bergelson lab released genotyping data for 1307 Arabidopsis ecotypes using a 250k SNP chip (Horton, 2012) at http://bergelson.uchicago.edu/regmap-data/regmap.html/. The Ecker lab has sequenced 128949 new T-DNA insertions by "TDNA-seq", 64354 of which are mapped inserts in the original SALK lines (different from the existing location in the Salk TDNA Express database). Another 40117 are new inserts in new lines, which will be released to the ABRC during this year. The inserts are available at http://signal.salk.edu/cgi-bin/tdnaexpress. The Schneeberger lab released an improved SHOREmap method for accelerating genetic mapping using next-generation sequencing and synteny (Galvão, 2012). The Nordborg lab's GWAPP application permits easy genome-wide association mapping across more than 1300 Arabidopsis ecotypes for which sequence information is available (Seren, 2012) at http://gwas.gmi.oeaw.ac.at/. The Weigel lab's easyGWAS application has a similar functionality: https://easygwas.tuebingen.mpg.de/. Joshua Heazlewood's group has released a 1001 Proteomes portal for accessing Arabidopsis proteomics data across many accessions (Joshi, 2012) at http://1001proteomes.masc-proteomics.org/.

Big Data and Tools for Small/Large Non-Coding RNAs and Methylation Patterns

The Ecker lab released methylation and transcriptome data for 152 Arabidopsis ecotypes (Schmitz, 2013) at http://neomorph.salk.edu/1001_epigenomes.html. An epigenomics and strand-specific transcriptome database hosted by the Lam lab at Rutgers University (Luo, 2013) at http://epigenome.rutgers.edu was published. The Chua lab at Rockefeller University released its Plant Long noncoding RNA Database, PLncDB (Jin, 2013) encompassing long noncoding RNAs from flowers, leaves and roots of Arabidopsis, and methylation and small RNA data from other sources at http://chualab.rockefeller.edu/gbrowse2/homepage.html. Arabidopsis methylation data from wild-type and mutant Arabidopsis plants from Steve Jacobsen's lab at UCLA (Stroud, 2013) were posted at http://genomes.mcdb.ucla.edu/AthBSseq/. The data from the above resources and from other such data sets will be incorporated into the EPIC (Epigenomics of Plants International Consortium)-CoGE Browser, currently being built by Eric Lyons (U. Arizona) and Brian Gregory (U. Pennsylvania) at http://genomevolution.org/wiki/index.php/EPIC-CoGe. AthaMap from Reinhard Hehl's group at the Technical University of Braunschweig introduced a tools to identify Micro RNA Targets and Small RNA Targets (Bülow, 2012) at http://www.athamap.de/miRNA_ident.php and http://www.athamap.de/smallRNA_targets.php.

Other Big Data

The Benfey lab released novel data sets covering cell-type-specific miRNA and proteomic data in the Arabidopsis root (Breakfield, 2012; Petricka, 2012). Brian Ellis' lab release the results of an extensive immunoprofiling analysis in stem cross-sections, where it's possible to see which cell wall components are present in specific cell types of the maturing Arabidopsis stem (Hall, 2013) at http://www.wallmabdb.net.

Other Tools

The iRootHair Database, a database of root hair genomics information to assist in the study of root hair development and system biology (Kwasniewski, 2013) was released at http://www.iroothair.org/. For translational genomics efforts, the Provart lab published their Expressolog method for identifying homologs with similar patterns of expression in equivalent tissues in 10 different plant species (Patel, 2012) at http://bar.utoronto.ca/expressolog_treeviewer/. RobinA, an all-in-one R/Bioconductor solution for the mapping of RNA-seq reads, through read counting to final statistical evaluation with an easy-to-use graphical user interface (Lohse, 2012) was released at http://mapman.gabipd.org/web/guest/robin. Brian Gregory's lab also posted a nice tool for exploring RNA secondary structure for Arabidopsis transcripts (Li, 2012a) at http://gregorylab.bio.upenn.edu/annoj_at9_structure/. The GeneSharingNetworks tool permits the identification of genes that are leptokurtically expressed in Arabidopsis, that is, that are strongly expressed in only one or a few cell types or tissues (Li, 2012b) at http://genesharingnetworks.org/. The very useful "Subcellular location of proteins in Arabidopsis" database was updated to SUBA3 (Tanz, 2013), see http://suba.plantenergy.uwa.edu.au/.

Work towards creating a new Arabidopsis Information Portal by the International Arabidopsis Informatics Consortium proceeded (International Arabidopsis Informatics Consortium, 2012), with community meetings at ICAR in Vienna last summer, and at the PAG Conference in San Diego in January 2013. Christopher Town of the J. Craig Venter Institute submitted a grant application to the NSF to fund the development of the framework and certain key modules for this new portal. The group has been asked to prepare a detailed Project Execution Plan in preparation for a reverse site visit at NSF, likely in late April or early May. Nicholas Provart and Stephen Wright were successful in obtaining funding from Genome Canada/Ontario Genomics Institute to build 7 modules for the new portal. Eva Huala and colleagues at TAIR meanwhile have been working with iPlant to keep TAIR data accessible after the end of the funding period in August 2013. See the IAIC section of this report for further updates.

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Clone-Based Functional Genomics Resources (ORFeomics)

By Motoaki Seki (Chair) and Joe Ecker (Co-chair)

The ORFeomics subcommittee keeps tracking progress made towards the production of full-length cDNAs and open reading frame clones for all annotated Arabidopsis protein-coding genes. We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Table 2). The revised ones are shown in bold. New clones include 5,414 mbSUS clones (Frommer et al.) and 192 ORF clones from Guillaume Pilot.

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/sheen-web/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
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	pIX-HALO vector			12.069		ABRC
Guillaume Pilot	**pDONRZEO vector**	**Membrane protein**	**5′ and 3′ end seq**	**192**		**ABRC**
cDNA clones						
RIKEN/SSP/Salk Insitute	λ ZAP or λ PS		Full sequence/ 5′ and 3′ end seq.	25.000	www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml	BRC
MPI-MG	Gateway expression		5′ end seq.	4.500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28.866	www.genoscope.cns.fr/Arabidopsis	CNRGV

Metabolomics

By Kazuki Saito (Chair) and Wolfram Weckwerth (Co-chair) with contributions from subcommittee members

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

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

The subcommittee website has been launched www.masc-metabolomics.org. In summer of 2012, the 8th Annual International Conference of the Metabolomics Society in conjunction with The Plant Metabolomics Forum has been held in Washington DC, US, June 25 – 28 http://www.metabolomics2012.org/. Metabolomics study on Arabidopsis was one of the major topics of this meeting. Metabolomics 2013 meeting will take place in Glasgow, UK, July 1 - 4, 2013 < http://www.metabolomics2013.org/>. Based on the joint NSF (US) and JST (Japan) funding, four joint US and Japanese research teams have been awarded funding in-total about $12 million (about Yen 960 million) to develop new environmentally-friendly techniques to increase the production of renewable biofuel and reduce pesticide use based on cutting-edge metabolomics research. Two project teams (Lloyd Sumner/Kazuki Saito, Oliver Fiehn/Masanori Arita), which focus on metabolite and gene annotation of Arabidopsis and bioinformatics have been granted by this joint program. The kick-off meeting for these joint granting teams has been held in Narita, Japan, February 16 – 18, 2012. Discussions about setting up similar US-German programs have been initiated and look promising.

Arabidopsis metabolome expression databases 'AtMetExpress development' (Matsuda., 2010) and 'AtMetExpress 20 ecotypes' (Matsuda., 2011) have been established at http://prime.psc.riken.jp/ (Sakurai., 2013). A web portal of Arabidopsis Metabolomics Consortium at <www.plant-metabolomics.org> that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants has been publicized (Bais., 2010, Bais 2012, Quanbeck., 2012). Mass spectral databases, MassBank <http://www.massbank.jp/index.html?lang=en> (Horai., 2010) and ReSpect for Phytochemicals <http://spectra.psc.riken.jp/> (Sawada., 2012) have been publicly available. The Madison-Qingdao metabolomics consortium database (http://mmcd.nmrfam.wisc.edu/) has emphasis on Arabidopsis and contains both NMR and MS data of metabolites.

A major initiative driven by the European Bioinformatics Institute deserves mention here. MetaboLights (http://www.ebi.ac.uk/metabolights) is a database for Metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments and is a collaborative multi-laboratory effort including groups specialising in plant metabolism. A publication describing the database is published in Haug (2013).

Two substantial EU funded consortia projects META-PHOR< http://www.meta-phor.eu/> and DEVELONUTRI <http://www.develonutri.info/welcome>, although not focused on Arabidopsis, are technology orientated and aim to provide platforms for co-ordination of plant metabolomic data collection across different laboratories. Though both projects are finished now, this kind of activity should be encouraged for Arabidopsis to allow facilitate integration of data from different sources.

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Natural Variation and Comparative Genomics

By J. Chris Pires (Co-chair, piresjc@missouri.edu) and Brian Dilkes (Co-chair, bdilkes@purdue.edu) with contributions from subcommittee members

Subcommittee Goals and Priorities

Goals of the Natural Variation and Comparative Genomics towards the 2020 From Bench to Bountiful Harvests Roadmap

A) Build a predictive model of an Arabidopsis plant from its molecular parts. Build predictive models with insights from:

- natural variation within Arabidopsis and comparisons to other related species of plants.
- information gained from other species to enhance our knowledge of Arabidopsis; for example, whole genome duplications in Brassica increase the resolution of conserved noncoding region detection.
- Develop 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

- Explore the variation in Arabidopsis and related species at numerous levels of biological organization to infer biological networks from various –omics datasets, including genomic, epigenomic, proteomic, metabolomic, ionomic, interactomic, and phenomic.
- Analyze Arabidopsis ecotypes and related plant species in association with their rhizosphere, endophyte and epiphyte communities (metagenomics) in various ecological and agricultural settings.
- Integrate 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.
- Generate 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.
- Develop computational resources to understand and utilize the natural variation of Arabidopsis and related species. This will include interactions among the all the MASC subcommittees with the 1001 Arabidopsis Genomes project, Multinational Brassica Genome Project (MBGP), and Brassicales Map Alignment Project (BMAP) to consider natural variation and comparative 'omics in the roadmap. Ensure that the Arabidopsis Information Portal (AIP) be built to work for Brassica and other plant species.
- Create germplasm resources that are publicly available (e.g., Brassica diversity, Reg Map panel) and create a database for managing diversity (e.g., Brassibase, brassica.info)

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

- Actively pursue systems biology research programs and analyze –omics datasets in other plant systems using key knowledge gained through the analysis of Arabidopsis, starting with the crop Brassicas (vegetables and oilseeds), biofuel crops (e.g., Camelina), and other economically important species (e.g., horseradish, wasabi, etc.).
- Establish data standards and ontologies to provide uniform data on growth conditions and experimental metadata to enable modeling from controlled environments to the field.
- Develop 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 International Arabidopsis Informatics Consortium (IAIC), an international informatics and data infrastructure

- Integrate -omics data and informatics infrastructure in Arabidopsis with other species.
- Develop 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.

- Develop open access ontology-driven database tools and promote the adoption of uniform vocabularies and machine-readable formats for describing experimental data and metadata.

E) Deepen International Cooperation and Coordination

- Undertake 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.
- Continue to offer BMAP workshops at international conferences to coordinate efforts, share expertise, and develop -omics standards and comparative ontologies. Share information on standards, lists of species being sequenced, and emerging international

The study of natural variation within Arabidopsis and comparative 'omic and systems biology investigations in related species is central to understanding plant biology and plant environment interactions.

Natural Variation

Accomplishments

Understanding how genetic variation can control phenotypic variation is a fundamental goal of modern biology. A major push has been made using genome-wide association mapping in all organisms to attempt and rapidly identify the genes contributing to phenotypes such as disease and nutritional disorders. New methods for genome-wide association studies have been developed (Chan, 2011, Kerwin, 2011). Additional progress was made in generating the genome sequences of 816 genomes of the Arabidopsis 1001 genome project (released on April 17, 2013).

Needs

Creating improved and "user friendly" resources are a major area where the Natural Variation community should invest future efforts. It is important to develop web-based resources that make sequence data (as well as the raw data) easily available for researchers to reutilize. For example, much of these sequencing data have been generated under the expectation of their usefulness for genome-wide association (GWA). Many labs would therefore greatly benefit from developing web-based interfaces that allow easy access and friendly GWA analysis of these data. There have been some encouraging and positive developments in this area, and the various ongoing efforts to integrate the Arabidopsis 1001 genomes (e.g., EU transPLANT project (www.transplantdb.eu/). However, fostering open-source public availability of web resources and data remains paramount if this data and others are to be made available in a useful form to the larger community. Another area of current need is the collection of site metadata and sample provenance; it is essential that work in this area continue.

Ongoing Justification

One goal of plant biology has been to link variations in natural populations to genotypic variation, with the aim of understanding evolution within a species and moving beneficial traits into plants of agricultural importance. Arabidopsis has proven to be an efficient plant model for evolutionary analyses because of the ease of manipulation, breadth and depth of understanding of genetic and biochemical pathways, and its abundance of natural variation. Combined, these attributes have allowed the largest number of genes and nucleotide polymorphisms underlying natural variation to be uncovered in Arabidopsis compared to any other plant species. However, it still remains a considerable challenge to map genotype to phenotype. In part this is because we observe results from complex, quantitative, multi-gene traits, which are greatly influenced by environmental factors. However, providing access to this unexploited wealth of variation, Arabidopsis researchers can begin to link phenotypic differences with genotypic variations on a global scale. In addition to variation in DNA sequence, large data sets from other 'omic' technologies such as proteomics, metabolomics, ionomics, and epigenomics are also being used to assess the variation that exists at different levels of biological organization and molecular regulation. By combining large scale 'omic' data sets obtained across populations it is possible to bring the power of systems biology to quantitative genetics and environmental genomics. This approach can be used to construct and infer biologically meaningful regulatory networks that can reveal the molecules that contribute to systems robustness, plasticity and the survival and adaptation of species.

Comparative Genomics

Accomplishments

The relationships among the crop Brassicas are beginning to be elucidated (Arias and Pires, 2012) and ongoing studies for multi-locus nuclear phylogenies for the *Brassicaceae* are in progress. Following the 2011 genome sequences publications for *Arabidopsis lyrata*, *Brassica rapa*, and *Thellungiella parvula*, 2012 has been a year to make progress on dozens of other genomes in the *Brassicales*: Aethionema, Arabis, Boechera, Brassica, Cardamine, Caulanthus, Cleome, Euclidium, Leavenworthia, Sisymbrium, and Thlaspi. The Brassicales Map Alignment Project (BMAP) has a centralized list of species being sequenced in the Brassicales (that is updated semi-annually on brassica.info); the DOE JGI Community Sequencing Program funded BMAP project is now sequencing 20 genomes. In addition, Brassibase (Koch, 2012) has been created, which is an online-accessible knowledge and database system for *Brassicaceae* taxonomy, systematics and evolution. The database includes chromosome numbers, character traits, germplasm resources, and accurate enumeration of all species, genera and tribes. Biological knowledge of the mustard family is exponentially increasing; however, biological material and resources, either collected directly in the wild or held in germplasm collections,

have often been misidentified; and only very rarely has the material been further characterized and documented. A DFG funded knowledge base (priority programme Adaptomics 1529) has been established entitled "Evolutionary plant solutions to ecological challenges / Molecular mechanisms underlying adaptive traits in the Brassicaceae"(see http://www.ruhr-unibochum.de/dfg-spp1529/Seiten/index.html). The project centers on the Brassicaceae and aims to obtain fundamentally novel, comprehensive and increasingly predictive insights into the molecular solutions that plant species develop to match local environmental demands.

Needs

The integration of population genomics and comparative genomics is ongoing in Arabidopsis, Brassica, and other plant species. As outlined by the International Arabidopsis Informatics Consortium (IAIC)(2012), the major strategic challenges include not only gathering high-throughput data, but also organizing and integrating the data into broadly accessible bioinformatics platforms. Current investigations examine both within-species comparisons of natural variation and cross-species comparative -omics. However, the ability to retrieve a specific region of the genome across a large set of Arabidopsis accessions, let alone to other species, is not a simple task. It is essential that any future informatics platform integrate data, tools and resources for comparative studies. For example Phytozome (Goodstein, 2012), CoGe (http://genomevolution.org/CoGe/), and PLAZA (Van Bel, 2012) could all act as providers for a comparative module of the AIP. The current idea is to replace the centralized TAIR database with the centralized Arabidopsis Information Portal (AIP) that would connect to multiple databases, tools and resources. It is fundamental that the AIP serves not only Arabidopsis, but also related plant species such as the crop Brassicas. Indeed, the portal will need to be flexible enough in design to work for any species. The design of the AIP should provide core functions whilst remaining flexible to encourage constant innovation from multiple contributors. We would recommend that the community portal include these basic components: databases for genomic and molecular stocks, gold standard genome annotations, curation of functional data, transcriptome (expression level, e.g., Movahedi, 2012), epigenomics (including small RNAs), proteomics, protein-protein interactome, metabolomics, and phenomics. The AIP should also contain search engines that can integrate cross-species information, such as PosMed-plus. Data made accessible via the AIP should be linked and attached to literature to permit data mining and meta analyses. For example, ranking candidate genes to prioritize experimentation can be accomplished by connecting phenotypic keywords to genes through linked data of biological interactions. Representatives from the Brassicales Map Alignment Project (BMAP), Multinational Brassica Genome Project (MBGP), MASC, IAIC, and Brassibase will be coordinating efforts with each other and emerging international partners to ensure that the new platform meets the needs of the plant community.

Ongoing Justification

Natural variation and comparative genomics are providing insights into fundamental questions in biology. Arabidopsis and sequenced relatives provide an unsurpassed set of tools to analyze the genetic basis of developmental, metabolic or physiological differences. Comparative genome sequence analysis is a useful tool to investigate homologous gene families, define conserved gene functions between orthologs, and identify lineage- and species-specific genes. Most annotations of newly sequenced genomes are based on similarity with sequences for which functional information is available; thus, it is imperative to gather –omics data across species. Genomewide data describing functional properties including gene expression, protein–protein interactions and protein–DNA interactions are becoming available for an increasing number of model organisms. Consequently, the integration of functional genomics information, apart from gene sequence data, provides an additional layer of information to study gene function and regulation across species. Downstream comparative sequence analysis of differentially expressed genes between different species makes it possible to identify evolutionary conserved responsive gene families as well as species-specific components. In addition, unknown genes showing a conserved response shared between multiple species are interesting targets for detailed molecular characterization (Movahedi, 2012).

There is ongoing debate whether the Arabidopsis networks are under neutral evolution, dosage constraints, or selection (Bekaert, 2012) and investigating networks in the context of copy number variation in Arabidopsis and additional whole genome duplications (e.g. *Arabidopsis suecica*, Brassica and Camelina) should add insight into network evolution. By combining the power of emerging technologies with the extensive knowledge base that has built up in previous decades, the community of researchers investigating Arabidopsis, Brassica and other species in the Brassicales communities are poised to lead the way in the utilization of natural variation, systems biology and comparative –omics to understand how sequence variation affects biological and evolutionary processes and inform crop improvement efforts.

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Phenomics

By Robert Furbank (Co-chair) and Fabio Fiorani (Co-chair) with contributions from the subcommittee members and the wider Arabidopsis community

Summary

In 2012 the plant phenotyping community has continued to respond towards alleviating the 'phenomics bottleneck' (Furbank and Tester, 2011; Fiorani and Schurr, 2013) by increasing the capacity and throughput of existing infrastructure and by establishing new, non-invasive methodologies based on a growing number of imaging modes (from RGB to fluorescence and multi-spectral imaging) characterized by a various level of automation of both plant cultivation and imaging routines, and data analysis pipelines. Several plant phenotyping installations dedicated to quantitative and dynamic analyses of *Arabidopsis thaliana* macro- (shoot and root), analyses of microscopic traits (e.g. chloroplast morphology) and to allow high-throughput and reproducibility of molecular phenotypes are routinely exploited to generate rich data sets for key genetic material. This includes the 1001 genomes sequenced within the 1001 genome project, the RIKEN Arabidopsis Activation Tagging lines, new gene knockout collections (miRNA-induced gene silencing), and numerous Recombinant Inbred Lines populations (summarized in Table 3). The number of phenotyping approaches and their throughput are increasing and national and international platforms and projects are established (Table 4). The need to continued efforts for bringing results to the community through databases that are inter-operable remains high. In this respect, we consider that defining best practices for phenotyping experiments and ontology driven approaches to plant phenomics data structures and repositories remains high-priority to link genome and phenome data and enable feasible data integration roadmaps (Lavagi et al, 2012).

Development of Hardware and Software Infrastructure for Routine High-throughput Plant Phenotyping, and Validation of Methodologies

The Montpellier Plant Phenotyping Platform (M3P), LEPSE, INRA, Montpellier France

Three platforms are now fully operational at the Laboratory of Plant Ecophysiology in response to Environmental Stresses (PHENOARCH, PHENODYN and PHENOPSIS, at LEPSE, INRA, Montpellier). New phenotyping technologies and image analysis procedures have been developed extending the phenotyping capacity of the PHENOPSIS platform. Today, this platform can be used to grow and phenotype 1516 *Arabidopsis thaliana* plants in individual pots simultaneously. Automated routines include watering and imaging (top and side RGB cameras views, infra-red and fluorescence imaging systems). Reproducibility of plant phenotypes by using this platform has recently been demonstrated in a multi-scale analysis of leaf growth response to a moderate soil water deficit at the proteomics, transcriptomics, cellular and the whole leaf scales (Baerenfaller, 2012). Recent technological developments allow measuring developmental and physiological traits associated to water use efficiency, in particular: photosynthesis, transpiration, leaf surface temperature and leaf insertion angles, in response to drought treatments and heat stresses (Pantin, 2012; Vile, 2012). Mathematical models have been developed explaining multi-scale phenotypic inter-relationships among these traits and the genetic basis of biological laws describing the relationships driving growth and resource-use strategies in plants (usually described across a wide diversity of taxa) has been identified in specific cases (Vile, 2012; Vasseur, 2012). Technical expertise and software tools developed at LEPSE have been shared with other groups to support collective development of phenotyping technologies aimed at understanding the basis of the genetic and environmental controls of growth and water use efficiency in *Arabidopsis thaliana*. Images and phenotyping data derived from experiments conducted in PHENOPSIS are publicly available via a web portal interfacing with the database (Fabre, 2011; http://bioweb.supagro.inra.fr/phenopsis/). PHENOPSIS is part of the PHENOME project funded by the French Investment for the Future and part of its capacity is offered thourgh the European Plant Phenotyping Network (EPPN) funded by the FP7 Research Infrastructures Program of the European Union. In this context, the platform has been opened to different external users in 2012.

The High Resolution Plant Phenomics Centre, Canberra, Australia

Two new phenotyping platforms, CabScan and Trayscan, part of the Australian Plant Phenomics Facility, are now operational at the Commonwealth, Scientific, and Industrial Research Organisation, CSIRO division of Plant Industry; the latter platform is also duplicated at the Australian National University. Cabscan is an in-cabinet imaging robot platform, using visible stereoscopy and infrared imaging,

to monitoring the growth of model plants such as Brachypodium distachyon and *Arabidopsis thaliana*. The system enables digital analysis of plant growth with high spatial and high temporal resolution, images 20 plants at once, up to four times per hour, day and night. The growth chamber, in which the robot roams, is equipped with a multi-wavelength enrichment system providing high level of spectral control. The growth chamber can accommodate 320 plants at once. Trayscan is a new automated phenotyping platform equipped with a conveyor system, which is enclosed in an acclimation chamber allowing control of light and temperature (up to 500 mmol m-2 s-1). The system has a throughput of approximately 2500 plant per day. Plants are grown individually in template trays of 20 plants. The system processes 15 trays at once in a sequential manner. It is equipped with an automatic watering system which weight 5 individual pots at once, an infrared imaging station, a multi-angular visible imaging station and a pulse modulated fluorescence imaging station (plant can be dark adapted within the system). A complete image analysis pipeline is currently being implemented for analyzing growth of plants in 2D, 2.5D, 3D and 4D.

Institute of Bio- and Geo-Sciences: IBG2 Plant Sciences - The Jülich Plant Phenotyping Centre (JPPC) at Forschungszentrum Jülich, Germany

Two climate chambers dedicated to the analysis of *Arabidopsis thaliana* rosettes growth dynamics are operational and have a total capacity of 2400 plants grown in 70cm-wide pots. This robotized system (SCREEN-Chamber) executes plant-to-sensor routines during which pots are cultivated using a tray format, typically of 40 pots per tray. There are four XYZ positioning systems, two per chamber, equipped with measuring heads mounting cameras for active fluorescence protocols. To increase daily throughput and design more flexible routines, the imaging positions within the chambers have been retrofitted with RGB cameras (top view) for automated segmentation of projected shoot area. Watering stations are also implemented in this system. Typical experiments include imposing water and nutrient limitation treatments. Low air temperature to about 10oC can be achieved in these growth chambers and several light regimes are possible. Next to this system, an agar based screening system is used (SCREENROOT-SP) to measure root and shoot growth dynamics of Arabidopsis seedlings. Also, a new robotized cultivation and a 2D imaging system for plants grown in large (90x60x3.4cm) soil-filled rhizoboxes was constructed and validated using model monocot and dicot species (Nagel, 2012). Arabidopsis (Col-0) plants cultivated in rhizoboxes for 5 weeks in the greenhouse reached depths of about 40cm and displayed a large proportion of the root system at the transparent plate of the rhizoboxes (up to about 80%) in our conditions. This highlights opportunities for root phenotyping in soil for Arabidopsis genetic resources. The typical simultaneous root and shoot imaging throughput for this system is of about 50 rhizoboxes/hour. For a comprehensive description of phenotyping infrastructure including MRI for 3D reconstructions of plant roots grown in soil and other imaging systems for which access is offered through the European Plant Phenotyping Network (EPPN) see also http://www.fz-juelich.de/ibg/ibg-2/EN/methods_jppc/methods_node.html. Significant progress in data acquisition, storage and retrieval pipelines was achieved in 2012 with the deployment of the distributed plant database PHENOMIS architecture (Schmidt et al, 2013). This effort will enable data sharing and reuse as well in the coming years. IBG2 and JPPC phenotyping infrastructure undergoes continued and sustainable development within the German Plant Phenotyping Network (DPPN) and part of its capacity is offered through the EU-funded project, the European Plant Phenotyping Network (EPPN). Within the EPPN network about 20 phenotyping projects including several Arabidopsis ones were selected for access and were ongoing in 2012 http://www.plant-phenotyping-network.eu/eppn/selected_projects.

Wageningen University, the Netherlands

A robotic phenotyping infrastructure based on chlorophyll fluorescence, visible light and near-infrared imaging of Arabidopsis has been developed for the analysis of QTLs and use QTL markers in plant breeding (Harbinson et al, 2012). The imaging system has been built into a growth cabinet to ensure wide-ranging and accurate climate control and is comprised of a plant cultivation system and a camera module. The cultivation system can accommodate up to 1440 plants, grown individually in rockwool blocks, in two groups, with each group having an independently controlled fertigation system. A mobile camera module is positioned above the plants in the cultivation system and can scan and image them in any chosen order. The camera module is fitted with an optical filter wheel and LED light sources and different imaging modes (e.g., narrow band, broad band or fluorescence) are selected by means of a filter wheel and activation of specific LED measuring light sources. Using chlorophyll fluorescence imaging the photosynthetic light-use efficiency and other photosynthetic properties of the plants, such as non-photochemical quenching, can be measured as frequently as once per hour. The visible and NIR imaging modes allows conventional colour images to be taken, as well as nocturnal imaging and imaging of chlorophyll and anthocyanin content. Using these imaging options, the phenotyper can be used to measure the physiological and growth (via projected plant area) responses of Arabidopsis and other small plants and seedlings to the environmental changes and stresses. Arabidopsis plants grown under unstressed conditions can be observed for about 3 weeks from the time of germination, after which they begin to overlap each other making automated image analysis difficult.

The plant-environment responses that we observe with the system are useful in their own right, but we make use of these responses to the localize the genetic factors that give rise to them. Using this approach of combined phenotyping and genetic analysis we are exploring the genetic basis of natural variation in environmental physiological traits, especially in

relation to photosynthesis and nutrition. Currently we have identified QTL and even candidate genes for phenotypic variation in photosynthetic capacity and NPQ, pigmentation, plant growth related traits and leaf movement. Most of these traits were not only analyzed in standard conditions but also in response to an environmental change such as to low temperature, to fluctuating and increasing light conditions, and to phosphate and nitrate deficiency. The Arabidopsis phenotyping equipment is in a state of continuous improvement, especially with regards to the software for control of the phenotyping robotics and the subsequent analysis of the raw data produced by the system. Particular goals for the coming year (2013) are improvements in the imager to permit z-axis movement in addition to x-y scanning, and improvements in data curation and sharing.

RIKEN and Other Developments in Japan

RIKEN has continued developing the integrated database of Plant Omics Data https://database.riken.jp/sw/en/The_integrated_database_of_plant_omics_data/ria301i/ within the RIKEN information system https://database.riken.jp (Tetsuro Toyoda) Phenotypic data include summaries of qualitative observations captured using annotations using controlled vocabularies and images. The Chloroplast Function Database II (Fumiyoshi Myouga and Kazuo Shinozaki) has been generated. This database is used to compare the phenotypes of visually identifiable mutants with their plastid ultrastructures and to evaluate their potential significance from characteristic patterns of plastid morphology in vivo. Information includes more than 300 morphological mutants and 1,740 homozygous lines with wild-type phenotypes as well as 48 images of plastid morphologies of mutants by transmission electron microscopy.

Other developments in Japan include: rice root development using root image analysis system (NIAS Advanced Genome Center, Dr. Habu, Y.) and the software CARTA (clustering-aided rapid training agent) for autolearning system (Dr. Kutsuna, N. and Hasezawa, S.; Kutsuna, 2012)

Aberystwyth University, UK

New phenotying systems have been commissioned in 2012.

The "SmartHouse" is based on a commercial system (LenmaTec) for the automated handling of over 800 RFID tagged plant containers moved on a programmable conveyor system between growth, imaging and sampling areas. Each carriage conveys one large plant (up to 2m tall) or a tray of 4-6 small plants (i.e. Arabidopsis). Environmental, nutrient and watering controls enable the application of single or combinatorial stresses, allowing mapping populations and diversity collections to be characterized under defined conditions. The Centre provides a range of sensors (RGB, thermal, UV, near IFR) to record plant characteristics non-destructively and dynamically. Imaging techniques under development including: Hyperspectral imaging and Laser scanning.

Large scale Flow Solution Nutrient Culture (hydroponics with dynamic ion uptake monitoring systems). This automated hydroponics research system provides non-destructive continuous measurement of net uptake of NO3- , NH4+ , K+ and other ions as required, at the whole plant level, under defined environmental conditions (air conditioned pressurised greenhouse) and rhizosphere pH. It is ideally suited to characterisation of nutrient uptake/remediation and assimilation under conditions of (a) constant external nutrient concentrations, (b) constant relative addition rates (where performance under limiting nutrient supply is of interest) and (c) controlled episodic regimes of supply. Resolution of uptake rates is from 10 min to 10 weeks and capacity is between 200-600 plants, depending on size. The system may be used for short (i.e. <24 h) or long-term (12 weeks) studies/screens.

MPI for Developmental Biology

MPI has developed methods to study segregation distortion in hundreds of F2 populations derived from natural accessions. These methods make use of bulk segregation analysis and Illumina sequencing, and combine the power of experimental crosses with GWAS.

MPI has developed a new dominant knockout technique, miRNA-induced gene silencing (MIGS), that can be used for facile, dominant knockout of multiple genes in transgenic plants (Felippes et al, 2012).

Selected Publications

- Duke University

Root phenotyping with root array:

Busch W, Moore BT, Martsberger B, Mace DL et al. (2012) A microfluidic device and computational platform for high-throughput live imaging of gene expression. Nat Methods (11):1101-6.

Galkovskyi T, Mileyko Y, Bucksch A, Moore B et al. (2012) GiA Roots: software for the high throughput analysis of plant root system architecture. BMC Plant Biol 12:116.

- Carnegie Institution

Root phenotyping with RootChip:

Grossmann G, Guo WJ, Ehrhardt DW, Frommer WB et al. (2011) The RootChip: an integrated microfluidic chip for plant science. Plant Cell 23(12):4234-40.

- University of Potsdam, Germany

Arvidsson S, Pérez-Rodríguez P, Mueller-Roeber B (2011) A growth phenotyping pipeline for Arabidopsis thaliana integrating image analysis and rosette area modeling for robust quantification of genotype effects. New Phytol 191(3):895-907.

- INRA - Institut Jean-Pierre Bourgin, Versailles, France

Tisné S, Serrand Y, Bach L, Gilbault E et al. (2013) Phenoscope: an automated large-scale phenotyping platform offering high spatial homogeneity. Plant J [Epub ahead of print].

- Center for Genomics and Systems Biology, New York University, New York

Ristova D, Rosas U, Krouk G, Ruffel S et al. (2013) RootScape: A Landmark-Based System for Rapid Screening of Root Architecture in Arabidopsis. Plant Physiol 161(3):1086-96.

Key Genetic Resources and Traits Phenotyped in 2012

Table 3. List of novel and known genetic resources and key traits for which phenotyping to various level has been undertaken or has continued in 2012.

Institution	Genetic resources	Key plant traits and research topics
INRA-LEPSE	Known genetic resources available in other groups have been used such as epigenetic recombinant lines (Reinders J, et al., 2009 Genes Dev.); population of recombinant inbred lines and near isogenic lines (Alonso-Blanco et al., 1998 Plant J, Keurentjes et al., 2007 Genetics); Salk T-DNA insertion lines (O'Malley and Ecker, 2010 Plant J); selected panels of mutants in hormonal, carbon metabolism and cell cycle pathways	Genetic and environmental control of rosette growth and functioning (phenology, cell division, endoreduplication, water use efficiency,photosynthesis, transpiration, leaf surface temperature and leaf insertion angles)
Jülich Plant Phenotyping Centre (JPPC) at IBG2-FZJ	1001 genomes project: first 80 sequenced lines were phenotyped at low and control T (agar system SCREENROOT SP, root and shoot growth), and at reference, non limiting conditions in pots (SCREEN CHAMBER) Selected panels of mutants in hormonal pathways	Water and nutrient use efficiency; rosette growth dynamics, photosynthesis; root growth dynamics and architecture; abiotic stresses; modeling of responses to the environment
MPI for Developmental Biology	New gene knock-out method MIGS	Growth-immunity trade off
National Institute of Agro-biological Science (NIAS)	Japonica and Indica rice	Root morphology
University of Tokyo	Arabidopsis cells, BY2 JST Project (http://www.jst.go.jp/pr/announce/20120829-2/index.html)	Pattern of epidermal cells and guard cells of Arabidopsis leaves; evaluation of morphological measurement
RIKEN	RIKEN Arabidopsis Activation Tagging lines (http://amber/gsc.riken.jp/act/top.php) (Minami Matsui collaboration with NEC Soft co ltd.) Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA over-eXpressing) lines (Minami Matsui).	
RIKEN	Ac/Ds transposon lines (http://rarge.gsc.riken.jp/phenome/)(http://rapid.psc.database.riken.jp) (Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki)	
RIKEN	Arabidopsis Ds/Spm and T-DNA-tagged mutants of nuclear genes encoding chloroplast proteins (http://rarge.psc.riken.jp/chloroplast) (Fumiyoshi Myouga and Kazuo Shinozaki)	Photosynthesis; plastid morphologies of mutants by transmission electron microscopy
RIKEN	Database SciNetS (https://database.riken.jp)	
Wageningen University	Created a range of cytoplasmic swaps in Arabidopsis thaliana (ie moving cytoplasmic genomes into different nuclear backgrounds and vice versa); collected 120 new A. thaliana from Ireland. Borevitz A. thaliana Hap Map collection; Nordbrg A. thaliana Reg Map collection; the Versailles A. thaliana RIL, Bur X Col, Shah X Col and Can X Col populations, and a Brassica rapa RIL population, and Brassica oleracea cultivars	Photosynthetic capacity and NPQ, pigmentation, plant growth related traits and leaf movement; most traits were analyzed in standard conditions and in response to low temperature, to fluctuating and increasing light conditions, and to phosphate and nitrate deficiency.
Aberystwyth University	Arabidopsis RILs (O'Niell et al., 2008) and MAGIC populations (Kover et al., 2009) are being phenotyped on soil, under limiting nutrient conditions (hydroponics) and for tolerance to environmental pollutants. Natural diversity collections for oats, Miscanthus, clover, legumes, Brachypodium are also being developed and phenotyped for similar traits.	Biomass accumulation; Nutrient Use efficiency Seed biology; "Green" Chemical Feedstocks; cell wall composition; climate change related traits such as cold/heat/flooding tolerance Machine learning; data integration; ontologies

Projects and Collaborative Research

Table 4. National and international consortia and initiatives focusing on development and collaborative use of hardware and software infrastructure dedicated to plant phenomics including Arabidopsis and other model species.

Project	Web Link
Australian Plant Phenomics Facility (APPF)	http://www.plantphenomics.org.au
European Plant Phenotyping Network (EPPN)	http://www.plant-phenotyping-network.eu
German Plant Phenotyping Network (DPPN)	http://www.dppn.de/dppn/EN
International Plant Phenomics Network (IPPN)	http://www.plantphenomics.com
iPlant Collaborative (iPG2P)	http://www.iplantcollaborative.org/challenge/iplant-genotype-phenotype
PHENOME France	http://www.inra-transfert.fr/en/page.php?optim=phenome
Phenotype RCN (Plant Working Group)	http://www.phenotypercn.org
UK Plant Phenomics Network	http://www.ukppn.org.uk

Priorities and Prospects for Coordinated Actions

We consider that the non-exhaustive list of points indicated here below require continued attention and coordinated actions. As an outlook, we envisage that some of these themes may result in specific working groups. In following reports the Subcommittee will aim at describing activities that have developed to tackle these issues and that go in the direction of tighter coordination.

- Urgent requirement to exploit models to predict traits in Arabidopsis and diverse crops.
- Coordination of experimentation across phenotyping centers regarding germplasm used for sequencing within the 1001 genome project would be desirable.
- There is a need to promote best practices in phenotyping experimentation including e.g., requirements for optical and environmental sensor calibration and for simplified but precise schemas for reporting experimental meta-data.
- There is a need to promote in depth understanding of the physics of non-invasive technologies
- Ontology driven approaches to databases towards interoperability, data reuse and meta-analytical approaches, virtual laboratory environments and genome to phenome linkages.
- Phenotyping across environments – how do lab and indoor phenotypes translate into the field or landscape to inform us about adaptation and evolution?
- Automation of operations in plant phenotyping – at what scale does it reduce costs significantly?

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Proteomics

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

The past year has seen the subcommittee develop approaches to support the objectives of the Arabidopsis road map. This has included the development of a proteomics portal (1001 Proteomes) to enable exploitation of natural variation sequence data by Arabidopsis proteomic researchers. In the next few years, the ability to employ targeted proteomic approaches will likely become a more widely used approach for analysis of biochemical pathways and processes. The recent integration of Arabidopsis data into MRMaid represents the first stages in supporting these approaches. In combination with the ProMEX resource, Arabidopsis researchers now have advanced access to develop targeted proteomic approaches. The proteomics subcommittee has also actively been continuing our interactions with other proteomics organizations including Human Proteome Organization (HUPO) through the iMOP program and with the International Plant Proteomics Organization (INPPO). The development of these new resources and the continued interactions with complementary international organizations are part of the subcommittee's commitment to the road map aimed at increasing data integration and increasing international coordination in this area of research.

Recent Activities

A proteomics workshop was held in July 2012 at ICAR (Vienna, Austria) organized by Wolfram Weckwerth and Stefanie Wienkoop (University of Vienna, Austria). Speakers included Sandra Tanz (Australia) presenting an update to SUBA, Klaas Jan van Wijk (USA) outlining the use of QCONCAT and Stefanie Wienkoop (Austria) discussing absolute quantitation in proteomics experiments.

A workshop organized by Alex Jones (The Sainsbury Laboratory, UK), Hirofumi Nakagami (RIKEN Plant Science Center, Japan) and Jesús Jorrín Novo (University of Cordoba, Spain) was held in Kyoto, Japan at the XV International Congress on Molecular Plant-Microbe Interactions. The focus of this workshop was "Proteomics in plant pathology, challenges and advances" with the organizers discussing various approaches including phosphorylation, natural variation and 2-DE approaches to dissect plant pathology.

A proteomics workshop will be held at the upcoming ICAR 2013 in Sydney, Australia. The workshop will focus on proteomic approaches to identify receptor complexes and signaling events. Organizers are Joshua Heazlewood, Alex Jones and Harvey Millar and speakers will be selected from the conference abstracts.

In collaboration with the 1001 Genomes project (http://www.1001genomes.org/), we have developed a portal to enable the visualization of non-synonymous SNPs resulting from large scale sequencing of Arabidopsis natural variants (http://1001proteomes.masc-proteomics.org/). The 1001 Proteomes portal provides a simple interface to assess amino acid changes in Arabidopsis proteins. The proteomes of each of these natural variants (based on the SNP calls) are also available to the community to support proteomic experiments in these lines.

Recently Arabidopsis data in the EBI mass spectral repository PRIDE (http://www.ebi.ac.uk/pride/) has been incorporated into the MRMaid utility (http://www.mrmaid.info/). The portal assists in identifying transitions for targeted approaches in mass spectrometry (SRM / MRM / mass western) by profiling experimental spectra. This enables a more rational approach for the selection of protein specific tags for these experiments. The inclusion of Arabidopsis as an option in this resource was driven by Alex Jones.

Collectively the members of MASCP continue to contribute and update public resources focused on plant proteomics to support community research programs. A collection of these online repositories can be found at http://www.masc-proteomics.org/mascp/index.php/Databases. Major updates that occurred in the past year include SUBA (http://suba.plantenergy.uwa.edu.au/) which has been updated to SUBA3 and now includes a SUBAcon providing a subcellular prediction based on data within the resource. The mass spectral reference database ProMEX (http://promex.pph.univie.ac.at/promex/) was updated and now houses spectral data from a variety of plant species totaling over 100,000 spectra. The GelMap database (http://www.gelmap.de/arabidopsis/) is continuing to incorporate more annotated gel reference maps with recent additions of 2D-BN for chloroplasts and a 2DE for mitochondria and the pep2pro database has added new datasets which are available at http://www.pep2pro.ethz.ch.

Selected Publications

There were a number of contributions published in the past year (2012-2013) that significantly advanced proteomics in Arabidopsis and these include:

- Two independent studies were published in the past year employing differential organelle isolation approaches and proteomics to characterize the poorly examined Golgi apparatus in Arabidopsis. These studies have considerably expanded our knowledge of proteins and novel pathways within this organelle.

Parsons HT, Christiansen K, Knierim B, Carroll A et al. (2012) Isolation and proteomic characterization of the Arabidopsis Golgi defines functional and novel targets involved in plant cell wall biosynthesis. Plant Physiology (159): 12-26.

Nikolovski N, Rubtsov D, Segura MP, Miles GP et al. (2012) Putative glycosyltransferases and other plant Golgi apparatus proteins are revealed by LOPIT proteomics. Plant Physiology (160): 1037-1051.

- The genome sequencing of Arabidopsis natural variants will significantly contribute to our understanding of the subtleties of gene regulation and its effect on phenotype. This study has provided a simple visualization tool to view non-synonymous SNPs in these data as well as enabling easy access for proteomic studies.

Joshi HJ, Christiansen KM, Fitz J, Cao J et al. (2012) 1001 Proteomes: A functional proteomics portal for the analysis of Arabidopsis thaliana accessions. Bioinformatics (28): 1303-1306.

- The publications highlight the involvement that the MASC proteomics subcommittee has in developing international connections to proteomics communities both in the area plant research (INPPO) and more broadly with model systems (HUPO).

Jones AM, Aebersold R, Ahrens CH, Apweiler R et al. (2012) The HUPO initiative on Model Organism Proteomes, iMOP. Proteomics (12): 340-345.

Agrawal GK, Sarkar A, Agrawal R, Ndimba BK et al. (2012) Boosting the globalization of plant proteomics through INPPO: current developments and future prospects. Proteomics (12): 359-368.

- Application of quantitative proteomics connects the loss of photosynthetic capacity with other chloroplast and cellular functions, such as protein folding and stability, plastid protein import and the expression of stress-related genes.

Motohashi R, Rödiger A, Agne B, Baerenfaller K and Baginsky S. (2012) Common and specific protein accumulation patterns in different albino/pale green (apg) mutants reveals regulon organization at the proteome level. Plant Physiology (160): 2189-2201.

- The study describes that protein and transcript levels correlate well during leaf development, with some notable exceptions, and that diurnal transcript level fluctuations are not matched by corresponding diurnal fluctuations in the detected proteome. Also, it was found that continuous reduced soil water content results in reduced leaf growth but the plant adapts at molecular levels without showing a typical drought response.

Baerenfaller K, Massonnet C, Walsh S, Baginsky S et al. (2012) Systems-based analysis of Arabidopsis leaf growth reveals adaptation to water deficit. Molecular Systems Biology. 8 (1).

- Quantitative proteomics was used to examine changes in components of the mitochondrial electron transfer chains major respiratory complexes in response to cold and various chemical stresses.

Tan Y-F, Millar AH and Taylor NL (2012) Components of mitochondrial oxidative phosphorylation vary in abundance following exposure to cold and chemical stresses. Journal of Proteome Research (11): 3860-3879.

- In the publication, the proteomes of stay-green1 (sgr1) and Col-0 were examined before the initiation of senescence and this revealed a number of quantitative differences in a range of soluble plastid proteins.

Grassl J, Pružinská A, Hörtensteiner S, Taylor NL and Millar AH (2012) Early events in plastid protein degradation in stay-green Arabidopsis reveal differential regulation beyond the retention of LHCII and chlorophyll. Journal of Proteome Research (11): 5443-5452.

- The review provides a summary of the advances in mitochondrial proteomics in Arabidopsis thaliana over the past 5 years.

Lee CP, Taylor NL and Millar AH (2013) Recent advances in the composition and heterogeneity of the Arabidopsis mitochondrial proteome. Frontiers in Plant Science (4): 4.

- This publication proposes how the use of selected reaction monitoring (SRM) mass spectrometry that has been developed in Arabidopsis could be applied to decipher the molecular mechanisms of abiotic stress tolerance in crop plants.

Jacoby RP, Millar AH and Taylor NL (2013) Application of selected reaction monitoring mass spectrometry to field grown crops to allow dissection of the molecular mechanisms of abiotic stress tolerance. Frontiers in Plant Science (4): 20.

Goals Supporting the Arabidopsis Road Map: From Bench to Bountiful Harvests

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

- Build on large scale proteogenomic mapping efforts and integrative subcellular profiling to further enhance and expand current whole plant and subcellular protein expression maps in Arabidopsis
- Create a resource of validated Arabidopsis proteotypic peptides that can be employed for SRM-based quantitative analyses of proteins by mass spectrometry (e.g. AtSRM Atlas)
- Continue to expand and integrate new proteomics resources through the MASCP Gator

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

- Construct a 1001 proteomes portal for community exploitation and visualization of proteomes from Arabidopsis natural variants
- Undertake a coordinated proteomic analysis of Arabidopsis accessions to both validate genomics data and to identify specific SRM markers (based on nsSNPs) for specific proteins from accessions for future quantitative analyses

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

- Assist in the coordination proteomics activities in other plant systems through representations as the Arabidopsis committee on the International Plant Proteomics Organization (INPPO)
- Actively pursue proteomics research programs in other plant systems using key knowledge gained through the analysis of Arabidopsis

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

- Maintain and enhance existing informatics infrastructure in Arabidopsis proteomics

- Create new resources to exploit emerging technologies (e.g. AtSRM Atlas)
- Develop international proteomics standards in coordination with the iMOP program
- Continue to coordinate the integration of Arabidopsis proteomics resources through the MASCP Gator
- Integrate proteomics data resources with other informatics resources in Arabidopsis

E) Deepen International Cooperation and Coordination

- Represent Arabidopsis proteomics activities and develop proteomics standards through interactions with the initiative on Model Organism Proteomes program (iMOP) as part of the Human Proteome Organization (HUPO)
- Represent Arabidopsis proteomics interests as representatives of the International Plant Proteomics Organization (INPPO)
- Continue to offer proteomics workshops at international conferences

Systems Biology

By Siobhan Brady (Chair) and Malcolm Bennett (Co-chair) with contributions from subcommittee members

Key Aims

Promote systems biology research in Arabidopsis research. Systems approaches involving computational and mathematical modeling are becoming much more important as our knowledge of the regulatory signals and pathways controlling plant growth and development become increasingly detailed and their network behavior and outputs less intuitive.

Help bridge the 'genotype to phenotype gap', by encouraging researchers to move beyond the network and cellular scales, and use multiscale modelling to predict emergent dynamics at the tissue, organ and organismal levels through the use of virtual organ models and digital organisms.

Underpin synthetic biology applications in crops by facilitating translation of knowledge generated using systems approaches in Arabidopsis and other plant species.

Recent Activities

Several members of the MASC subcommittee contributed to a special issue of Plant Cell containing 4 reviews describing recent efforts to model network to multi scale systems in plants (see October 2012 edition).

Co-organizing training activities promoting systems biology approaches in Arabidopsis research. Recent examples include the Mathematics in the Plant Sciences Study Group (25-28 March 2013; http://www.cpib.ac.uk/events/mpssg/). Study groups are meetings to facilitate interactions between theoretical and life scientists. Plant sciences researchers are invited to present a problem that will be tackled by a team of mathematicians and computer scientists during the workshop. Problems can be from any area of plant and crop science but need to be amenable to modelling approaches. Following four days of intensive work, each group presents the progress they have made on their problem. Links are established between the theoretical and plant scientists attending the meetings so that problems discussed during the study group can be followed up in more detail. Previous meetings in the series have resulted in successful grant proposals, studentships and publication. This years problems came from plant researchers based in the US (such as Tobias Baskin from UMass Amherst and Dan Roberts from Univrersity of Tennessee) and Europe (Siobhan Braybrook, Cambridge Laboratory, UK and Catherine Bellini, SLU Umea, Sweden).

Co-organizing research workshops promoting systems biology research. Recent examples include the systems themed symposium at the Anuual SEB Meeting (June 28th-July 2nd 2012 held in Salzburg, Austria) entitled "Generating new biological insights from complex data: methodology, data gathering, inference, modeling, validation, integration and solutions.'

To achieve our ambitious aims, we are establishing a subcommittee website for efficient exchange of information and dissemination of our activities to be launched in 2013.

Recent and Upcoming Research Meetings and Training Events

- Workshops offered at meetings included an International Workshop on Synthetic Biology in Santiago Chile (organized by Rodrigo Gutierrez) – lectures and lab training were offered and the connections between synthetic biology and systems biology were explored.
- A Cold Spring Harbor meeting on High Throughput Image Analysis – co-organized by Philip Benfey.
- Two Systems Biology sessions at ICAR2012 in Vienna, Austria; one was a workshop co-organized by Siobhan Brady and Wolfgang Busch and related specifically to root development
- The Agricultural Model Intercomparison and Improvement Project (AgMIP) is organizing a "hack-a-thon" on February 4-8, 2013 at the Texas Advanced Computing Center in Austin, Texas, with the goal of facilitating the swift development of applications and tools for use by the AgMIP research community. AgMIP is a major international effort that brings together experts in the fields of climate, crop, and economic modeling through the use of cutting-edge information technologies. Goals of the project include improving the ability of the models to simulate the effects of climate change on agriculture, and training a new generation of researchers to use the models effectively. The iPlant Collaborative is funded by the National Science Foundation, with the goal of building cyberinfrastructure and computational tools to solve grand challenges in plant biology.

- CPIB Summer School: Mathematical Modeling for Biologists. The sixth Mathematical Modelling for Biologists course is planned for 9-12 September 2013 (http://www.cpib.ac.uk/events/cpib-summer-school/). The aims of the summer school are to introduce modelling and quantitative approaches to biologists; to explain where models come from, and how to investigate the behaviour of those models; to introduce differential equation models, parameter estimation and sensitivity, randomness and spatial models; to show how to create, simulate and analyse models using appropriate software. Examples include applications to gene regulation, biochemical reactions, population dynamics, and epidemiology.

Systems Related Plant Databases

BAR's Arabidopsis Interactions Viewer now contains 28,000 experimentally-determined PPIs and about 70,000 predicted interactions based on interacting orthologs available through the the PSICQUIC registry.

Department of Energy Systems Biology Knowlegebase: Integration and modeling for predictive biology. The goal of KBase is to incorporate community data and provide services through an application programming interface (API) to facilitate user interaction for data visualization and data exploration. One component of this relevant to systems biology is "Network Analysis" where the stated goal is to create co-expression networks, ontology analysis of these networks and to recommend genes based on guilt by association. Transcript based modeling of metabolism for plant genomes will also occur. Plant genomes incorporated in K-base include poplar, Arabidopsis, Sorghum, Chlamydomonas, Brachypodium, Miscanthus and switchgrass. Network interactions will include public data and data computed in KBase. For protein-protein interaction networks this will include IntAct data for Arabidopsis and interologs in poplar, Sorghum and Brachypodium. For tissue and condition-specific coexpression networks and clusters this data will primarily come from Arabidopsis and poplar. Functional association networks will incorporate AraNet and PoplarNet. Regulatory network data will come from AGRIS.

SynthSys hosts PlaSMo, a database of diverse plant models in XML formats (www.plasmo.ed.ac.uk), BioDare a database of low volume time series data (i.e. not array data) (www.biodare.ed.ac.uk), and SBSI a model simulation and optimisation infrastructure for high-performance computing (www.sbsi.ed.ac.uk).

Selected Publications

Cruz-Ramirez et al. (2012) A Bistable Circuit Involving SCARECROW-RETINOBLASTOMA Integrates Cues to Inform Assymetric Stem Cell Division., Cell.

Huang et al. (2012) Mapping the Core of the Arabidopsis Circadian Clock Defines the Network Structure of the Oscillator. Science, 336:775-779.

Band et al, (2012) Root gravitropism is regulated by a transient lateral auxin gradient controlled by a tipping-point mechanism. PNAS 109:4668-73.

Petricka et al (2012) The protein expression landscape of the Arabidopsis root. PNAS 109:6811-8.

Analysis and Recommendations of MASC

The history of Arabidopsis research is rather short compared to traditional model organisms with agricultural importance. Within the last 20 years the impact of Arabidopsis in basic research and also applied research drastically increased. Nowadays *Arabidopsis thaliana* serves as an established model and reference plant to study new hypothesis, develop new techniques and discover fundamental principles and applied insights into plant form and function that can be transferred to other species. Arabidopsis research and associated resources developed by the Arabidopsis community underpin aspects of the agricultural industry, which exploits the potential use of Arabidopsis for knowledge transfer and as test system for applications.

The tremendous knowledge gained by research on Arabidopsis was only possible due to the continuous support by funding bodies all over the world. In line with the growing financial support the Multinational Arabidopsis Steering Committee was founded in order to organize the international research efforts on Arabidopsis. MASC strives to coordinate research on the level of individual research labs and the whole community to avoid redundancy and to maximize the output by combined efforts. During the last two decades the community formulated two road maps that aimed to inform scientists, funding bodies and decision makers on the future foci of Arabidopsis research. The Arabidopsis community was very successful in achieving the formulated goals, i.e. the sequencing of the Arabidopsis genome as first plant reference genome and commencing functional characterization of Arabidopsis genes.

In 2012 the third road map entitled "From Bench to Bountiful Harvests" was published that outlines the goals of the international Arabidopsis community as guidelines and information resource for Arabidopsis researchers, funding bodies and decision makers (Lavagi, 2012). The main aim is to build functional networks at many levels of biological organization from molecules, single cells, tissues to the whole plant and ecological issues of plant communities. The connection from the lab to the field and *vice versa* will be strengthened to help to address the current global challenges of a growing population and global climate change.

Analysis

In the last decade molecular tools advanced from single functional genomics approaches to the level of 'omics' studies allowing to monitor whole genomes, transcriptomes, proteome and metabolomes in single experiments. This development was accompanied by the creation of vast volumes of different types of data. Many of these databases have been established and are maintained by members of the MASC subcommittees (see Reports of the MASC Subcommittees on page 13 ff.). One major challenge we are facing now is to create a new platform that will allow all researchers to analyze and combine these data to address specific biological questions and to reveal putative functions to further characterize genes and their interplay. A key goal will be to develop tools that are of use to all researchers, within and without the Arabidopsis community and to all disciplines from ecology to bioinformatics.

MASC and the international Arabidopsis community recognized this need early on and founded the International Arabidopsis Informatics Consortium (IAIC) in 2011 (http://www.arabidopsisinformatics.org/, see Arabidopsis Community Projects and Resources on page 9 ff.). In 2011, during a workshop the online platform Arabidopsis Information Portal (AIP) was designed and the results were published in Plant Cell last year (Baerenfaller, 2012). The core module for this data assembly is the "Gold Standard Genome Annotation" developed by TAIR (Li, 2012; Swarbreck, 2008). Thereby the Arabidopsis community began to approach one major short term goal of the road map. Subsequently the proposal for funding of the development of AIP was submitted to the U.S. National Science Foundation and the full AIP implementation plan was already requested (see Reports of the MASC Subcommittees on page 13 ff., Country Reports of the International Arabidopsis Community on page 42 ff.). The attempt to link individually curated databases with web-interfaces will ensure Arabidopsis to be a primary reference organism for other biological systems once again (Joshi, 2012; Joshi, 2011).

There are many fundamental improvements in the AIP, most important it is indeed a portal for all databases. The AIP and its resources are being developed in such a manner that it will function as a portal, not a static website that provides links to other sites. The databases that will be implemented in the AIP represent repositories of molecular data and imply the potential to build robust predictive models of various aspects of plant physiology, ecology and evolution. Statistic model approaches allow to reveal correlations between metabolites, proteins, transcripts and phenotypes (Weckwerth, 2003). For example in several studies on kinetic or structural modeling the biochemical and regulatory networks were reconstructed based on the functionally annotated genome of *Arabidopsis thaliana* (Dal'Molin, 2010; Mintz-Oron, 2012; Poolman, 2009). Subsequently, these models on genome-scale pathways need to be tested with experimental data to identify active and non-active pathways, alternative routes and regulatory circuits. Here in a recent study stochastic modeling allowed to interpret metabolite dynamics with

respect to pathway regulation by linking metabolomics data with genome-scale metabolic reconstruction (Doerfler, 2012; Weckwerth, 2011). Moreover model approaches were applied for developmental and gene regulatory processes such as flower and root development, auxin transport and circadian rhythm (Band and King 2012; Peret, 2012; Pokhilko, 2013; Roeder, 2011). In order to better understand allele variation and adaptive traits statistic models on population dynamics can be built with Arabidopsis data. In the context of generating robust predictive models for various plant processes *Arabidopsis thaliana* fulfills its prophecy by Friedrich Laibach as being a model plant for genetics and developmental physiology (Laibach 1943; Weigel 2012).

The Arabidopsis community has also made progress concerning many other projects of the road map (Lavagi, 2012). For example the transition of the TAIR resource to iPlant is being processed (see Arabidopsis Community Projects and Resources on page 9 ff.), new databases of polymorphisms for future studies on adaptation and evolution were created (Horton, 2012; Huang, 2012; Joosen, 2012; Kover and Mott 2012; Kronholm, 2012; Lee and Mitchell-Olds 2012; Schmitz and Ecker 2012) and especially the IAIC and the MASC subcommittees have been and are still highly active, which was also reflected by the program of the international Conference on Arabidopsis Research (ICAR), Vienna, 2012 (see Progress and Activities of MASC on page 8 ff., Reports of the MASC Subcommittees on page 13 ff.).

In the current and in coming decades a major theme of Arabidopsis research is to translate the knowledge of fundamental plant processes into applied systems, especially crop plants and breeding. To support the exchange between applied and basic research several new organizations were founded such as the Asia-Oceania-Agricultural Proteomics Organization (AOAPO). In 2012 many MASC members were present as speakers at the 4th International Symposium on Frontiers in Agriculture Proteome Research sponsored by the AOAPO to enhance the discourse which is necessary to translate Arabidopsis research into applied plant biotechnology.

Recommendations

Research on the reference organism *Arabidopsis thaliana* was fruitful in the past and leveraged research on other model plants of agricultural importance. Arabidopsis has proven to be useful to transfer knowledge and as powerful system to establish new techniques and generate and test new hypotheses. The future success of Arabidopsis as reference plant will depend and was always dependent on the continuous support by funding bodies and decision makers. As we move into the post-genomic era an emerging view is there might be less of a need for a reference plant, but that is if you think plant biology would be just about DNA. With respect to a more holistic view of critical mass, interconnected databases, resources and biological insights Arabidopsis certainly continues to be the prime reference organism for plant sciences. Indeed, as knowledge from other developing models such as Brachypodium grows the power of comparative 'omics' will come to the forefront and this requires a reference organism like Arabidopsis. It is important to support the unique Arabidopsis community that is characterized by highly active researchers and their practice of open and free exchange of data, ideas and technologies. Basic and applied research are essential counterparts that contribute valuable solutions to the challenges we face. The Multinational Arabidopsis Steering Committee recommends for 2013 (see also "Detailed Goals" next page):

1. Development of the Arabidopsis Informatics Portal and communicating the status to the plant science community
2. Translating the fundamental understanding of processes such as flowering, stress physiology, developmental processes etc. into applied systems, especially crop plants and breeding studies, for example development of strategies for common conferences and symposia
3. Intensification of the analysis of natural genetic variation in *Arabidopsis thaliana*
4. Development of *in silico* models of Arabidopsis from molecular to organismic level

Detailed goals for 2013 according to the road map: "From Bench to Bountiful Harvests"

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

- Collect and collate accurate and quantifiable data obtained at multiple levels of abstraction (ongoing)
- Continue to develop collections of mutants and mutant lines accompanied by support of public and accessible stock centers (ongoing)
- Develop new research tools and experimental methods to address the lack of global assays for a number of plant processes (ongoing)
- Fully exploit emerging technologies (ongoing)
- Provide training for plant scientists in computational science and theoretical approaches (ongoing)
- Encourage further collaboration between plant biologists and theoretical scientists (ongoing)

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

- Continue to develop genomic sequencing and computational resources in order to understand and utilize the natural variation of Arabidopsis and related species (short/medium term)
- Develop tools and techniques to facilitate the identification of QTLs that have subtle effects on plant genotypes (ongoing)
- Utilize the information gathered in Arabidopsis and related species to undertake comparative genomics/ comparative evolution / comparative ecological genomics (ongoing)
- Develop appropriate open access informatics and data infrastructure for storage, retrieval and analysis of variation and QTL data (short/medium term)
- Develop accessible statistical and computational methods for the analysis of natural variation and QTL data (short/medium term)
- Develop high-throughput methods for measuring phenotypes in the lab and in the field (ongoing)

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

- Undertake the approaches outlined in sections A and B to help us understand important complex traits (ongoing)
- Promote active dialogue, knowledge and data exchange between plant communities and various fields of expertise (ongoing)
- Develop a data and informatics infrastructure in which underpinning knowledge generated in Arabidopsis can flow easily to plant breeding (short/medium term)
- 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) (ongoing)
- Promote exchanges of information and personnel between Arabidopsis groups and those working on other plant species and vice versa (ongoing)
- Promote knowledge exchange with data providers/users of other model organism communities and facilitate interactions with computational/theoretical researchers (ongoing)

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

- Develop the Arabidopsis Information Portal (AIP) infrastructure that is flexible enough to respond to new/future approaches in data management, access and integration (short term)
- Develop appropriate data standards and establish their widespread use in the community (short term)
- 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 (short/medium term)
- Ensure all data and resources generated are available via the appropriate public data repositories (ongoing)
- Ensure there is interoperability between the data and resources generated by the Arabidopsis community and those generated by other communities (ongoing)
- Establish strong links with other data providers/users and computational experts to allow exchange of information and best practice (ongoing)

(E) Deepen international cooperation and coordination

- Continue to represent each country that is undertaking Arabidopsis research around the globe (ongoing)
- Increase awareness of the richness of international Arabidopsis research via the production and distribution of the annual MASC report and the International Conference on Arabidopsis Research (ICAR) (ongoing)
- Help coordinate international Arabidopsis research, to minimize duplication of efforts and maximize efficient use of resources through collaboration (ongoing)
- Promote open communication and free exchange of data, materials, resources and ideas among the Arabidopsis research community (ongoing)
- Liaise with funding agencies supporting Arabidopsis research (ongoing)
- Provide coordination for the "Bench to Bountiful Harvests" road map (ongoing)
- Periodically assess the status of the "Bench to Bountiful Harvests" (ongoing)

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Arabidopsis Basic Research and its Impact on Applied Research

Scientific Highlights in 2012

In 2012 the annual number of publications involving Arabidopsis research has increased once again. The number of peer-reviewed articles in 2012 in rice was slightly lower than that of Arabidopsis but appeared to follow the same trend (Figure 1). Over the past 20 years the Arabidopsis community has enjoyed the ease of manipulation of this plant and the availability of a wide range of resources that have been developed. Resources include chemically generated mutants; homozygous T-DNA insertion mutant lines; RNAi resources, artificial microRNAs; cDNA and ORF clones; large-scale microarray data; RILs and other mapping populations. Resources that are more recent additions include expanded information about the Arabidopsis proteome, metabolome and methylome, and the natural diversity found in Arabidopsis accessions. Web-based databases and browsers are also proliferating, reflecting the need to manage the vastly increasing number of datasets developed by the many Arabidopsis research groups worldwide. The constant development of resources that adapt to the evolving needs of the community have greatly facilitated a large body of cutting-edge research that allows for rapid advances in plant biology.

With the population the need for food increases and we are facing the effects of climate change, therefore some governments are placing a greater emphasis on plant science research. However, the time lapse between an original scientific discovery and its biotechnological application is often rather long and studying an organism that is easier to manipulate may be beneficial in the long term. Indeed, Arabidopsis lends itself exceptionally well to studying most aspects of basic plant biology; its well-known features include its small genome, size, high fecundity, diverse natural populations, ease of genetic manipulation and transformation, and short generation time. Studies in Arabidopsis have also greatly benefited from strong international collaborations first established over 40 years ago and strengthened during the Arabidopsis Genome project spanning the last decade across several countries and continents. With the release of the reference sequence in 2000, the 'genomic era' of Arabidopsis research truly began, allowing a rapid increase in discoveries and publications (Figure 1).

Considered alongside classic model organisms such as corn, the Arabidopsis publication record remains impressive, reflecting its ease of use as a genetic system, advanced resources and datasets, and the collegiality of the worldwide community, each of which contributed to its development as reference plant. Between 1994 and 2012, the number of peer-reviewed Arabidopsis publications increased more than 10-fold, while rice and corn publications increased about 5.5-fold and 2.9-fold, respectively (Figure 1). Over 4,000 peer-reviewed Arabidopsis publications were produced in the past year, many of which contain exciting new breakthroughs that will no doubt have impacts on studies in plants and other species.

The following section provides summaries of just a few significant advances; notably, most publications involve collaborators from two or more countries, reflecting the collegiality and truly international nature of the Arabidopsis community.

A Nano Sensor to Assay *in vivo* Auxin Distribution

Plant development is guided by the interplay and gradual distribution of several small molecules, called plant hormones. In recent years, the knowledge about hormone perception mechanisms drastically increased. Today most receptors of the "classical" hormones i.e. auxins, cytokinins, giberrellins and ethylene were identified as well as promising candidates for abscisic acid perception exist (Santer, 2013). The insights into the molecular mechanism of hormone perception enable the development of new nano sensors to map the hormone distribution *in vivo* at a high spatio-temporal resolution.

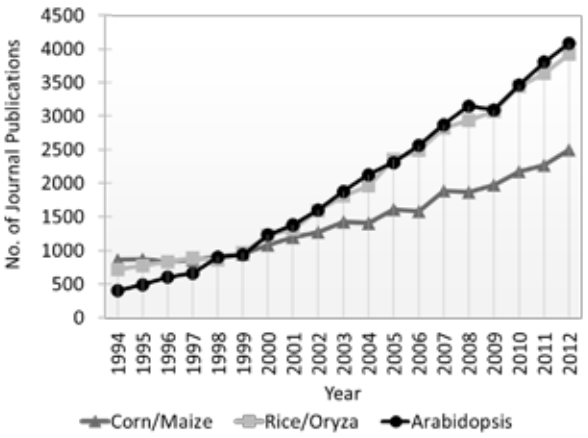

Figure 1. Number of Journal Publications from 1994 until 2012 citing the model organisms Arabidopsis, rice or corn,
Source: http://www.ncbi.nlm.nih.gov/pubmed query e.g.: Arabidopsis[Title/Abstract] AND ("journal article"[Publication Type] OR "review"[Publication Type]) AND ("2012"[PDAT] : "2012"[PDAT]).

In 2012 Brunoud and colleagues published the first plant hormone nano sensor by overexpression of a fusion protein of an auxin co-receptor domain with a fast maturing yellow fluorescent protein. Previously it was shown that the DII domain of Aux/IAA proteins interact via auxin with TIR1, which is a component of the $SCF^{TIR1/ABF1-5}$ complex that targets the Aux/IAA to degradation by the 26S proteasome. The authors validated that the DII domain of IAA28 fused to Venus (DII-Venus) is degraded upon presence of auxin. With this new DII-Venus reporter line they were able to monitor the inverse auxin distribution during developmental responses without any further perturbation. The decrease in DII-Venus fluorescence signal in root and shoot is comparable to the *DR5* promoter-reporter expression studies and unraveled also previously unknown regions. Time course experiments to monitor auxin distribution during auxin application, gravitropism and organ initiation revealed the auxin distribution dynamics in tissues and single cells.

The design of more *in vivo* nano sensors especially for hormones is essential to build robust models of developmental processes, which will be substantial for future computer based models to predict plant development under various circumstances.

Brunoud G, Wells DM, Oliva M, Larrieu A et al. (2012) A novel sensor to map auxin response and distribution at high spatio-temporal resolution. Nature 482(7383):103-6.

Santer A, Estelle M (2013) Recent advances and emerging trends in plant hormone signalling. Nature 459:1071-8.

Getting Connected – Egg Cell Secreted Proteins Induce Sperm Plasma Membrane Modifications

More than a century ago it was observed that two sperm cells are delivered by the pollen tube to fertilize the plant egg cell and the central cell. The mechanisms that govern the fusion of the plant egg and sperm cell, especially the factors required for intercellular communication are almost unknown.

In 2012 Sprunck and colleagues published a new model about the intercellular communication of gametes by Egg cell 1 (EC1) proteins, which are secreted by the egg cell, activate the sperm cell prior fusion and help to orientate the gametes. The authors showed that EC1 proteins are expressed in the egg cell before and during fertilization. The N-terminal secretion peptide is likely to direct EC1 proteins to exocytosis, which takes place upon sperm cell arrival and during double fertilization. Indeed, quintuple *ec1* mutants displayed a female gametophytic effect because sperm cells did not fuse with the egg cell. Gamete interaction studies indicated that EC1 secretion upon sperm cell arrival and during fusion with the egg cell activates the sperm cell to fuse with the egg cell. EC1 peptides caused the reallocation of HAP2/GCS1 (Hapless2/Generative cell specific 1) from endomembranes to the sperm plasma membrane. HAP2/GCS1 was described previously to be involved in the late step of gamete interactions. The observations by the authors also suggest that EC1 perception by the sperm cell might help to orientate the gametes during the fusion process.

It can be speculated that the overall intercellular communication between egg and sperm cell is far more complex because EC1 seems to facilitate only this fusion but not the fusion between the central and the sperm cell. Sprunck and colleagues provided first evidence for the complex communication during fertilization and they showed that the mutual activation of gametes is necessary as it was described for other sexual reproducing organisms.

Sprunck S, Rademacher S, Vogler F, Gheyselinck J et al. (2012) Egg cell-secreted EC1 triggers sperm cell activation during double fertilization. Science 338(6110):1093-7.

Another Mode of Action - Small RNAs are Involved in DNA Break Repair

Small RNAs play diverse and conserved roles in eukaryotes. They mediate transcriptional and post-transcriptional regulation of gene expression. In plants the RNA-directed DNA methylation (RdDM) pathway confers gene silencing of transposons and other repetitive DNA sequences by the most abundant heterochromatic small interfering RNAs.

In 2012 Wei and colleagues characterized a new class of DNA-double strand break small RNAs (diRNAs) involved in homologous recombination to repair DNA-double strand breaks (DSB). To analyze the efficiency of DSB repair in plants and human cells the authors used DSB inducible reporter lines. The DSB repair of the reporter after induction of DSB was reduced in the Arabidopsis mutants *dicer like 2* (*dcl2*), *dcl3* and *dcl4* that are defective in small RNA processing. This suggests a role for small RNAs in DSB repair. The mutant lines had reduced levels of specific diRNAs after DSB induction that matched to the flanking region of the reporter sequence. Because the detected small RNAs always mapped close to the DSB induced region, diRNAs might function in *cis*. The RNA-Polymerase IV and V also seem to be involved in the DSB repair whereas components of the RdDM pathway did not affect DSB repair in the DSB inducible reporter lines. Furthermore, Wei and colleagues could show that Argonaute 2 (AGO2) seems to load the diRNAs that flank the reporter where DSB was induced. This observation is in accordance with previous experiments in which AGO2 expression was induced after γ-irradiation. One of the first steps in DSB repair is phosphorylation of histone H2AX, which seems to be independent of diRNAs. The function of diRNAs seems to be downstream of histone phosphorylation for example to recruit DSB repair complexes or guide other histone modifying enzymes.

The study provides evidence that small RNAs are involved in the repair of DNA double strand breaks. The precise mechanism and components of the mechanism need to be discovered in future. The experimental set up of Wei and colleagues suggests that diRNA functions seem to be conserved in humans like it is known for other small RNAs.

Wei W, Ba Z, Gao M, Wu Y et al. (2012) A role for small RNAs in DNA double-strand break repair. Cell 149(1):101-12.

Where Sugar Transport Begins

Crop improvement focuses to shift the balance of sugar translocation to harvestable organs but the mechanisms that influence the translocation efficiency are almost unknown. The first step in sugar allocation is the transport from the mesophyll cells to the phloem, where sucrose is loaded from the apoplast by sucrose-H^+ co-transporter SUT1 (*At*SUC2) into the sieve element-companion cell complex and transported to sink organs. The sucrose transport mechanism from the mesophyll to site of phloem import was a matter of debate. For example symplastic transport by plasmodesmata and thus, sucrose efflux into the apoplast close to the sites of phloem import was suggested. However, apoplastic transport and sucrose efflux more distant from the phloem could not be excluded.

In 2012 Chen and colleagues identified the sucrose efflux transporters *At*SWEET11 and 12 localized to the plasma membrane of the phloem. Their results clearly supported the model of the symplastic sugar transport from the mesophyll to the phloem. Members of the clade III SWEET family of rice and Arabidopsis were shown to transport sucrose by FRET sensor uptake assays in human embryonic kidney cells. The low-affinity, pH-independent transport of sucrose by *At*SWEET12 supports a uniport mechanism. The double mutants of the close paralogs *At*SWEET11 and 12 were smaller compared to wild type at high light conditions and accumulated starch and hexoses at higher levels in leafs, which is comparable to plants defective in phloem loading. Furthermore, the slightly reduced root growth caused by sugar allocation deficiency of the *atsweet11;12* mutant was rescued by addition of sucrose to the media. Localization studies revealed that *At*SWEET11 and 12 are most likely in the plasma membrane of phloem parenchyma cells and not in companion cells. The regulation of sucrose efflux from phloem parenchyma cells into the apoplast and influx into phloem companion cells requires a tight control mechanism and intercellular communication. This is of special importance because growth of biotrophic pathogens depends on the apoplastic available sugars. For example in rice previous experiments showed that the expression of clade III SWEETs was induced after pathogen infection. Chen and colleagues speculate that the diversity of SWEET genes is an evolutionary tool to enhance the robustness of plant resistance against pathogens and to ensure that only a limited amount of sugars is present in the phloem apoplast.

The characterization of clade III SWEETs adds an important component to the mechanism of sugar allocation in plants, which will be essential to understand and adjust changes in sugar transport for crop improvement.

Chen LQ, Qu XQ, Hou BH, Sosso D et al. (2012) Sucrose efflux mediated by SWEET proteins as a key step for phloem transport. Science 335(6065):207-11.

Biogenesis of Chloroplasts Depends on Sufficient Protein Turnover

Over 90% of the proteome of plastids is imported into the plastid and hence encoded in the nucleus. In response to developmental or environmental changes plastids can interconvert between photosynthetic active and inactive variants. For example etioplasts in dark grown seedlings interconvert to chloroplasts after the transition to light, chromoplasts develop during the process of fruit ripening and at the end of the life cycle chloroplasts become gerontoplasts during senescence. These processes require overall changes in the proteome of plastids, which might include alterations in the plastid import machinery.

Ling and colleagues identified Suppressor of plastid protein import1 locus 1 (SP1) a RING-type ubiquitin E3 ligase that directs components of the chloroplast import machinery for degradation by the 26S proteasome and thereby alters the biogenesis of chloroplasts. *SP1* was identified by a forward genetic screen to suppress the *toc33* (*ppi1*) chlorotic phenotype. The translocon at the outer envelope of chloroplasts (TOC) system facilitates the translocation of pre-proteins into the chloroplasts. TOC33 is localized to the cytosolic site of the outer membrane and recognizes precursors of the photosynthetic apparatus. The *ppi1 sp1* double mutant indeed showed an improved protein import capacity and improved chloroplast development compared to *ppi1*. The SP1 protein has two membrane spanning domains anchored to the outer membrane of the chloroplast and the RING domain exposed to the cytosol. *In vitro* experiments revealed that SP1 interacts with TOC33 and some TOC proteins relevant for the import of housekeeping pre-proteins but not with other components of the chloroplast import machinery. SP1 facilitates ubiquitination of itself and its interacting partners and thereby directs the proteins towards degradation. By *in vivo* analyses they verified elevated amounts of TOC proteins in sp1 mutants and reduced amounts in SP1 overexpression lines. The effect of the protein degradation machinery on the TOC proteins by SP1 could be validated in different experiments. Furthermore, the authors demonstrate that the turnover of TOC proteins mediated by SP1 is essential for rapid plastid biogenesis. De-etiolation is slowed down in *sp1* mutants and accelerated in SP1 overexpression lines and in case of senescence the authors observed the reciprocal effect.

The study of Ling and colleagues identified the first mechanism that governs the action of the pre-protein import machinery of plastids. The turnover of import proteins seems to define the speed at which plastids interconvert. For example etioplasts interconvert to chloroplasts more rapidly as well as chloroplasts to gerontoplasts, if TOC proteins have an accelerated protein turnover. Thereby the TOC protein turnover seems to influence the change of the proteome of plastids which is essential for plastid interconversion.

Ling Q, Huang W, Baldwin A, Jarvis P (2012) Chloroplast biogenesis is regulated by direct action of the ubiquitin-proteasome system. Science 338(6107):655-9.

Tipping the Scale – The Role of Salicylic Acid Perception in the Life-and-death Decision Upon Pathogen Attack

Plants have decisive mechanisms to cope with pathogens. At the site of pathogen infection host cells can undergo either programmed cell death (PCD) known as hypersensitive response (HR) or they react by systemic acquired resistance (SAR) due to the memory of previous pathogen attacks. In both processes salicylic acid seems to play a key role. In case of an initial perception of an effector by a host resistance protein the immune response usually leads to PCD, also known as effector-triggered immunity (ETI). The increase in salicylic acid levels induces a global transcriptional reprogramming especially in the neighboring cells that leads to SAR.

In 2012 Fu and colleagues were able to postulate a new model how plants define the borders of PCD and the degree of SAR. They identified two receptors of salicylic acid Nonexpresser of PR genes 3 (NPR3) and NPR4 that function as adaptors to modulate the degradation of NPR1 under different salicylic acid concentrations. NPR1 is the molecular switch that triggers transcriptional reprogramming during SAR. By *in vitro* pull down and co-immunoprecipitaion assays they showed that NPR3 and NPR4 both function as adaptors between NPR1 and cullin 3 E3 ligase (CUL3) to trigger the degradation of NPR1 by the proteasome. NPR3 interacts with NPR1 only when salicylic acid is present, whereas NPR4 interacts with NPR1 only in the absence of salicylic acid. Saturation and dissociation experiments led to the characterization of the binding affinities of both receptors. NPR3 binds with low affinity and is expected to trigger NPR1 degradation on sites of high salicylic acid levels. In contrast NPR4 binds salicylic acid with high affinity at physiological concentrations and is assumed to fine tune NPR1 levels in a concentration dependent manner. Based on these results the authors suggest a model for the concentration-dependent salicylic acid function. Low levels of salicylic acid trigger the NPR1 degradation by NPR4 and CUL3 and thereby suppress SAR. During pathogen attack the salicylic acid levels increase to the site of the infection which progressively prevents NPR1 from degradation especially close to sites of PCD and thus accelerates the immune response. In cells where ETI takes place the salicylic acid concentration is highest and causes the degradation of NPR1 by NPR3 and CUL3 enabling PCD. The mutant analyses with *npr3 npr4* support this model because pathogen growth was reduced compared to wild type whereas *npr1* and *npr1 npr3 npr4* were more susceptible and none of these mutants were capable to establish SAR.

The salicylic acid perception once again highlights the concept of protein degradation by the proteasome after hormone perception to modulate specific cellular responses. Here the stability of NPR1 is modulated in a concentration dependent manner by two distinct salicylic acid receptors NPR3 and NPR4 which seems to be decisive for plant cells to make the life-and-death decision during pathogen infections.

Fu ZQ, Yan S, Saleh A, Wang W et al. (2012) NPR3 and NPR4 are receptors for the immune signal salicylic acid in plants. Nature 486(7402):228-32.

Soil Matters – The *Arabidopsis thaliana* Root Microbiome

Soil composition influences plant growth not only by its chemical properties but also by its microbe community. Especially endophytes and microbes of the rhizosphere that colonize plant roots affect plant health and biomass. Therefore, the characterization of the root microbiome would be of high interest for e. g. the assessment of soil quality, the investigation of plant-microbe interaction, or the development of plant probiotics to increase crop productivity.

For a long time little was known about the *Arabidopsis thaliana* root microbiome. In 2012 two publications from Bulgarelli et al. and Lundberg et al. characterized the composition of the Arabidopsis root microbiome with a resolution of up to the family level by pyrosequencing of 16S ribosomal RNA and *in situ* hybridization by CARD-FISH. Both groups showed independently that the soil itself is an important variable that influences the qualitative and quantitative composition of the root colonizing endophytes. Another general conclusion was the clear difference between the designated operational taxonomic units (OTU) of the root extracts compared to those from the rhizosphere and pure soil. Both groups also stated a minor but significant effect of the host genotype on the endophyte composition, which is most likely of quantitative nature. In general, the *Arabidopsis thaliana* microbiome undergoes a loss of diversity from the external rhizosphere to the endophytic compartment. In both studies the root fractions were significantly enriched in *Actinobacteria* (predominantly *Streptomycetaceae*) and it is known that some of this class exude antimicrobial secondary metabolites. Different families of the class of *Proteobacteria* were either enriched or depleted in the root microbiome. This suggests that soil microbes are either actively excluded by the host immune system, out competed by other bacteria or metabolically unable to colonize. Furthermore, Lundberg and colleagues could show that OTUs representing *Acidobacteria*, *Gemmatimonadetes* and *Verrucomicrobia* are generally reduced in roots compared to soil and rhizosphere. Bulgarelli and colleagues narrowed down the relevant OTUs even more by comparison with results obtained from colonized wood splinters. Thereby, they were able to differentiate between rather saprophytic microbia, bacteria that are excluded rather due to features of the cell wall and endophytes (predominantly *Actinobacteria*) that depend on metabolically active plant cells.

The limited number of bacterial taxa that colonize *Arabidopsis thaliana* roots across diverse soils suggests similar host needs across ecotypes and will allow for a detailed characterization of these endophytes and their broad metabolic potential. The previous assumptions together with the identification of genotype-specific endophyte associations point to general principles, which were also described for

mammalian enterobacteria before. In future, the identification of beneficial endophytes possibly contributes to the development of plant probiotics to increase plant health and biomass amongst other applications.

Bulgarelli D, Rott M, Schlaeppi K, Ver Loren van Themaat E et al. (2012) Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. Nature 488(7409):91-5.

Lundberg DS, Lebeis SL, Paredes SH, Yourstone S et al. (2012) Defining the core Arabidopsis thaliana root microbiome. Nature 488(7409):86-90.

Lignin - The Building Block of the Casparian Strip

The Casparian strip of the endodermis is the primary diffusion barrier in young roots and its function is comparable to tight junctions in animal cells. Unlike tight junctions the plant cell wall of the Casparian strip is impregnated with a kind of polymer that is resistant to chemical treatment and thus its chemical composition was a dispute for more than a century.

The study by Naseer and colleagues should end this dispute because they provide compelling evidence for lignin being the impregnating polymer of the Casparian strip and not suberin. The fluorescent dye propidium iodide doesn't diffuse through the Casparian strip and thus marks the zone of endodermis formation. Application of suberin dye together with promoter:GUS fusions of suberin biosynthetic genes indicated the formation of suberin significantly later or in other words further away from the root meristem. This conclusion was supported by the analysis of plants lacking endodermal suberin due to the expression of CUTICLE DESTRUCTION FACTOR 1 (CDEF1) in the endodermis. Although CDEF1 and other cutinases degrade suberin the roots of the transgenic plants still resembled wild type. In contrast the inhibition of lignin biosynthesis by two inhibitors delayed the formation of the Casparian strip, which could be complemented by the exogenous application of coniferyl and sinapyl alcohols. Furthermore, they were able to biochemically analyze the composition of the Casparian strip by using the *arabidopsis histidin transfer protein 6* (*ahp6*) mutant. A mild cytokinin treatment delays the formation of xylem enabling the isolation of endodermis tissue without xylem. The ratios of lignin units in samples with and without xylem were comparable. The results by Naseer and colleagues unambiguously demonstrate that lignin is the polymer that facilitates the impregnation of the Casparian strip.

The authors speculate that scaffolded protein domains exist containing recently identified Casparian strip membrane domain proteins (CAPs), transporters of monolignol substrates and lignin polymerizing enzymes. Therefore, the endodermis is a promising cellular model to study the mechanisms that guide the subcellular formation of lignin.

Naseer S, Lee Y, Lapierre C, Franke R et al. (2012) Casparian strip diffusion barrier in Arabidopsis is made of a lignin polymer without suberin. PNAS 109(25):10101-6.

Impact on Applied Research and Industry

The prevalent focus of applied research is on the development of applications with commercial value which for studies of plant species of agricultural importance are essentially required, like for instance rice, corn, soybean or legumes. 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 last 20 years the division of labor between the public and private sector has proven to be tremendously successful in case of plant biology.

In the 1990's Arabidopsis was established as new model plant in basic research possible due to the large support by government agencies. Already in 1999 and 2000 the number of peer-reviewed publications referring to rice, corn or Arabidopsis reached comparable levels and since then publications on Arabidopsis and rice exceeded those on maize (Figure 1). Clearly the continuous and ongoing success of Arabidopsis as reference plant ever since was dependent on the indispensable constant funding by government agencies. During the last decades the Arabidopsis community leveraged the applied research fields. For example in 2000 the Arabidopsis genome was published as reference genome, which was followed by functional genomics studies, the prosperity of 'omics' and network approaches and concomitant the development of a plethora of new technologies that should not be underestimated. 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 usually 10 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. An indication of what impact Arabidopsis research had in the past and what we might expect from translating Arabidopsis research into crop species and commercial products can be roughly estimated by the sole number of filed patents in recent years (Figure 2). Since the mid 1990's the amounts of filed patents that mentioned Arabidopsis, rice or corn steadily increased until 2012 and a positive future trend can be proposed at least concerning US utility patents, European published applications and international patents. The development of the filed patents over the last 18 years follows the same trend like the number of journal publications. Although patents on corn and rice far exceed those citing Arabidopsis, the translation of Arabidopsis knowledge and technologies to crop species cannot be underestimated. The continuous funding of Arabidopsis basic research by government agencies is crucial to further develop Arabidopsis as reference plant and to leverage applied studies in other plant species.

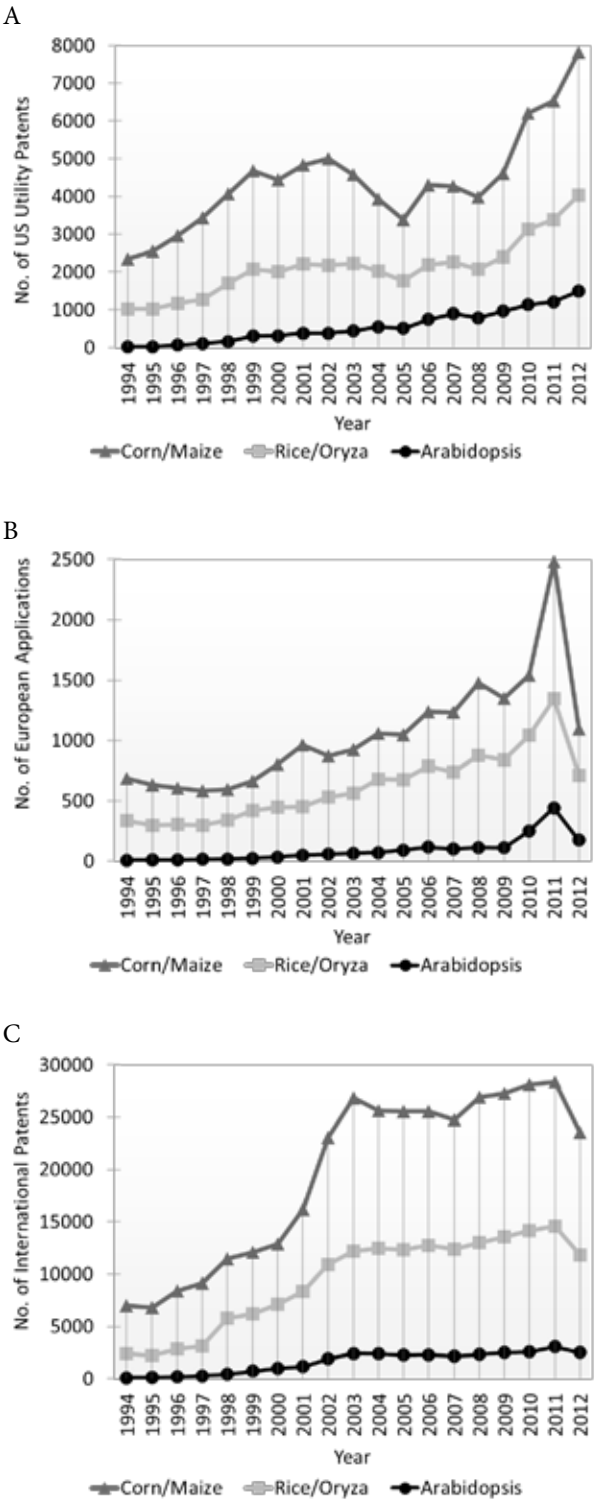

Figure 2. Trend of published patents from 1994 until 2012 in the United States (A), Europe (B) and internationally according to WIPO (World Intellectual Property Organization, 146 contractig states) (C).
Searches were performed via: A) http://patft.uspto.gov/netahtml/PTO/search-adv.htm, e.g. query: SPEC/rice OR SPEC/oryza AND ISD/20120101->20121231; B) http://worldwide.espacenet.com/advancedSearch?locale=en_EP, select EP collection, e.g.: Keyword(s) in full text: rice OR oryza, Publication date: 2012; C) http://patentscope.wipo.int/search/en/structuredSearch.jsf, select any field, e.g. English all: rice OR oryza, Publication date: 2012.

In the following section we summarized just a few recent examples of translational research to demonstrate that Arabidopsis serves as invaluable reference for applied research and how knowledge gained in this reference organism can be translated into real world applications and applied research in general.

Increasing Crop Stress Tolerance - Chemical vs. Genetic Approach

Increasing tolerance against abiotic stress factors is one of the major targets of agricultural research to prevent loss of yield in crops. In recent years not only the major conserved response pathways were characterized in detail like reactive oxygen species or abscisic acid signaling but also the knowledge about their interconnection increased. A common response to abiotic stress is the accumulation of metabolites like anthocyanins, which causes the typical brown/purple leaf coloration of stressed plants. Already 15 years ago the poly(ADP-ribose)-polymerases (PARPs) were shown to play a major role in plant abiotic stress response. Genetic studies with RNAi and knockdown lines revealed a correlation of reduced PARP levels with increased resistance against several abiotic stresses.

In 2012 European Arabidopsis scientists together with researchers from Bayer CropScience published a new approach to modulate abiotic stress tolerance by chemical inhibition of PARP enzyme activity. First they identified the optimal concentration of the inhibitor 3-Methoxybenzamide, which facilitates enhanced growth and reduced brown leaf coloration under mild stress conditions comparable to the RNAi lines. In a second step they analyzed the effects caused by the chemical PARP inhibition in Arabidopsis in detail. Gene expression and metabolite profiling revealed that PARP inhibition influences the phenyl-propanoid pathway and the authors observed a reduced stress-induced accumulation of anthocyanins after stress treatment at various growth stages. Expression analysis and mutant studies provide evidence to assume that the reduced anthocyanin accumulation during PARP inhibition is caused by transcriptional repression of key transcription factors and biosynthetic enzymes of the anthocyanin biosynthesis pathway. In long-term experiments the authors could show that chemical PARP inhibition increased the NAD+ content, like it was previously reported for the RNAi lines. Futhermore, the levels of defense molecules were reduced but the chlorophyll content was not altered and no negative effect on photosynthesis due to reduced anthocyanin accumulation during chemical PARP inhibition could be detected.

The study shows that chemical PARP inhibition at optimal concentration improves abiotic stress tolerance in whole plants like it was shown in genetic studies before. This opens the perspective to use chemical inhibitors as alternatives to genetic approaches that specifically target groups of enzymes to increase tolerance to abiotic stress and therefore leads to higher crop yield.

Schulz P, Neukermans J, Van der Kelen K, Mühlenbock P et al. (2012) Chemical PARP inhibition enhances growth of Arabidopsis and reduces anthocyanin accumulation and the activation of stress protective mechanisms. PLoS One 7(5):e37287.

Single Gene Approach to Increase Grain Yield in Soybean

Over the last decades the overall crop yield increased especially in major crops. Some crops like soybean have lagged behind others i.e. maize. A standard approach to protect crop yield are commercialized transgenic crops with herbicide and insect resistance. A new approach to increase crop productivity is the heterologous overexpression of single genes for instance from Arabidopsis in crops. An advantage of this approach is that promising candidate genes can be characterized in Arabidopsis in detail and thus, allows to expand the knowledge to possibility discover additional targets.

Several years ago Mendel Biotechnology and the Monsanto Company initiated a program to screen transgenic soybean in field trials that overexpressed single Arabidopsis genes to increase yield. In 2011 they published that Arabidopsis B-Box32 (BBX32) is involved in light signaling by suppressing light-induced genes in etiolated seedlings and the interplay with the circadian clock pathway was suggested (Holtan, 2011). One year later the companies published their first results on the overexpression of *Arabidopsis thaliana* B-Box32 (BBX32) in soybean, which correlates with a significant increase in grain yield in multi-location field trials over several years. Expression of *At*BBX32 in soybean delays senescence at a specific developmental phase decisive for soybean grain yield. Time course microarray experiments revealed that *At*BBX32 overexpression modulates the expression of circadian clock genes like *Gm*TOC1 and *Gm*LCL2 at dawn. Phylogenetic analyses identified *Gm*BBX52 and *Gm*BBX53 as putative homologs of *At*BBX32 and overexpression of the respective genes in soybeans leads to comparable phenotypes. Based on the results of *At*BBX32 overexpression in soybean the authors speculate on a role for this B-Box protein as integrator of light and clock pathways to regulate the duration of developmental stages after transition to flowering. Their results provide evidence for a conserved function of *At*BBX32 and its homologs in soybean, which implies that more conserved pathways exist.

Therefore the results obtained for BBX32 soybean are a very promising and successful example for the approach to increase crop yield by expression of single Arabidopsis genes in crops and basic Arabidopsis research helps to understand the molecular changes that lead to increased yield.

Preuss SB, Meister R, Xu Q, Urwin CP et al. (2012) Expression of the Arabidopsis thaliana BBX32 gene in soybean increases grain yield. PLoS One 7(2):e30717.

Holtan HE, Bandong S, Marion CM, Adam L et al. (2012) BBX32, an Arabidopsis B-Box protein, functions in light signaling by suppressing HY5-regulated gene expression and interacting with STH2/BBX21. Plant Physiol 156(4):2109-23.

Two for one: Engineering Phosphorus Metabolism

Since the green revolution in the 1960s the excessive use of fertilizers and herbicides facilitated a steady increase in crop yield. Both fertilizers and herbicides still need to be applied in increasing amounts due to herbicide resistant weeds and soils that do not meet nutritional requirements for plant cultivation. One major component of fertilizers is phosphorus, which is a non-renewable resource with reserves lasting for 70-200 years given the current use. For example about 67% of soils used for agriculture are limited in available orthophosphate crucial for photosynthesis. Orthophosphate availability in soils is limited and only 20-30% of the applied orthophosphate can be acquired by the plant. Excessive orthophosphate that gets run-off into rivers and oceans promotes major ecological problems like toxic algae blooms. The development of new approaches is necessary to ascertain the need for food of a growing population.

A strategy to reduce phosphate fertilization and weed growth altogether was published in 2012 by López-Arrendondo and Herrera-Estrella. They introduced the phosphite-specific oxidoreductase from Pseudomonas stutzeri WM88 (*ptxD*) into Arabdiopsis and tobacco plants, which enables the plants to utilize phosphite as sole phosphorus source. Phosphite is classified as organic fertilizer that is not toxic to humans or animals and already used as fungicide. Naturally plants can utilize only orthophosphate and not phosphite. Arabidopsis plants overexpressing the *ptxD* gene were able to metabolize phosphite and grew vigorously on plates supplemented with phosphite comparable to wild type plants fertilized with orthophosphate. Unfertilized wild type and transgenic plants displayed reduced growth and wild type with phosphite as sole phosphorus source showed even more reduced growth and died early. Comparable results were obtained by experiments with transgenic tobacco plants grown on sterile, natural low-orthophosphate alkaline or acidic soils. Only half of the amount of phosphite compared to orthophosphate was necessary to yield the same amount of seeds and biomass in transgenic and wild type tobacco, respectively. The authors also tested the effect of phosphite on plant growth of five weeds. All tested agronomical important weeds displayed reduced growth after phosphite treatment but did not die in natural soils.

Therefore, the phosphite based fertilization system seems to be a promising approach for agro-ecological agriculture. The authors suggest to apply this weed control and phosphorus fertilization technology in future as foliar fertilizer to reduce the influence on soil bacteria composition. The potential of the *ptxD* gene to outcross into wild is expected to be rather low due to its lack in natural soils. Although this system needs to be tested under field conditions it is a promising candidate to reduce the application of phosphorus and herbicides in a single treatment.

López-Arredondo DL, Herrera-Estrella L (2012) Engineering phosphorus metabolism in plants to produce a dual fertilization and weed control system. Nat Biotechnol 30(9):889-93.

Predicting the Performance of Complex Heterotic Traits in Hybrid Maize

A major success of plant breeding programs was the concept of hybrid breeding. Two parental inbred lines are crossed and yield a superior hybrid line, a phenomenon called heterosis or hybrid vigour. The molecular mechanisms behind hybrid success are not understood and so far no criteria to successfully predict hybrid performance exist. Standard breeding procedures like quantitative trait loci mapping have failed to predict the performance of the highly polygenic traits due to the large number of QTL loci. So far it was inevitable for breeders to perform testcrosses to estimate the general combining ability of inbred lines. The accurate prediction of the value of inbred lines is therefore desirable to reduce the number of testcrosses and to accelerate the breeding process.

In 2012 Riedelsheimer and colleagues presented a new approach to predict the performance of highly polygenic maize traits by whole genome nucleotide polymorphism (SNP) and quantitative metabolic data acquisition of parental inbred lines. The authors applied an approach previously developed by hybrid biomass studies in *Arabidopsis thaliana* (Gärtner, 2009 and Steinfath, 2009). In the actual study 285 inbred maize lines were crossed with two single-cross testers and the hybrid generation was comprehensively phenotyped. In the parental lines 56,110 SNPs and 130 metabolites were analyzed and used individually or combined for ridge regression-best linear unbiased prediction models to predict hybrid performance. The prediction accuracies ranged from 0.72 to 0.81 with the SNP data and 0.6 to 0.8 with the metabolite data, the combination of both data sets didn't improve the SNP accuracies. In Arabidopsis it was shown that the combination of some selected parental and metabolic markers allowed to improve the prediction accuracy but in general the predictions in maize were better.

In future these whole genome SNP based prediction models will allow to screen underutilized Genebank accessions and other highly diverse materials prior field trials with testcrosses. The whole genome prediction approach to evaluate maize inbred lines is a powerful tool to enhance breeding of highly polygenic traits and complements genome-wide association studies in maize. However, additional training populations will be needed to predict hybrid performance in traits that separately evolved from those analyzed in the study by Riedelsheimer.

Gärtner T, Steinfath M, Andorf S, Lisec J et al. (2009) Improved heterosis prediction by combining information on DNA- and metabolic markers. PLoS One 4(4):e5220.

Riedelsheimer C, Czedik-Eysenberg A, Grieder C, Lisec J et al. (2012) Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nat Genet 44(2):217-20.

Steinfath M, Gärtner T, Lisec J, Meyer RC et al. (2010) Prediction of hybrid biomass in Arabidopsis thaliana by selected parental SNP and metabolic markers. Theor Appl Genet 120(2):239-47.

Relax – It's Time to Flower

One of the most important agricultural crops besides cereals are legumes. In comparison to cereals the knowledge about genetic changes that underlie domestication and adaptation in legumes is less advanced. For instance the majority of cultivated peas presumably originated from wild Pisum sativum var. humile distributed in the Near East. In its natural range wild pea germinates in autumn and flowers after winter in response to long day conditions. Cultivated pea accessions differ in their flowering time behavior for example cultivars grown in higher latitudes, where the growing season in limited, flower under short day conditions. The analysis of the early history of wild and cultivated accessions is a helpful tool to unravel new molecular targets in legumes like pea that can be used to improve breeding.

Weller and colleagues compared flowering time and photoperiod responsiveness of wild and cultivated pea by genetic and phenotypic analysis. They identified the previously known quantitative trait locus HIGH RESPONSE TO PHTOTOPERIOD (HR) and a new major QTL, both of which explain 88% of the adaptive changes in flowering time in pea. They determined the recessive hr allele to be associated with early flowering, reduced branching and reduced sensitivity to high red:far red ratios under short day conditions. The circadian clock pathway is known to influence responses to photoperiod and light quality. Indeed hr homozygous lines showed altered expression of genes entrained by circadian rhythm. The authors inferred the location of genes in pea that were described in Arabidopsis to function like HR. Thereby they identified the location of putative pea orthologs of ELF3 and FRI to be located near HR. Reanalysis mapped the putative PsELF3 less than 0.3 cM distant from HR. Sequencing of hr cDNA of one accession revealed an insertion in exon1 at the ELF3 locus that causes a frame shift and truncation of the ELF3 protein. Expression of the putative PsELF3 ortholog restores wild type phenotype in Arabidopsis elf3-1 mutants, whereas the mutant version of the hr allele did not. Resequencing of all initial accessions revealed that the hr allele is widespread across cultivated pea and reflects mutant versions of the PsELF3 gene. Furthermore, the authors could show that mutation of the lentil ortholog ELF3 also contributed to flowering time variation in lentil.

The results suggest that impaired ELF3 function is linked to flowering under short day conditions in legumes. The ELF3 locus as well as the other identified QTL can be used as new molecular markers for breeding. The data also impliy that other associated clock genes are involved in the regulation of flowering time in legumes and thus, might constitute new molecular targets for breeding. This study again highlights the conserved adaptation of flowering time by loss of gene function that control photoperiod responsiveness, which leads to a relaxation of mechanisms that under unfavorable conditions would delay flowering.

Weller JL, Liew LC, Hecht VF, Rajandran V et al. (2012) A conserved molecular basis for photoperiod adaptation in two temperate legumes. Proc Natl Acad Sci 109(51):21158-63.

Country Reports of the International Arabidopsis Community

Country Highlights

Argentina

- Five new research grants have been awarded by the Agencia Nacional de Promoción Científica y Technológica
- Arabidopsis scientists published 26 internationally recognized publications

Australia & New Zealand

- ICAR 2013 – 24th International Conference on Arabidopsis Research held in Sydney, Australia, June 24th -28th 2013
- Notable published highlight: Munns R et al. (2012) Wheat grain yield on saline soils is improved by an ancestral Na+ transporter gene. Nat Biotechnol

Austria

- Three new research consortia have been awarded for funding: Stress-induced nucleosome dynamics, Strigolactones and UV-B radiation
- New PhD school on RNA-Biology was started

Belgium

- Belgian national research project grant on the topic of root-shoot interactions in plants and additional projects on plant science have been awarded all of which Arabdiopsis research has major impact
- Seven publication on Arabidopsis with high impact have been published in 2012

Canada

- ICAR 2014 – 25th International Conference on Arabidopsis Research will be held in Vancouver, Canada, July 28th-August 1st 2014

China

- Three key project on Arabidopsis research with the topics stem cell and sexual reproduction were renewed
- Official inauguration of the "Shanghai Centre for Plant Stress Biology"

Czech Republic

- The two joint research centers "Centre of the Region Hana for Biotechnological and Agricultural Research" and "Central European Institute of Technology (CEITEC)" were successfully established and still recruit new researchers and open new labs
- Notable publication: Petrovská B et al. (2012) Plant Aurora kinases play a role in maintenance of primary meristems and control of endoreduplication. New Phytol

Finland

- Notable published highlights: Vatén A et al. (2012) Callose biosynthesis regulates symplastic trafficking during root development. Dev Cell. and Suorsa M et al. (2012) PROTON GRADIENT REGULATION5 is essential for proper acclimation of Arabidopsis photosystem I to naturally and artificially fluctuating light conditions. Plant Cell

Germany

- Arabidopsis Functional Genomics Network (AFGN) Final Report was published in 2012 and AFGN continues its work as section of the German Botanical Society (DBG)
- New collaborative research center awarded "Priming and memory of organismic responses to stress"

Hungary

- Notable publication: Terecskei K et al. (2012) The circadian clock-associated small GTPase LIGHT INSENSITIVE PERIOD1 suppresses light-controlled endoreplication and affects tolerance to salt stress in Arabidopsis. Plant Physiol
- T-DNA insertion mutagenesis program has been established in the Institute of Plant Biology, BRC

India

- Dr. R Sowdhamini's group at NCBS, Bangalore has created a unique plant stress regulatory genomics data platform called STIFDB2

Ireland

- Scientific Highlight: Liu F, Bakht S, Dean C (2012) Co-transcriptional role for Arabidopsis DICER-LIKE 4 in transcription termination. Science.

Italy

- A laser-microdissection service for Arabidopsis has been established at Fondazione Filarete, Milano

Japan

- New projects were started with the focus to transfer knowledge obtained by Arabidopsis research to useful crops
- Scientific Highlight: Oda Y, Fukuda H (2012) Initiation of cell wall pattern by a Rho- and microtubule-driven symmetry breaking. Science

Spain

- Scientific Highlight: Huang W et al. (2012) Mapping the core of the Arabidopsis circadian clock defines the network structure of the oscillator. Science

Sweden

- Swedish Metabolomics Centre in Umeå is a national resource, inaugurated March 2013
- A de novo assembly of the >20Gbp Norway spruce genome was recently produced.

United Kingdom

- UK Plant Sciences Federation (UKPSF) was established in late 2011 to provide 'one voice for UK Plant Science'
- The ERA-Net for Coordinating Action in the Plant Sciences (ERA-CAPS) launched its first joint call for proposal its total budget is around €20M
- Amongst the scientific highlights: Ling Q et al. (2012) Chloroplast Biogenesis Is Regulated by Direct Action of the Ubiquitin-Proteasome System. Science

United States

- NAASC will organize the 2014 ICAR, which is scheduled for the University of British Columbia in Vancouver (July 28 – August 1)
- Proposal for funding to develop the Arabidopsis Informatics Portal (AIP), which will replace TAIR, the current core informatics resource, submitted to the U.S. National Science Foundation (NSF)
- Simon Chan, a talented and promising early-career Arabidopsis researcher, passed away in August 2012

Argentina

http://www.arabidopsis.org/portals/masc/countries/Argentina.jsp
Contact: Jorge J. Casal (casal@ifeva.edu.ar)
IFEVA, Faculty of Agronomy, University of Buenos Aires

General Activities

New Grants from Agencia Nacional de Promoción Científica y Tecnológica (www.agencia.gov.ar):

- PICT-0148. Regulation of alternative splicing in plants. Alberto Kornblihtt. Universidad de Buenos Aires.
- PICT-0054. Molecular bases of polar cell expansion in root hairs in Arabidopsis. José Manuel Estevez. Consejo Nacional de Investigaciones Científicas y Técnicas. Buenos Aires.
- PICT-0967. Epigenetic control of abiotic stress responses in plants. Norberto Daniel INSEM. Universidad de Buenos Aires.
- PICT-2383. Role of Nitric Oxide in stress responses in photosynthetic organisms. Lorenzo Lamattina. Universidad Nacional de Mar del Plata.
- PICT-0041. Lights and shadows in the interactions between plants and microorganisms. Carlos Luis Ballaré. Universidad de Buenos Aires.

Selected Publications

Iñigo S et al. 2012) Proteasome-mediated turnover of arabidopsis MED25 is coupled to the activation of FLOWERING LOCUS T transcription. Plant Physiology 160, 1662-1673.

Chorostecki U et al. (2012) Identification of new microRNA-regulated genes by conserved targeting in plant species. Nucleic Acids Research 40, 8893-8904.

Giacomelli JI et al. (2012) Role of recently evolved miRNA regulation of sunflower HaWRKY6 in response to temperature damage. New Phytologist 195, 766-773.

Cerrudo I et al. (2012) Low red/far-red ratios reduce arabidopsis resistance to Botrytis cinerea and jasmonate responses via a COI1-JAZ10-dependent, salicylic acid-independent mechanism. Plant Physiology 158, 2042-2052.

Boccalandro HE et al. (2012) Phototropins but not cryptochromes mediate the blue light-specific promotion of stomatal conductance, while both enhance photosynthesis and transpiration under full sunlight. Plant Physiology 158, 1475-1484.

Campi M, et al. (2012) Participation of chromatin-remodeling proteins in the repair of ultraviolet-B-damaged DNA. Plant Physiology 158, 981-995.

Debernardi JM et al. (2012) Functional specialization of the plant miR396 regulatory network through distinct microRNA-target interactions. PLoS Genetics 8, art. no. e1002419.

Australia & New Zealand

www.Arabidopsis.org/info/2010_projects/Australia.jsp
Contact: Barry Pogson (Barry.Pogson@anu.edu.au)
Australian National University, Canberra

General Activities

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

Major areas of Arabidopsis research and functional genomics are Canberra, Melbourne, Adelaide and Perth. Major sites of plant science with foci on crops include Queensland, Tasmania, South Australia, ACT and NSW. Centres with a strong focus on Arabidopsis include the Australian Research Council (ARC) Centres of Excellence in Plant Energy Biology (www.plantenergy.uwa.edu.au/) and Plant Cell Walls (www.plantcellwalls.org.au) and CSIRO Plant Industry (www.pi.csiro.au), plus numerous researchers across all the Universities.

Increasing numbers of New Zealand plant scientists are incorporating Arabidopsis thaliana into their research, and several are using functional genomics approaches. In addition to the projects being conducted at the universities, research programs are carried out at the Government-owned Crown Research Institutes.

New Academic Appointments

Iain Searle, University of Adelaide; Matt Gilliham, University of Adelaide; Josh Mylne, University of Western Australia.

Notable Awards

Harvey Millar (Plant Energy Biology Deputy Director, UWA) was the first Australian to receive the American Society of Plant Biology Charles Shull Award and also received the 2012 Fenner Medal. John Evans (ANU) and David Day (Flinders U) were elected to the Australian Academy of Science and Graham Farquhar (ANU) as a Foreign member of the USA National Academy of Science. The 2012 Goldacre award was to Josh Mylne (UWA) and the 2013 Asutralian Academy of Science Fenner Medal to Ulrike Mathesius (ANU). The ASPS and FPB Best paper award was to Dr Arati Agarwal (Deakin University).

Research Highlights

Rana Munns, Matt Gilliham and colleagues (Nature Biotechnology 30: 360) demonstrated a 25 % increase in tolerance to saline soils in Durum wheat – a finding built upon translational research in Arabidopsis and wheat. ANU and ARC Plant Energy Biology Researchers led by Murray Badger are participants in a Bill and Melinda Gates Grant to improve photosynthetic performance in Crops.

doi: 10.1038/nbt.2120.

Munns R, James RA, Xu B, Athman A et al. (2012) Wheat grain yield on saline soils is improved by an ancestral Na^+ transporter gene. Nat Biotechnol 30(4):360-4.

Conferences and Meetings

- Arabidopsis 2013, Sydney, 24th – 28th June. The 24th International Conference on Arabidopsis Research will be held in Sydney, Australia. The Venue is ideally located at the Sydney Convention Centre on Sydney Harbour, 15 minutes from the airport. Chair: Barry Pogson (barry.pogson@anu.edu.au).
- COMBIO – Combined Biology Societies Annual Conference. See http://www.asps.org.au/ for details

Arabidopsis genomies tools and resources

- NCRIS Plant Phenomics (www.plantphenomics.org.au). The Canberra and Adelaide nodes were officially opened in 2009. This offers cutting-edge growth and automated non-invasive analytical facilities. Analyses include root and shoot growth, photosynthetic rates, infra-red and hyper-spectral imaging of Arabidopsis and crop plants in growth chambers, glasshouses and field sites. The Facility is available to national and international researchers at the marginal cost of running the facility. Several international collaborations have been established and more are encouraged. For more information please contact Bob Furbank (Robert.Furbank@csiro.au). More details can be found in the Phenomics Subcommittee section of this annual report.
- SUBA (a SUBcellular location database for Arabidopsis proteins). The SUBA database provides a powerful means to assess protein subcellular localisation in Arabidopsis (http://www.suba.bcs.uwa.edu.au).
- Anno-J: Interactive web-based genome browsing in Arabidopsis for large datasets in functional genomics Julian Tonti-Filippini and A. Harvey Millar (hmillar@cyllene.uwa.edu.au), ARC Centre of Excellence in Plant Energy Biology, M316. The University of Western Australia, Perth, WA, 6009, Australia.

Major Funding Agencies

- Australian Research Council (www.arv.gov.au)

Austria

http://arabidopsis.org/portals/masc/countries/Austria.jsp Contact: Marie-Theres Hauser (marie-theres.hauser@boku.ac.at) BOKU-University of Natural Resources & Life Science, Vienna; Wolfram Weckwerth (wolfram.weckwerth@univie.ac.at) University Vienna

General Activities

Projects are undertaken at six Austrian institutions (BOKU-University of Natural Resources & Applied Life Science Vienna, University of Vienna, GMI-Gregor Mendel Institute of Molecular Plant Biology, MFPL-Max F. Perutz Laboratories, University of Salzburg, IST-Institute of Science and Technology, Austria) on:

Chromosome biology: *Karel Riha* telomeres and genome stability (www.gmi.oeaw.ac.at/rkriha.htm); *Peter Schlögelhofer* meiotic recombination (http://www.mfpl.ac.at/mfpl-group/group/schloegelhofer.html)

Development, hormones and stress responses: *Lindy Abas* membrane proteins and hormone transport (www.dagz.boku.ac.at/11133.html); *Andreas Bachmair* Protein modifiers in plants and retrotransposon biology (www.mfpl.ac.at/mfpl-group/group/bachmair.html); *Eva Benkova* hormonal cross-talk and root architecture (http://ist.ac.at/de/forschung/forschungsgruppen/benkova-gruppe/); *Wolfgang Busch* regulatory networks of root development (www.gmi.oeaw.ac.at/research-groups/wolfgang-busch); *Jiri Friml* auxin transport, cell polarity and endocytic trafficking (http://ist.ac.at/de/forschung/forschungsgruppen/friml-gruppe/); *Thomas Greb* vascular tissue development (www.gmi.oeaw.ac.at/research-groups/thomas-greb); *Marie-Theres Hauser* development, stress (www.dagz.boku.ac.at/11135.html?&L=1); *Claudia Jonak* stress signaling and adaptation (www.gmi.oeaw.ac.at/research groups/claudia jonak); *Jürgen Kleine Vehn* phytohormonal crosstalk and differential growth regulation (www.dagz.boku.ac.at/dagz.html?&L=1); *Barbara Korbei* membrane protein transport in plants (www.dagz.boku.ac.at/19987.html?&L=1); *Christian Luschnig* auxin, chromatin (www.dagz.boku.ac.at/7968.html?&L=1); *Irute Meskiene* Cell signalling control by MAPK phosphatases (www.mfpl.ac.at/mfpl-group/group/meskiene.html); *Andrea Pitzschke* signaling events in stress response (www.dagz.boku.ac.at/17707.html?&L=1); *Markus Teige* Plant stress signalling by CDPKs and organellar signalling (www.mfpl.ac.at/research/group-teige.html)

Epigenetics: *Ortrun Mittelsten Scheid* epigenetic regulation in plants (www.gmi.oeaw.ac.at/oms.htm); *Hisashi Tamaru* chromatin during pollen development (www.gmi.oeaw.ac.at/htamaru.htm); *Michael Nodine* small RNA functions in small embryos (www.gmi.oeaw.ac.at/research-groups/michael-nodine)

Glycobiology: *Lukas Mach* glycosylation enzymes, proteinases, vacuolar proteins (www.dagz.boku.ac.at/7967.html); *Georg Seifert* arabinogalactan proteins, cell elongation biosynthesis of nucleotide sugars for cell wall polymers (www.dapp.boku.ac.at/ips.html?&L=1); *Richard Strasser*

N-glycosylation (www.dagz.boku.ac.at/12349.html?&L=1); *Raimund Tenhaken* biosynthesis of nucleotide sugars for cell wall polymers, programmed cell death (www.uni-salzburg.at/zbio/tenhaken)

Plant pathogen interactions: *Gerhard Adam* mycotoxins in plant-pathogen interactions (www.dagz.boku.ac.at/11137.html?&L=1); *Holger Bohlmann* Nematode induced syncytia (www.dnw.boku.ac.at/2238.html?&L=1); *Julia Hofmann* Molecular pathophysiology (www.dnw.boku.ac.at/2238.html?&L=1)

Population genetics: *Magnus Nordborg* genome-wide association studies, local adaptation (www.gmi.oeaw.ac.at/research-groups/magnus-nordborg)

Systems biology and ecology: *Wolfram Weckwerth* proteomics database resource for Arabidopsis http://promex.pph.univie.ac.at/promex/ and Arabidopsis metabolomics database and COVAIN, a metabolomics toolbox for metabolic modelling and multivariate statistics (www.univie.ac.at/mosys/wolfram_weckwerth.html)

RNA metabolism: *Andrea Barta* splicing and alternative splicing in plants, SR proteins in development and stress response, non-sense mediated RNA decay (www.mfpl.ac.at/index.php?cid=68)

Current research consortia

- "Chromosome dynamics - unravelling the functions of chromosomal domains" is a multiorganismal project (Arabidopsis represented by Peter Schlögelhofer) (www.mfpl.ac.at/research/research-networks/chromosome-dynamics.html?a=1)
- "Fusarium Metabolites and Detoxification Reactions" SFB 37 coordinated by Gerhard Adam from the BOKU-Univ. of Natural Resources & Life Sciences, Vienna (www.dagz.boku.ac.at/14676.html)
- "PASAS: Alternative splicing and abiotic stress in plants" ERA-NET Plant Genomics with J. Brown (UK), A. Barta (Austria), R. Fluhr (Israel), A. Jarmolowski (A. Mickiewicz, Poland)
- "RNA Regulation of the transcriptome" SFB 43, coordinated by Renee Schroeder, Max F Perutz Labs (www.mfpl.ac.at/rna-biology/network/)
- "MeioSys-Systematic analysis of factors controlling meiotic recombination in higher plants", a collaborative project funded by the EU (FP7) (www.meiosys.org/)
- "Ecological and evolutionary plant epigenetics" (EpiCOL): ESF EEFG project www.esf.org/activities/eurocores/running-programmes/euroeefg/collaborative-research-projects/epicol.html
- "Metabolic reprogramming by induction of transcription" (MERIT): an EU-funded Marie-Curie Initial Training Network (http://theory.bio.uu.nl/MERIT/html/index.html)
- "Stress-induced nucleosome dynamics in plants", bilateral project between FWF and ANR (France)
- "UV-B radiation: A specific regulator of plant growth and food quality in a changing climate (UV4growth)" (www.cost.eu/domains_actions/fa/Actions/FA0906)
- "Strigolactones: biological roles and applications" (www.cost.eu/domains_actions/fa/ Actions/FA1206)

Public Relations - Education

- Fascination of Plants Day 18.5.2013 www.plantday12.eu/
- "Dialog Gentechnik/Open Science" an independent non-profit society dedicated to provide scientific information on molecular biology and different aspects of biotechnological applications is organizing the Vienna Open Lab where hands on courses are offered to school classes and the general public. (www.viennaopenlab.at/en_index.php)
- Vienna Biocenter International PhD Programme: international competitive program offer up to 4 years Arabidopsis research projects. www.univie.ac.at/vbc/PhD/
- Max F. Perutz International PhD Program: www.projects.mfpl.ac.at/mfpl-phd-selection/
- PhD School "Chromosome Dynamics". Coordinated by Peter Schlögelhofer. http://gscd.gmi.oeaw.ac.at/
- PhD School "RNA Biology". Cooridated by Andrea Barta. www.mfpl.ac.at/rna-biology/doctoral-program/
- VBC Summer School is a ten week research and teaching programme for undergraduates from around the world (www.vbcsummerschool.at)

Meetings and Conferences

Viennese Plant Network meetings: biannual minisymposia of all plant Institutes of the Viennese area.

Selected Publications

Dal Santo S, Stampfl H, Krasensky J, Kempa S et al. (2012) Stress-induced GSK3 regulates the redox stress response by phosphorylating glucose-6-phosphate dehydrogenase in Arabidopsis. Plant Cell. 2012 Aug;24(8):3380-92.

Korte A, Vilhjálmsson BJ, Segura V, Platt A et al. (2012) A mixed-model approach for genome-wide association studies of correlated traits in structured populations. Nat Genet 44(9):1066-71.

Kurzbauer MT, Uanschou C, Chen D, Schlögelhofer P (2012) The recombinases DMC1 and RAD51 are functionally and spatially separated during meiosis in Arabidopsis. Plant Cell 24(5):2058-70.

Leitner J, Petrášek J, Tomanov K, Retzer K et al. (2012) Lysine63-linked ubiquitylation of PIN2 auxin carrier protein governs hormonally controlled adaptation of Arabidopsis root growth. Proc Natl Acad Sci U S A 109(21):8322-7.

Marquez Y, Brown JW, Simpson C, Barta A, Kalyna M. (2012) Transcriptome survey reveals increased complexity of the alternative splicing landscape in Arabidopsis. Genome Res. 22(6):1184-95.

Belgium

http://arabidopsis.org/portals/masc/countries/Belgium.jsp
Contact: Lieven De Veylder (lieven.deveylder@psb.vib-ugent.be)
Plant Systems Biology, VIB-Ghent University

General Activities

Belgian Arabidopsis projects are funded by university-, regional- or federal-level grants, but not within calls specifically targeting this model plant species or plants. In addition VIB, the Flanders Institute for Biotechnology, provides significant support to the Department of Plant Systems Biology (over 5 million Euros per year) in which about half the research activities are dedicated to Arabidopsis studies.

- A Belgian national research project (IAP), coordinated by D. Inzé, focuses on how root and shoot influence each other and how this interaction contributes to the development of the plant. This program also involves T. Beeckman, F. Van Breusegem G. Beemster, L. De Veylder, M. Boutry, X. Draye, N. F. Chaumont, and C. Périlleux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project. More info, see www.iuap-mars.be/
- The group of N. Verbruggen obtained an ARC (Action de Recherche Concertée) project on the study of nutrition and circadian rhythms (in collaboration with Jean-Christophe Leloup) and a FNRS (Fonds de la Recherche Scientifique) project focusing on metal hyperaccumulation (in collaboration with Marc Hanikenne and Moreno Galleni).
- Two FWO (Research Foundation – Flanders) research grants were appointed to T. Beeckman to study lateral root initiation, one focusing on formative divisions (in collaboration with D. Van Damme) and one dealing with chemical genomics (in collaboration with D. Audenaert).

Other current Arabidopsis research topics in Belgium include cell cycle regulation (D. Inzé, L. De Veylder, P. Dhonukshe), root and leaf growth and development (T. Beeckman, G. Beemster, M. Van Lijsebettens, K. Vissenberg), oxidative stress and cell death (F. Van Breusegem; P. Motte, H. Asard), genome annotation and evolution (Y. Van de Peer, P. Rouzé, K. Vandepoele), proteomics (G. De Jaegher), 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. Vandamme, 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).

Selected Publications

Andriankaja M, Dhondt S, De Bodt S, Vanhaeren H et al. (2012) Exit from Proliferation during Leaf Development in Arabidopsis thaliana: A Not-So-Gradual Process. Dev Cell 22, 64-78.

Bassard, JE, Richert L, Geerinck J, Renault H et al. (2012) Protein-Protein and Protein-Membrane Associations in the Lignin Pathway. Plant Cell 24, 4465-4482.

De Rybel B, Audenaert D, Xuan W, Overvoorde P et al. (2012) A role for the root cap in root branching revealed by the non-auxin probe naxillin. Nat Chem Biol. 8, 798-805.

Eloy NB, Gonzalez N, Leene JV, Maleux K et al. (2012) SAMBA, a plant-specific anaphase-promoting complex/cyclosome regulator is involved in early development and A-type cyclin stabilization. Proc Natl Acad Sci U S A 109, 13853 - 13858.

Gudesblat GE, Schneider-Pizoń J, Betti C, Mayerhofer J et al. (2012) SPEECHLESS integrates brassinosteroid and stomata signalling pathways. Nat Cell Biol. 14, 548-554.

Péret B, Swarup K, Ferguson A, Seth M et al. (2012) AUX/LAX genes encode a family of auxin influx transporters that perform distinct function during Arabidopsis development. Plant Cell 24, 2874 - 2885.

Whitford R, Fernandez A, Tejos R, Pérez AC et al. (2012) GOLVEN secretory peptides regulate auxin carrier turnover during plant gravitropic responses. Dev Cell. 22, 678-685.

Arabidopsis Genomics 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/).

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)

Canada

http://arabidopsis.org/portals/masc/countries/Canada.jsp
Contact: Dario Bonetta (dario.bonetta@uoit.ca)
Ontario Institute of Technology

General Activities

Approximately 55 groups conduct research with Arabidopsis in Canada. Updates from those groups that might be of interest to the Arabidopsis community include:

- Brian Ellis' (University of British Columbia) has released the results of a broad analysis of stem cross sections using immunoprofiling to query the cell wall composition in different cell types of maturing Arabidopsis stems (http://www.wallmabdb.net).
- Hall HC, Cheung J, Ellis BE (2013) Immunoprofiling reveals unique cell-specific patterns of wall epitopes in the expanding Arabidopsis stem. The Plant Journal (74): 134-147.
- Nicholas Provart's group (University of Toronto) reported on the development of the BAR expressolog which facilitates the prediction of orthologous genes in different plant species (http://bar.utoronto.ca/expressolog_treeviewer/cgi-bin/expressolog_treeviewer.cgi).
- Patel RV, Nahal HK, Breit R, Provart NJ. (2012) BAR expressolog identification:expression profile similarity ranking of homologous genes in plant species. Plant Journal (71):1038-1050.

Although no specific funding is targeted for Arabidopsis research, Genome Canada (http://www.genomecanada.ca) continues to be an important source of funding for large-scale projects across disciplines. The research funded by Genome Canada includes aspects of human health, agriculture, fisheries and aquaculture, forestry, the environment, and energy. The Canadian government has committed $165 million in new funding for genomics research in 2013.

The Natural Science and Engineering Research Council (NSERC) is one of three federal funding agencies in Canada that supports most of the basic research involving Arabidopsis. The total budget for basic research as a whole has continued to remain flat over the past six years with a drift towards research in areas of priorities set by the government or by NSERC. This has meant an increased trend of research awards from NSERC that are tied to partnerships with industry or specific programs which are driven by application rather than discovery. The current funding environment has therefore placed added pressures on conducting basic research in the plant sciences.

Meetings and Conferences

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

Selected Publications

Frank F, Hauver J, Sonenberg N, Nagar B (2012) Arabidopsis Argonaute MID domains use their nucleotide specificity loop to sort small RNAs. EMBO J 31(17):3588-95.

González-Lamothe R, El Oirdi M, Brisson N, Bouarab K (2012) The conjugated auxin indole-3-acetic acid-aspartic acid promotes plant disease development..Plant Cell 24(2):762-77.

Indriolo E, Tharmapalan P, Wright SI, Goring DR (2012) The ARC1 E3 ligase gene is frequently deleted in self-compatible Brassicaceae species and has a conserved role in Arabidopsis lyrata self-pollen rejection. Plant Cell 24(11):4607-20.

McCann HC, Nahal H, Thakur S, Guttman DS (2012) Identification of innate immunity elicitors using molecular signatures of natural selection. Proc Natl Acad Sci U S A 109(11):4215-20.

Ren M, Venglat P, Qiu S, Feng L et al. (2012) Target of rapamycin signaling regulates metabolism, growth, and life span in Arabidopsis. Plant Cell 24(12):4850-74.

Schattat MH, Griffiths S, Mathur N, Barton K et al. (2012) Differential coloring reveals that plastids do not form networks for exchanging macromolecules. Plant Cell 24(4):1465-77.

Wang L, Shen W, Kazachkov M, Chen G et al. (2012) Metabolic interactions between the Lands cycle and the Kennedy pathway of glycerolipid synthesis in Arabidopsis developing seeds. Plant Cell 24(11):4652-69.

Arabidopsis Genomics Tools and Resources

- The Canadian reverse genetic TILLING facility, CAN-TILL (http://www3.botany.ubc.ca/can-till/) is operated by George Haughn and Erin Gilchrist at the University of British Columbia.
- The Botany Array Resource (BAR) (http://bbc.botany.utoronto.ca) has added a tool (NGM) for positional cloning using a next-generation sequencing platform (http://bar.utoronto.ca/ngm) and the Expressolog Tree Viewer tool mentioned above. The BAR continues to be an essential source of web-based tools for bioinformatics.

Major Funding Sources

- NSERC (http://www.nserc.ca)
- Genome Canada and associated five regional Genome centres (http://www.genomecanada.ca)
- Agriculture Canada (http://www.agr.ca)

China

http://arabidopsis.org/portals/masc/countries/China.jsp
Contact: Weicai Yang (wcyang@genetics.ac.cn) Institute of Genetics And Developmental Biology (IGDB)

General Activities

The current foci of funding of Arabidopsis research by the National Science Foundation of China (NSFC) are on hormone signaling and development, sexual plant reproduction, stem cell, and plant-microbe interactions. The eight-year program on phytohormones funded by NSFC continues to support research projects in Arabidopsis. Three key projects, coordinated by Dr. Yu-Xin Hu of Beijing Institute of Botany, Dr. Meng-Xiang Sun of Wuhan University, and Dr. Xian-Sheng Zhang of Shandong Agricultural University, on stem cell and sexual plant reproduction were renewed successfully for another five years by the "Reproduction and Development Initiative" and "Stem Cell Initiative" under the National Long-term Basic Research Plan of the Ministry of Science and Technology of China (MOST). These funds will promote Arabidopsis research in China as a whole although no special project on functional genomics was initiated.

The Shanghai Centre for Plant Stress Biology (http://www.scpsb.ac.cn/index.asp), Chinese Academy of Sciences headed by Dr. Jian-Kang Zhu was officially inaugurated on April 28, 2012. The Center aims to host about 200 researchers and establish six departments, including plant stress biology, epigenetics, developmental and reproductive biology, plant signal transduction, and plant biotechnology. The Center is located in the Shanghai Chenshan Botanical Garden about 50 km west of the Shanghai city center in Songjiang district. This creates a lot of opportunities for young researchers who want to come to China.

Selected Publications

Feng F, Yang F, Rong W, Wu X et al. (2012) A Xanthomonas uridine 5'-monophosphate transferase inhibits plant immune kinases. Nature 485(7396):114-8.

Liu T, Liu Z, Song C, Hu Y et al. (2012) Chitin-induced dimerization activates a plant immune receptor. Science 336(6085):1160-4.

Qian W, Miki D, Zhang H, Liu Y et al. (2012) A histone acetyltransferase regulates active DNA demethylation in Arabidopsis. Science 336(6087):1445-8.

Wei W, Ba Z, Gao M, Wu Y et al. (2012) A role for small RNAs in DNA double-strand break repair. Cell 149(1):101-12.

Wu D, Hu Q, Yan Z, Chen W et al. (2012) Structural basis of ultraviolet-B perception by UVR8. Nature 484(7393):214-9.

Arabidopsis Genomics Tools and Resources

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

Major Funding Sources

The National Science Foundation of China: No. 83 Shuangqing Road, Haidian District, Beijing 1000085. Tel: (086) 010 62327087. http://www.nsfc.gov.cn/Portal0/default106.htm

The Ministry of Science and Technology of China, Department of Basic Research, No. 15 Fuxing Road, Beijing 100862. Tel: 86-10-58881515, http://www.most.gov.cn/eng/index.htm

Czech Republic

http://arabidopsis.org/portals/masc/countries/Czech_Republic.jsp
Contact: Viktor Zarsky (viktor@natur.cuni.cz ; zarsky@ueb.cas.cz) Charles University and Academy of Sciences of the Czech Republic, Prague

General Activities

In the Czech republic Arabidopsis research is focused mostly on the three major areas– cell biology, plant growth regulators biology and cytogenetics/genome biology. Along with the traditional centers of experimental plant research at the institutes of the Academy of Sciences of the Czech republic (esp. Institute of Experimental Botany, Institute of Biophysics and Institute of Plant Molecular Biology) and universities (Charles University in Prague, Masaryk University and Mendel University both in Brno and Palacky university in Olomouc) new joint research centers are established in Moravian cities Olomouc and Brno, both of them with plant biology as one of the crucial foci of research.

"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. Publication highlight for this year is the result of this research centre activity.(see further).

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

Both of these centers opened new labs and still recruit new researchers and group leaders also from abroad. In year 2012 Czech plant biologists published about 20 papers related to Arabidopsis – in many cases contributed as members of international author collectives.

Selected Publications

The report shows that RNAi silencing of Arabidopsis Aurora kinases, in addition to their function in regulating mitosis, are required also for maintaining meristematic activity and controlling the switch from meristematic cell proliferation to differentiation and endoreduplication. The colocalization and co-fractionation of AtAurora1 with AtTPX2, and γ-tubulin on microtubules in a cell cycle-specific manner suggests that AtAurora1 kinase may function to phosphorylate substrates that are critical to the spatiotemporal regulation of microtubule formation and organization.

Petrovská B, Cenklová V, Pochylová Z, Kourová H, Doskočilová A, Plíhal O, Binarová L, Binarová P. (2012) Plant Aurora kinases play a role in maintenance of primary meristems and control of endoreduplication. New Phytol. 193:590-604.

Arabidopsis Genomics Tools and Resources

In the Laboratory of Pollen Biology (Institute of Experimental Botany ASCR) on-line tool to access and analyze large sets of transcriptomic data is developed – "Arabidopsis Gene Family Profiler" (http://arabidopsisgfp.ueb.cas.cz/)

Major Funding Sources

The two major funding agencies for basic research are Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR). Both support regularly projects based on the use of Arabidopsis as a model plant and also bilateral projects with selected countries.

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

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

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

Finland

http://arabidopsis.org/portals/masc/countries/Finland.jsp
Contact: Ykä Helariutta (yrjo.helariutta@helsinki.fi)
University of Helsinki

General Activities

List of Community Members (PIs) in Finland

Eva-Mari Aro, Mikael Brosché, Paula Elomaa, Hiroaki Fujii, Adrien Gauthier, Ykä Helariutta, Kristiina Himanen, Niina Idänheimo, Jaakko Kangasjärvi, Saijaliisa Kangasjärvi, Markku Keinänen, Sirpa Kärenlampi, Ari-Pekka Mähönen, Paula Mulo, Kirk Overmyer, Tapio Palva, Eevi Rintamäki, Outi Savolainen, Teemu Teeri, Arja Tervahauta, Jari Valkonen, Michael Wrzaczek,

Functional Genomics Projects on Arabidopsis

- Kristiina Himanen is funded by the Academy of Finland for the project "Flower related Ubiquitin Proteasome System". 1.9.2011 - 31.8.2016. http://www.helsinki.fi/maatalousteet/tutkimus/ktt/index.html#research_groups
- Paula Mulo is funded by Academy of Finland for the project "Photosynthesis and alternative electron transfer" 1.8.2009-31.7.2014. http://www.sci.utu.fi/biokemia/en/research/plantphysiology/projects/mulo/index.html
- Mikael Brosche uses natural variation in Arabidopsis to study plant abiotic stress responses, with seeds from the stock center.
- Jaakko Kangasjärvi: Plant Receptor-like Kinases in ROS Signaling (PROSIG). 2009-2012. Funding ERA-PG/ Academy of Finland
- Sirpa Kärenlampi studies Heavy metal tolerance mechanisms with the specific aim to isolate and characterize putative genes and proteins conferring metal hyperaccumulation and tolerance traits. Interesting candidate genes are further examined for their function in yeast and Arabidopsis.http://www.uef.fi/biotieteiden-laitos/kasvibiotekniikka
- Eva-Mari Aro studies how plants regulatory the photosynthetic light reactions and keep them in balance with the needs and restrictions of the downstream metabolism.
- The Helariutta lab has recently developed a new method to spatially and temporally control symplastic trafficking based on identification of gain-of-function mutations in a CalS3 gene coding for a callose synthase isoform (Vaten et al. 2011 Developmental Cell 21:1144-55).

Functional genomics groups, collaborationg with groups in other countries

Jaakko Kangasjärvi is performing a comprehensive phenotypic and bioinformatic analysis of the CYSTEINE-RICH RECEPTOR-LIKE KINASE group in Arabidopsis together with several groups within the ERA-PG Jan Willem Borst (Netherlands, Wageningen University), Silke Robatzek (UK, Sainsbury Labs), David Collinge and Michael Lyngkjaer (Denmark, Copenhagen University), Stanislaw karpinski (Poland, Warsaw University of Life Sciences). Jaakko Kangasjärvi and Michael Wrzaczek as leaders of the consortium.

Conferences and Meetings

Meeting in Helsinki in 2012, April 17th: multinational, together with graduate school in plant biology on "Plant Stress Signalling: Perception and Pathways" - Mini-symposium. Oranizers: Jaakko Kangasjärvi and Michael Wrzaczek together with the FDPPS.

Selected Publications

Vatén A, Dettmer J, Wu S, Stierhof YD et al. (2012) Callose biosynthesis regulates symplastic trafficking during root development. Dev Cell 21(6):1144-55.

Suorsa M, Järvi S, Grieco M, Nurmi M et al. (2012) PROTON GRADIENT REGULATION5 is essential for proper acclimation of Arabidopsis photosystem I to naturally and artificially fluctuating light conditions. Plant Cell 24(7):2934-48.

Arabidopsis Genomics Tools and Resources

Jaakko Kangasjärvi has created a complete knockout collection for all CRKs in Arabidopsis. Comprehensive characterization of stress and developmental phenotypes has been done (publication in preparation).

Germany

http://arabidopsis.org/portals/masc/countries/Germany.jsp
Contact: Klaus Harter (klaus.harter@zmbp.uni-tuebingen.de) Center for Plant Molecular Biology (ZMBP), University of Tübingen

General Activities

The Arabidopsis Functional Genomics Network (AFGN)

The AFGN was founded in 2001 as a DFG-funded basic research program and the financial support by the DFG ended in October 2010 (http://www.uni-tuebingen.de/plantphys/AFGN/index.html). However, AFGN continues its coordinating function and work as a section under the umbrella of the German Botanical Society (DBG). The impressive progress of the AFGN members of the last funding period was recently published as a special issue in "Frontiers of Plant Physiology". The issue consists of an editorial and 20 reviews, mini-reviews and original papers (http://www.frontiersin.org/Plant_Physiology/researchtopics/Arabidopsis_2010_and_beyond_%E2%80%93_/344). In summary, the AFGN was an extraordinary success, not only with respect to science but also to the education of many diploma and PhD students and postdocs.

Selected Examples of Current Programmes

Priority Programmes:

- no. 1212: "Microbial reprogramming of plant cell development" (http://www.plant-micro.de/)
- no. 1529: "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)
- no. 1530: "Flowering time control: from natural variation to crop improvement" (http://www.flowercrop.uni-kiel.de/en)

Collaborative Research Centres:

- no. 648: "Molecular mechanisms of information processing in plants" (http://www.sfb648.uni-halle.de/)
- no. 973: "Priming and memory of organismic responses to stress" (http://www.sfb973.de/)

Research Training Groups:

- no. 1342: "Molecular and functional analysis of lipid-based signal transduction systems" (http://www.gk-1342.uni-wuerzburg.de/)
- no. 1525: "The dynamic response of plants to a changing environment" (http://www.igrad-plant.hhu.de/)

Research Units:

- no. 804: "Retrograde signalling in plants"
- no. 964: "Calcium signalling via protein phosphorylation in plant model cell types during environmental stress adaption" (http://www.uni-muenster.de/FOR964/)
- no. 1061: "Dynamic storage functions of plant vacuoles" (http://www.uni-kl.de/for1061/)

Cluster of Excellence:

- no. 1028: "Cluster of Excellence on Plant Sciences – from complex traits towards synthetic modules" (http://ceplas.eu/en/)

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

MASC Coordinator Funded by DFG

In 2012 a new grant has been awarded to Prof Klaus Harter and Prof Detlef Weigel for funding of an AFGN and MASC coordinator at the University of Tübingen. Dr Luise Brand has been appointed as AFGN and MASC coordinator from January 2013 - January 2016.

Conferences and Meetings

Together with colleagues from Austria and Switzerland, the AFGN members will continue to organize in a two-year rhythm the Tri-National Arabidopsis Meeting (TNAM). Cities like Cologne, Lutherstadt-Wittenberg, Neuchatel, Salzburg, Tübingen, Vienna and Zürich have officiated as excellent hosts for the meeting. In 2012, the 8th meeting was held in Lausanne and in 2014 the colleagues of the University of Heidelberg will host the 9th TNAM. The TNAM is predominantly funded by the German Research Foundation (DFG), is attended by around 200, prevailingly young scientists and is well-known for its convivial and very productive scientific atmosphere.

Selected Publications

Bulgarelli D, Rott M, Schlaeppi K, Ver Loren van Themaat E et al. (2012) Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. Nature 488(7409):91-5.

Manavella PA, Hagmann J, Ott F, Laubinger S et al. (2012) Fast-forward genetics identifies plant CPL phosphatases as regulators of miRNA processing factor HYL1. Cell 151(4):859-70.

Quint M, Drost HG, Gabel A, Ullrich KK et al. (2012) A transcriptomic hourglass in plant embryogenesis. Nature 490(7418):98-101.

Sprunck S, Rademacher S, Vogler F, Gheyselinck J et al. (2012) Egg cell-secreted EC1 triggers sperm cell activation during double fertilization.Science 338(6110):1093-7.

Major Funding Sources

Individual funding of Arabidopsis research is provided by the "Research Grant" to conduct at any time research projects with clearly defined topics and durations. Numerous, DFG-submitted plant "Research Grants" address scientific problems to be solved by using Arabidopsis as model organism. Furthermore, DFG-funded Arabidopsis functional genomics research is performed within the frame of the individual "Emmy Noether Programme" (support of young scientists), the Heisenberg "Programme" (support of researchers qualified for professorships) and the "Reinhart Koselleck Projects" (support of outstanding scientists with a proven scientific track).

The major funding source for Arabidopsis functional genomics is the DFG (http://www.dfg.de, Catherine Kistner: Catherine.Kistner@dfg.de).

Hungary

http://www.arabidopsis.org/portals/masc/countries/Hungary.jsp
Contact: László Szabados (szabados@brc.hu)
Biological Research Center Institute of Plant Biology, Szeged

General Activities

Arabidopsis research started in Hungary by György Rédei, an excellent geneticist, who pioneered Arabidopsis research. Rédei started Arabidopsis genetics in Hungary, but after emigrating to USA in 1957, he developed his scientific career in the University of Missouri in Columbia. Arabidopsis research was resumed in the beginning of 90s, when Csaba Koncz has established a research unit in the Biological Research Centre (BRC), in Szeged. Since that a number of scientists employed Arabidopsis as model plant in their research efforts.

Research with Arabidopsis is conducted in several research groups functioning in research institutes or universities. The most important center is the Biological Research Centre of Szeged (BRC), located in Southern Hungary. In the Institute of Plant Biology of the BRC (www.szbk.u-szeged.hu/plant_biology.php) Arabidopsis is used to study responses to different environmental signals such as light, osmotic and oxidative stress, salinity, regulation of cell division, differentiation and photosynthesis. Ferencz Nagy and his research team is interested in understanding regulation of light responses and circadian clock. Research topics include phytochrome-mediated light signalling, ultraviolet light-dependent signal transduction and control of circadian clock. Regulation of brassinosteroid biosythesis and signalling is one of their succesfull research program. Research unit of László Szabados investigates responses to salt and osmotic sresses trying to dissect osmotic, oxidative and ABA signals. Regulation of proline metabolism during stress is one of their research highlights. The group is involved in development of genetic tools to identify stress regulatory genes. Attila Fehér and his group is interested in Rho-type G proteins, which regulate cell polarity and differentiations. They are characterizing signalling pathways which connect receptor kinases (RLKs), G proteins and their downstream targets. Zoltán Magyar conducts research on regulation of cell proliferation, in particular cell cycle control by E2F transcription factors and the retinoblastoma (RB) tumour supressor protein.

The research group of Gábor Jakab in the University of Pécs is devoted to the characterization of pathogenesis-related lipase genes (PRLIPs), which are implicated in responses to different pathogens, including powdery mildew.

The Department of Plant Biology in the University of Szeged conducts is research on abiotic stress responses, photosynthesis and membrane transport. Research is focused on oxidative stress, signalling through reactive oxygen and nitrogen species (ROS, NO) and salicilic acid (SA) (Irma Tari, László Erdei, Ferenc Horváth).

Several groups use Arabidopsis as model in the Institute for Plant Biology in the Agricultural Biotechnology Centre, Gödöllő. The centre is known for pioneering research on virus-induced RNA silencing and suppression (József Burgyán), small RNA-mediated gene silencing in plant development (Zoltán Havelda, György Szittya) and regulation of Nonsense-mediated mRNA decay (NMD) in higher plants (Daniel Silhavy).

In the Agricultural Institute of the Centre for Agricultural Research responses to cold and other abiotic stresses is one of the main focus of plant research. Arabidopsis mutants are used in the group of Tibor Janda to study the regulatory roles of NO, salicilic acid and polyamines on responses to cold, in particular protection of photosynthesis during cold stress and adaptation.

Conferences and Meetings

There was no particular Arabidopsis-related workshop or congress in 2012. Results on Arabidopsis research were presented in several national or regional congresses including the followings:

- "Genetic Workshops in Hungary" Szeged, Hungary, date: 14/09/2012.
- "Oxidative stress tolerance in plants: from models to trees" Szeged, Hungary, date: 20/11/2012.

Selected Publications

Biro J, Farkas I, Domoki M, Otvos K et al. (2012) The histone phosphatase inhibitory property of plant nucleosome assembly protein-related proteins (NRPs). Plant Physiol Biochem 52: 162-168

Lehotai N, Kolbert Z, Peto A, Feigl G et al. (2012) Selenite-induced hormonal and signalling mechanisms during root growth of Arabidopsis thaliana L. J Exp Bot 63: 5677-5687

Majlath I, Szalai G, Papp I, Vankova R et al. (2012) Atnoa1 mutant Arabidopsis plants induce compensation mechanisms to reduce the negative effects of the mutation. J Plant Physiol 168: 1184-1190

Rigo G, Papdi C, Szabados L (2012) Transformation using controlled cDNA overexpression system. Methods Mol Biol 913: 277-290

Sokolova V, Bindics J, Kircher S, Adam E et al. (2012) Missense mutation in the amino terminus of phytochrome A disrupts the nuclear import of the photoreceptor. Plant Physiol 158: 107-118

Szalontai B, Stranczinger S, Palfalvi G, Mauch-Mani B et al. (2012) The taxon-specific paralogs of grapevine PRLIP genes are highly induced upon powdery mildew infection. J Plant Physiol 169: 1767-1775

Terecskei K, Toth R, Gyula P, Kevei E et al. (2012) The circadian clock-associated small GTPase LIGHT INSENSITIVE PERIOD1 suppresses light-controlled endoreplication and affects tolerance to salt stress in Arabidopsis. Plant Physiol 161: 278-290

Zsigmond L, Szepesi A, Tari I, Rigo G et al. (2012) Overexpression of the mitochondrial PPR40 gene improves salt tolerance in Arabidopsis. Plant Sci 182: 87-93

Arabidopsis genomics tools and resources

A T-DNA insertion mutagenesis program has been established in the Institute of Plant Biology, BRC. The program included random seuencing of t-DNA insertion sites and a gene trapping project using the promoterless firefly luciferase reporter gene. While this program was discontinued, T-DNA insertion lines are available for the research community (contact: L. Szabados, www.szbk.u-szeged.hu/personal_page.php?id=nb_szlá). More recently the Conditional cDNA Overexpressing System (COS) was established, comprising random cDNA library in the estradiol-inducible expression vector. The system was used with success to identify regulatory genes controlling stress responses or ABA signalling.

Major funding sources

In Hungary basic scientific research is mainly funded by the Hungarian Scientific Research Fund (OTKA, www.otka.hu), which supports plant science, including Arabidopsis research.

India

http://arabidopsis.org/portals/masc/countries/India.jsp
Contact: Jitendra P. Khurana (khuranaj@genomeindia.org)
Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi; R. Srinivasan (srinivasan53@gmail.com) National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi

General Activities

Dr. Sudip Chattopadhyay's group at NIT, Durgapur, has recently shown the functional interrelations of HY5 with ZBF1/MYC2 and ZBF2/GBF1 in light regulated Arabidopsis seedling development. The bZIP transcription factor, ZBF2, genetically and physically interacts with two other bZIP proteins, HY5 and HYH, to coordinately regulate Arabidopsis seedling development. Sudip's lab, in collaboration with Dr. Ashis Nandi's at JNU, has studied the role of light signalling in plant defense too. Dr. Ashverya Laxmi, at National Institute of Plant Genome Research, has provided significant evidence of interactions between glucose and phytohormone response pathways in controlling various plant growth and development features, especially root and hypocotyl directional growth. Among the studies focussed on photosynthesis related aspects, the effect of cold temperature and anaerobiosis on photosynthesis in Arabidopsis has been studied by Dr R Subramanyam from University of Hyderabad. Towards studies on abiotic and biotic stresses, Dr Anil Kumar's group has established the role of MAP kinase signalling pathway in the pathogenesis of Alternaria blight. In Arabidopsis, genome-wide analysis of certain gene families (plant-type II Ca2+ ATPases and in lectin receptor-like kinases) has been conducted for their relevance to abiotic and biotic stresses.

Selected Publications

Prasad BR, Kumar SV, Nandi A, Chattopadhyay S (2012) Functional interconnections of HY1 with MYC2 and HY5 in Arabidopsis seedling development. BMC Plant Biol 12:37.

Prasad VB, Gupta N, Nandi A, Chattopadhyay S (2012) HY1 genetically interacts with GBF1 and regulates the activity of the Z-box containing promoters in light signaling pathways in Arabidopsis thaliana. Mech Dev 129, 298-307.

Singh A, Ram H, Abbas N, Chattopadhyay S (2012) Molecular interactions of GBF1 with HY5 and HYH proteins during light-mediated seedling development in Arabidopsis thaliana. J Biol Chem 287, 25995-6009.

Gupta A, Singh M, Jones AM, Laxmi A (2012) Hypocotyl directional growth in Arabidopsis: a complex trait. Plant Physiol 159(4),1463-76.

Nellaepalli S, Kodru S, Subramanyam R (2012) Effect of cold temperature on regulation of state transitions in Arabidopsis thaliana. J Photochem Photobiol B 112, 23-30.

Nellaepalli S, Kodru S, Tirupathi M, Subramanyam R (2012) Anaerobiosis induced state transition: a non photochemical reduction of PQ pool mediated by NDH in Arabidopsis thaliana. PLoS One 7(11):e49839.

Kannan P, Pandey D, Gupta AK, Punetha H et al. (2012) Expression analysis of MAP2K9 and MAPK6 during pathogenesis of Alternaria blight in Arabidopsis thaliana ecotype Columbia. Mol Biol Rep. 39, 4439-44.

Vaid, N Pandey, PK Tuteja, N (2012) Genome-wide analysis of lectin receptor-like kinase family from Arabidopsis and rice. Plant Mol. Biol. 80, 365-388.

Arabidopsis Genomics Tools and Resources

Dr. R Sowdhamini's group at NCBS, Bangalore has created a unique plant stress regulatory genomics data platform called STIFDB2. STIFDB2 is an updated version of plant stress-responsive transcription factor database for Arabidopsis and rice, which can be used as an effective tool in the stress related functional genomics studies in plants.

Naika, M Shameer, K Mathew, OK Gowda, R Sowdhamini, R (2013) An updated version of plant stress-responsive transcription factor database with additional stress signals, stress-responsive transcription factor binding sites and stress-responsive genes in Arabidopsis and rice. Plant Cell Physiol. 54(2): e8 (1–15) DOI:10.1093/pcp/pcs185.

Major Funding Sources

The work on Arabidopsis in India is supported largely by the Department of Biotechnology (DBT), Council of Scientific and Industrial Research (CSIR), Department of Science and Technology (DST) and Indian Council of Agricultural Research (ICAR).

Ireland

http://www.arabidopsis.org/portals/masc/countries/Ireland.jsp

Contact: Prof. Charles Spillane (charles.spillane@nuigalway.ie) Plant & AgriBiosciences Research Centre (PABC), National University of Ireland Galway, Ireland

General Activities

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

Irish Arabidopsis research groups

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

- Prof Charles Spillane, Genetics and Biotechnology Lab, National University of Ireland Galway (NUIG), Ireland.
- Dr. Ronan Sulpice, Plant Systems Biology Lab, National University of Ireland Galway (NUIG), Ireland.
- Dr. Zoe Popper, Plant Cell Wall Lab, National University of Ireland Galway (NUIG), Ireland.
- Prof Tony Kavanagh, Plant Molecular Genetics, Smurfit Institute of Genetics, Trinity College Dublin, Ireland.
- Dr. Frank Wellmer, Plant Developmental Genetics, Smurfit Institute of Genetics, Trinity College Dublin.
- Dr. Paul McCabe, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Carl Ng, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Fiona Doohan, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
- Dr. Marcel Jansen, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.
- Dr. Ewen Mullins, Teagasc Crops Research Centre, Plant Biotechnology Unit, Oak Park, Carlow, Ireland.
- Dr. Fuquan Liu, School of Biological Sciences, Queens University Belfast, Northern Ireland.

Major Funding Sources

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

Selected Publications

Ali SS, Khan M, Fagan B, Mullins E, Doohan FM (2012) Exploiting the inter-strain divergence of Fusarium oxysporum for microbial bioprocessing of lignocellulose to bioethanol. AMB Express 2(1):16.

Baerenfaller K, Massonnet C, Walsh S, Baginsky S et al. (2012) Systems-based analysis of Arabidopsis leaf growth reveals adaptation to water deficit. Mol Syst Biol 8:606.

Chambers JP, Behpouri A, Bird A, Ng CK (2012) Evaluation of the use of the polyubiquitin genes, Ubi4 and Ubi10 as reference genes for expression studies in Brachypodium distachyon. PLoS One 7(11):e49372.

Fangel JU, Ulvskov P, Knox JP, Mikkelsen MD et al. (2012) Cell wall evolution and diversity. Front Plant Sci 3:152.

Islam MN, Jacquemot MP, Coursol S, Ng CK (2012) Sphingosine in plants--more riddles from the Sphinx? New Phytol, 193(1):51-7.

Jansen MA, Bornman JF. (2012) UV-B radiation: from generic stressor to specific regulator. Physiol Plant 145(4):501-4.

Jansen MA, Coffey AM, Prinsen E. (2012) UV-B induced morphogenesis: four players or a quartet? Plant Signal Behav 7(9):1185-7.

Kleessen S, Antonio C, Sulpice R, Laitinen Ret a. (2012) Structured patterns in geographic variability of metabolic phenotypes in Arabidopsis thaliana. Nat Commun 3:1319.

Kohler C, Wolff P and Spillane C (2012) Epigenetic mechanisms underlying genomic imprinting in plants. Ann Rev Plant Biol.

Liu F, Bakht S, Dean C (2012) Cotranscriptional role for Arabidopsis DICER-LIKE 4 in transcription termination. Science 335(6076):1621-3.

Newell CA, Natesan SK, Sullivan JA, Jouhet J et al. (2012) Exclusion of plastid nucleoids and ribosomes from stromules in tobacco and Arabidopsis. Plant J 69(3):399-410.

Ng CK, Coursol S. (2012) New insights into phospholipase d and sphingosine kinase activation in Arabidopsis. Front Physiol 3:67.

O'Connell MJ, Doyle AM, Juenger TE, Donoghue MTA et al. (2012) In Arabidopsis thaliana codon volatility scores reflect GC3 composition rather than selective pressure. BMC Research Reports.

Petti C, Reiber K, Ali SS, Berney M, Doohan FM. (2012) Auxin as a player in the biocontrol of Fusarium head blight disease of barley and its potential as a disease control agent. BMC Plant Biol 12:224.

Pyl ET, Piques M, Ivakov A, Schulze W et al. (2012) Metabolism and growth in Arabidopsis depend on the daytime temperature but are temperature-compensated against cool nights. Plant Cell 24(6):2443-69.

Riedelsheimer C, Czedik-Eysenberg A, Grieder C, Lisec J et al. (2012) Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nat Genet 44(2):217-20.

Riedelsheimer C, Lisec J, Czedik-Eysenberg A, Sulpice R et al. (2012) Genome-wide association mapping of leaf metabolic profiles for dissecting complex traits in maize. PNAS 109(23):8872-7.

Shinde S, Nurul Islam M, Ng CK. (2012) Dehydration stress-induced oscillations in LEA protein transcripts involves abscisic acid in the moss, Physcomitrella patens. New Phytol 195(2):321-8.

Shinde S, Shinde R, Downey F, Ng CK. (2012) Abiotic stress-induced oscillations in steady-state transcript levels of Group 3 LEA protein genes in the moss, Physcomitrella patens. Plant Signal Behav 6;8(1).

Wuest SE, O'Maoileidigh DS, Rae L et al. (2012) Molecular basis for the specification of floral organs by APETALA3 and PISTILLATA. PNAS 109(33):13452-7.

Italy

http://arabidopsis.org/portals/masc/countries/Italy.jsp
Contact: Giovanna Serino (giovanna.serino@uniroma1.it) Dept of Biology and Biotechnology, Sapienza Università di Roma

General Activities

Research on Arabidopsis in Italy is mainly carried out by laboratories from public Universities or from the National Research Center (CNR). Arabidopsis research in Italy focuses on the study of specific developmental processes: reproductive development (M.Cardarelli/P.Costantino on the male gametophyte; M.Kater/L.Colombo on the female gametophyte); root development (S.Sabatini/P.Costantino); seed germination (P.Vittorioso/P.Costantino); shoot control of root development (I.Ruberti). Other groups focused on Arabidopsis morphogenesis and differentiation (MM. Altamura), or cellular physiology (A.Carpaneto, E.Pedrazzini and MC.Bonza/MI.De Michelis/C.Olivari), or on different molecular mechanisms underlying specific processes (C.Tonelli on transcription factor families; G.Serino/P.Costantino on protein degradation). Collaborative joint research projects among members of these groups, as well as with international laboratories, have been funded in the past and present years, suggesting that a tight collaboration between different groups will be ensured also for the following years. Two collaborations in the field of plant epigenomis are already under development, and include the groups of C.Tonelli, I.Ruberti and S.Sabatini/P.Costantino, and the groups of F.Cervone/G.deLorenzo.

- Several groups were funded in 2012 by National Interest Research Grants (PRIN) from the Ministry of Education, University and Research National: A. Carpaneto, F. Cervone/G. deLorenzo; P. Costantino.
- Three groups were funded by EU grants: two by ERC grants: F. Cervone/G. deLorenzo (ERC advanced grant) and S.Sabatin (ERC consolidator grant), M. Kater/L. Colombo
- Institut Pasteur-Cenci Bolognetti foundation awarded grants to S.Sabatini; P.Vittorioso and to F. Cervone/G. deLorenzo, and the Cariplo Foundation to M. Kater/L. Colombo
- COST ACTION FA0903 Harnessing Plant Reproduction for Crop Improvement awarded to M. Cardarelli/P. Costantino and MM. Altamura
- Italian Ministry of Foreign Affairs for collaborative continues funding between Q. Xie (CAS, China) and L.J. Qu (Peking University), and the groups of G. Serino/P. Costantino and G.Frugis.
- C.Tonelli is member of a laboratory network funded by the SERRES-Selection of new grape rootstocks resistant to abiotic stresses through the development and validation of physiological and molecular markers by the Italian Consortium AGER (www.progettoager.it).

Conferences and Meetings

- P. Costantino, I. Ruberti and C. Tonelli were the organizers of the EMBO Conference "Plant Development and Environmental Interactions" held in Matera, Italy, May 27-30, 2012.
- C. Tonelli was the organizer of the 8th conference on the Future of Science, held in Venice on September 16-18, 2012.
- F. Cervone was the organizer of the 12th FISV Congress 24-27 September 2012 held in Rome, Italy.

Selected Publications

Bencivenga S et al. (2012) The transcription factors BEL1 and SPL are required for cytokinin and auxin signaling during ovule development in Arabidopsis. Plant Cell. 24:2886-97.

Dello Ioio R et al. (2012) A PHABULOSA/Cytokinin Feedback Loop Controls Root Growth in Arabidopsis. Curr Biol 25: 1699-704.

Petroni K et al. (2012) The promiscuous life of the expanded NF-Y subunits in plants. Plant Cell 24: 4777-92.

Rocchetti A et al. (2012) The putative K(+) channel subunit AtKCO3 forms stable dimers in Arabidopsis. Frontiers in Plant Science 3, 251:1-13

Sassi M et al. (2012) COP1 mediates the coordination of root and shoot growth by light through modulation of PIN1- and PIN2-dependent auxin transport in Arabidopsis. Development 139: 3402-3412.

Simonini S et al. (2012) Basic pentacysteine proteins mediate MADS domain complex binding to the DNA for tissue-specific expression of target genes in Arabidopsis. Plant Cell. 24:4163-72.

Arabidopsis Genomics Tools and Resources

- C. Tonelli and M. Galbiati have established, in addition to the RNAseq service (Illumina-based), a laser-microdissection service for Arabidopsis at Fondazione Filarete, Milano.
- A collection of multiple combinations of mutants in HD-Zip II and HD-Zip III genes has been generated by the group of Ida Ruberti and is available upon request.

Major Funding Sources

Major funding sources for Arabidopsis Research are the Italian Government, the European Union, as well as private Foundations.

Japan

http://arabidopsis.org/portals/masc/countries/Japan.jsp
Contact: Minami Matsui (minami@riken.jp)
RIKEN Plant Science Center

General Activities

In 2012 Plant Science in Japan additional new projects were started. BRAIN, DREB by MAFF, SATREPS by JST-JICA. All of them are to transfer the knowledge obtained by Arabidopsis research to useful crops. SATREPS is an international project. RIKEN terminated Plant Science Center (PSC) in 2013 March, and started a new center named RIKEN Center for Sustainable Resource Science (CSRS) by the coordination of plant science, chemical biology and chemistry for the contribution to Green Innovation and sustainable society. Biomass Engineering Program of RIKEN was integrated in RIKEN CSRS from April 2013. (http://www.csrs.riken.jp/en/, http://www.csrs.riken.jp/en/labs/index.html)

RIKEN BASE (Tetsuro Toyoda) (http://www.base.riken.jp/)

- Japan's national integrated database project covering Arabidopsis omics information resources (https://database.riken.jp/sw/links/en/crib158s39i/)
- PosMed (Positional Medline) for Arabidopsis genes is an intelligent search engine integrating genome information and literature (http://omicspace.riken.jp/PosMed/)
- GenoCon: International Genome Design Contest (http://genocon.org) (Tetsuro Toyoda, Minami Matsui).

RIKEN BRC

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

RIKEN PSC/CSRS(http://www.psc.riken.jp/english/index.html, www.csrs.riken.jp/en/)

- Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi). PSC established the Arabidopsis metabolomics platform (http://prime.psc.riken.jp/), which consists of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics. The publicly-available platform resources include Arabidopsis metabolome expression database AtMetExpress (http://prime.psc.riken.jp/lcms/AtMetExpress/); Arabidopsis MS/MS spectral tag (MS2T) viewer (http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html); standard spectrum search (http://prime.psc.riken.jp/?action=standard_index), ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (http://spectra.psc.riken.jp/); Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index); Drop Met (http://prime.psc.riken.jp/?action=drop_index); Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search). PRIMeLink (http://spectra.psc.riken.jp/menta.cgi/primelink/index) integrates the 3 above databases (AtMetExpress, MS2T and ReSpect) to provide a bi-directional searchable function from the gene or metabolite perspective.
- Hormonome platform and RIKEN Plant Hormone Research Network; (http://hormones.psc.riken.jp/) (Hitoshi Sakakibara and Yuji Kamiya)
- Phenome platform (http://amber/gsc.riken.jp/act/top.php) RIKEN Activation tagging lines Database and Full-length-cDNA-overexpressing (FOX) Arabidopsis lines (contact to Minami Matsui), Rice FOX Arabidopsis line Database (http://amber.gsc.riken.jp/ricefox/index.php) (Minami Matsui), Ds-transposon tagged lines (http://rarge.psc.riken.jp/phenome/) (http://rapid.psc.database.riken.jp) (Takashi Kuromori, Tetsuya Sakurai, Tetsuro Toyoda, Kazuo Shinozaki).
- Proteome platform (https://database.riken.jp/sw/links/en/ria1021i). PSC (Hirofumi Nakagami, Ken Shirasu) and Keiko University (Yasushi Ishihama, Naoyuki Sugiyama) developed a high-through-put shotgun phosphoproteomics tool for plants and phosphorylation site databases (http://phosphoproteome.psc.database.riken.jp, http://pepbase.iab.keio.ac.jp)
- The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/) for knockout Arabidopsis mutant lines for nuclear genes encoding chloroplast proteins (Fumiyoshi Myouga, Kazuo Shinozaki).
- Analysis of small Open Reading Frame (Kousuke Hanada, Minami Matsui, Motoaki Seki) Identification of ~8,000 sORFs with high coding potential in intergenic regions of the Arabidopsis genome. Design of an array and generation of an expression atlas for 7,901 identified coding sORFs.
- Mass Bank (Masanori Arita, Takaaki Nishioka, Kazuki Saito) The public repository of mass spectral data for sharing them among scientific research community. MassBank data are useful for the chemical identification and structure elucidation of chemical compounds detected by mass spectrometry. (http://www.massbank.jp/en/about.html)

- Genome-wide biochemical analysis using wheat cell-free-based protein array technology. The method that Ehime University (Keiichirou Nemoto and Tatsuya Sawasaki) and RIKEN PSC (Motoaki Seki and Kazuo Shinozaki) developed is useful for identification of substrates and interacting proteins for protein kinases, protein phosphatases and transcription factors.
- Transcriptome platform by using tiling array in collaboration with RIKEN BASE (http://omicspace.riken.jp/gps/) (Motoaki Seki, Tetsuro Toyoda, Kazuo Shinozaki)

KAZUSA DNA Reseach Institute

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

New and Ongoing Projects

- MEXT, Environmental sensing of plants: Signal perception, processing and cellular responses (2010-2015), Headed by Akira Nagatani, Kyoto University
- MEXT, Integrated Analysis of Strategies for Plant Survival and Growth in Response to Global Environmental Changes (2010-2015), Headed by Jian Feng Ma, Okayama University, Institute of Plant Science and Resources
- Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project on "Metabolomics for Low Carbon Society". Research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and Kazuki Saito (RIKEN PSC). Research led by Oliver Fiehn (Univ. of California at Davis) and Masanori Arita (Univ. of Tokyo)
- ERATO Higashiyama Live-Holonics Project (2010-2015) Headed by Tetsuya Higashiyama, Nagoya University. This project aims to study intercellular signaling in multicellular organisms with complete control of cells and molecules under the microscope, by developing new technologies for live-cell analysis.
- BMEP (Biomass Engineering Program) (www.riken.jp/bmep/english/index.html). RIKEN started BMEP in 2010. This program is focusing on the establishment and innovation for plant biomass production and renewable chemical materials and Bioplastics. Brachypodia as a model of grass biomass is used besides Arabidopsis in this program. This interdisciplinary program is organized by cooperation of chemists and plant biologists.
- Japan Advanced Plant Science Research Network has been started in 2011. In this program nine centers of excellence take roles to support plant researches for green innovation. Touhoku Univ.; Tracer analysis system using stable radioactive compounds. Univ. of Tsukuba; Transformation platform. Univ. of Tokyo; Ionome analysis, Metabolite analysis, Cell sorting and Photosynthesis measurement. RIKEN; Metabolome, Hormonone, Epigenome and Transcriptome analyses, Nagoya Univ.; Cell imaging, National Institute of Basic Biology; Next generation sequencing, Image analysis, NAIST; Cell signaling and Proteome analysis, Kyoto Univ.; Light and CO2 controlled growth room, Okayama Univ.; Multi-Stress evaluation system.
- BRAIN project. Discovery of key factors involved in osmosensing and their application to improvement of water-use-efficiency of crops (Kazuo Shinozaki, RIKEN)
- DREB project supported by MAFF. Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat in collaboration with IRRI, CIAT and CIMMYT (Kazuko Yamaguchi-Shinozaki JIRCAS and Kazuo Shinozaki RIKEN).
- NC-CARP (as a program in GRENE ;Green Network of Excellence). A new program "Network of Centers of Carbon Dioxide Resource Studies in Plants: NC-CARP (organizer: Professor Hiroo Fukuda)" started from 2011 as a 5-year project. This program aims at innovation of plant biomass technology by collaboration among Plant Science, Agriculture, Engineering and Chemistry, and at education of this new area. The centers include the University of Tokyo and Kobe University in addition to the nine centers belonging to the Japan Advanced Plant Science Research Network.
- JST-NSF (http://nsf.gov/funding/pgm_summ.jsp?pims_id=503558). A new 3-years project, "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society", started from 2011 by the support of the Strategic Japanese-US Joint Research Program (JST in Japan and NSF in US). Two teams devote to Arabidopsis-related projects: one led by Kazuki Saito of RIKEN, Japan, and Lloyd Sumner of Noble Foundation, US, and the other one led by Masanori Arita, Univ. of Tokyo, and Oliver Fiehn, Univ. of California at Davis.
- East Asia Science and Innovation Area Joint Research Program (e-ASIA), JST-NSTDA (Thailand)-MOST (Vietnam) on "Biomass and Plant Science". Research led by Motoaki Seki (RIKEN PSC), Ham Huy Le (Institute of Agricultural Genetics) and Jarunya Narangajavana (Mahidol University).

- SATREPS project supported by JST-JICA. Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant soybean in collaboration with Embrapa Brazil (Kazuko Yamaguchi-Shinozaki JIRCAS).

Selected Publications

Oda Y, Fukuda H (2012) Initiation of cell wall pattern by a Rho- and microtubule-driven symmetry breaking. Science 337(6100):1333-6.

Takeuchi H, Higashiyama T (2012) A species-specific cluster of defensin-like genes encodes diffusible pollen tube attractants in Arabidopsis. PLoS Biol 10(12):e1001449.

Kasahara RD, Maruyama D, Hamamura Y, Sakakibara T et al. (2012) Fertilization recovery after defective sperm cell release in Arabidopsis.Curr Biol 22(12):1084-9.

Arabidopsis Genomics Tools and Resources

RIKEN-BASE

- OMICSPACE (http://omicspace.riken.jp/gps)

RIKEN-BRC

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

RIKEN-PSC

- RPIMe (http://prime.psc.riken.jp/)
- AtMetExpress (http://prime.psc.riken.jp/lcms/AtMetExpress/)
- Arabidopsis MS/MS spectral tag (MS2T) viewer (http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html)
- Standard Spectrum Search (http://prime.psc.riken.jp/?action=standard_index)
- ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (http://spectra.psc.riken.jp/)
- Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index)
- Drop Met (http://prime.psc.riken.jp/?action=drop_index)
- Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search)
- PRIMeLink (http://spectra.psc.riken.jp/menta.cgi/primelink/index)
- RIKEN Plant Hormone Research Network (http://hormones.psc.riken.jp/)
- The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/)
- RIKEN Arabidopsis Activation Tagging Line Database (http://amber.gsc.riken.jp/act/top.php)
- RIKEN Arabidopsis Genome Encyclopedia (RARGE) (http://rarge.psc.riken.jp/)
- Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID) (http://rarge.gsc.riken.jp/phenome/)
- RIKEN Plant Phosphoproteome Database (RIPP-DB) (http://phosphoproteome.psc.database.riken.jp)

KAZUSA

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

Major Funding Sources

- RIKEN is supported by MEXT. Kazusa projects is supported by Chiba-Prefecture.
- Grants-in-Aid for Science from MEXT, (www.jsps.go.jp/english/egrants/grants.html)
- CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
- Program of Promotion of Basic Research Activities for Innovative Biosciences (www.brain.go.jp/welcome-e.html)
- ALCA (Advanced Low Carbon Technology Research and Development Program)(http://www.jst.go.jp/alca/en/index.html)
- A research and development-driven funding was started from 2011 for realization of low atmospheric carbon dioxide and wealthy society. For this purpose this funding supports game-change technologies leading to green-innovations.

Spain

http://arabidopsis.org/portals/masc/countries/Spain.jsp
Contact: Javier Paz-Ares (jpazares@cnb.csic.es)
Centro Nacional de Biotecnología, Madrid

General Activities

The most important Program on Arabidopsis functional genomics is TRANSPLANTA aiming to determine the function of Arabidopsis transcription factors. This Project involves 29 groups distributed all over Spain. Coordinator: Javier Paz-Ares; Budget 6 million Euros, start date: January 2008 end May 2013. Funding: Ministry of Science and Technology (Now Ministry of Economy and competitivity). Additionally three ERC starting grants have been awarded to Spanish scientist to work on circadian clock (Paloma Mas), sumoylation (Maria Luisa Lois) and translational control (Mar Castellano) in Arabidopsis. Finally, about 50 grants from the ministry Science and Competitivity fund Arabidopsis functional genomics projects at individual laboratories in Spain.

Conferences and Meetings

The TRANSPLANTA Project has hold a final meeting last Febraury in Alicante. The main message is that despite new technological developments make it now feasible implementing functional genomics approaches in virtually any plant species, the demonstrated power of Arabidopsis to generate reference knowledge an approaches justifies continued funding of research in this species

Selected Publications

Martínez-Macías MI, Qian W, Miki D, Pontes O et al. (2012) A DNA 3' phosphatase functions in active DNA demethylation in Arabidopsis. Mol Cell 45:357-70.

Lanza M, Garcia-Ponce B, Castrillo G, Catarecha P et al. (2012) Role of actin cytoskeleton in brassinosteroid signaling and in its integration with the auxin response in plants. Dev.Cell. 22:1275-85.

Huang W, Pérez-García P, Pokhilko A, Millar AJ et al. (2012) Mapping the core of the Arabidopsis circadian clock defines the network structure of the oscillator. Science. 336:75-9.

Arabidopsis Genomics Tools and Resources

As a result of the TRANSPLANTA project 400 transgenic lines conditionally overexpressing (estradiol inducible) different transcription factors have been deposited in the NASC stock center.

Sweden

http://arabidopsis.org/portals/masc/countries/Sweden.jsp
Contact: Maria E. Eriksson (maria.eriksson@plantphys.umu.se)
Umeå Plant Science Centre, Umeå University

General Activities

Swedish plant research typically uses Arabidopsis as a major model plant for functional genomics. This fast cycling model species often constitutes a first choice tool to address basic questions of growth and development, stress or other topics of specific relevance to crops in Agriculture and Forestry. The Arabidopsis community consists of several hundred researchers and is spread between more than ten universities in Sweden. It is engaged in vast areas of research from cell biology to ecological research. Traditionally there has been a strong focus on aspects of developmental biology, abiotic and biotic stress, plant growth regulators and photosynthesis. The research community is highly international, with a large part of researchers being recruited from abroad and extensive collaborations with peers in other countries. Due to the strong impact of the forestry industry in Sweden, forest tree model species are of great interest. Such model species are hybrid aspen (*Populus tremula x P. tremuloides*) and Norway spruce (*Picea abies*). There is also large interest among researchers of the community in using crops such as grains, canola and potato as additional plant model species to address specific topics.

Information, although not a complete list, on a few Departments across universities deploying Arabidopsis:

- Lund University, http://www4.lu.se/molecular-plant-biology and a plant research resource in Southern Sweden is Plant Link, http://www.plantlink.se/
- Gothenburg University, Department of Plant and Environmental Sciences, Plant Cell and Molecular Biology http://www.bioenv.gu.se/english/research/research-areas/Plant_molecular_biology/
- Uppsala University; http://www.ebc.uu.se/
- The Swedish University for Agricultural Sciences (SUAS) in Uppsala, http://www.slu.se/en/faculties/nl/about-the-faculty/departments/department-of-plant-biology-and-and-forest-genetics/research/
- The Linnean Centre; http://lcpu.se/, coordinates plant research in Uppsala.
- Umeå Plant Science Centre (UPSC; comprising Departments at Umeå University and SUAS in Umeå); http://www.upsc.se/Research/List/research-groups-at-upsc.html

Scientific Highlights

Professor Ove Nilsson, Umeå Plant Science Centre, SUAS was recently appointed Wallenberg Scholar which is a scheme funded by the Knut and Alice Wallenberg Foundation. He received this nomination with grants for his research focused on regulation of meristem identity and flowering time in Arabidopsis and Populus sp.

A de novo assembly of the Norway spruce (Picea abies) genome sequence was recently produced and gene prediction performed identifying that the genome contains ~30,000 well-suported gene loci and that it is largely composed of Long terminal Repeat (LTR) elements (Nystedt et al. 2013, Nature. In Press).

Also, the genomes of 110 accessions of the endogenous *Populus tremula* (European aspen) selected over a vast latitudinal cline are currently being sequenced. These efforts will ease extended, comparative studies across from Arabidopsis, Populus sp. to Norway spruce.

Selected Publications

The community of Swedish Arabidopsis scientis headed or contributed to about a hundred experimental papers in the last year, a selection is shown below.

Kradolfer D, Hennig H, Köhler C (2013) Increased maternal genome dosage bypasses the requirement of the FIS Polycomb Repressive Complex2 in Arabidopsis seed development. PLoS Genetics (9): e1003163.

Shen X, Pettersson M, Ronnegard L, Carlborg O (2012) Inheritance Beyond Plain Heritability: Variance-Controlling Genes in Arabidopsis thaliana. PLoS Genetics (8): e1002839

Cruz-Ramírez A, Díaz-Triviño S, Blilou I, Grieneisen VA et al. (2012) A Bistable Circuit Involving SCARECROW-RETINOBLASTOMA Integrates Cues to Inform Asymmetric Stem Cell Division. Cell (150): 1002-1015

Shaikhali J, Barajas-Lopéz JdD, Otvos K, Kremnev D et al. (2012) The CRYPTOCHROME1-Dependent Response to Excess Light Is Mediated through the Transcriptional Activators ZINC FINGER PROTEIN EXPRESSED IN INFLORESCENCE MERISTEM LIKE1 and ZML2 in Arabidopsis. Plant Cell (24): 3009-3025

Arabidopsis Genomics Tools and Resources

Science for Life Laboratory (SciLifeLab) is a newly established national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government, http://www.scilifelab.se

Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis http://www.upsc.se, found under "resources".

The Swedish Metabolomics Centre in Umeå is a national resource, inaugurated March 2013, for more information http://www.swedishmetabolomicscentre.se/

Major Funding Sources

- The Swedish Research Council (VR; http://www.vr.se) a core funder of researcher-initiated basic research.
- The Swedish Research Council Formas (http://www.formas.se) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.
- The Swedish Foundation for Strategic Research (http://www.stratresearch.se) supports strategic research in natural science, engineering and medicine.
- The Swedish Agency for Innovation Systems (VINNOVA; http://www.vinnova.se) promotes sustainable growth by funding needs-driven research and the development of effective innovation systems.
- The Royal Academy of Science (http://www.kva.se) and The Royal Academy of Agriculture and Forestry (http://www.ksla.se).
- The Wallenberg Foundations (http://www.wallenberg.com) is a private foundation supporting individual researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.
- Carl Tryggers Foundation for Scientific Research (http://www.carltryggersstiftelse.se/) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.
- The Kempe Foundations (http://www.kempe.com) private foundations devoted to support scientific research in Northern Sweden.

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

Research directions and funding possibilities

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

United Kingdom

Contact: Charis Cook (charis@garnetcommunity.org.u) GARNet - University of Warwick, Ruth Bastow (ruth@garnetcommunity.org.uk) GARNet - University of Warwick, Jim Beynon (jim.beynon@warwick.ac.uk) University of Warwick, Sean May (sean@arabidopsis.org.uk) NASC - University of Nottingham

General Activities

Over 300 research groups in the UK utilise the model plant Arabidopsis in their studies. Many of these groups are leaders in their field producing world-class research and publications in high impact journals. Arabidopsis research is largely project-focused, with work based in individual laboratories, multi-institutional collaborations or national Centres and Institutes. A UK institution, the University of Nottingham, hosts one of the two international Arabidopsis stock centres, NASC.

UK Arabidopsis Research Network

GARNet, currently funded via a five year grant (2009-2014) from BBSRC to support its coordination activities, aims to ensure that the full impact of the excellent UK plant science base is realised by acting as an information hub, providing a point of contact for researchers and funding agencies, promoting interactions between fundamental and applied plant science and increasing opportunities for UK plant science at the international level.

GARNet represents UK Arabidopsis researchers via a committee of 10 elected members and two ex-officio members, Prof Sean May and Dr Sabina Leonelli. Each year new members are elected to the GARNet committee as others rotate off. In December 2012 Nicolas Harberd, David Salt, and Antony Hall were elected to the committee for a three year term to join the current committee of Malcolm Bennett, Jim Beynon, John Doonan, Heather Knight, Smita Kurup, Jim Murray and Cyril Zipfel. GARNet is currently chaired by Jim Murray (since 1st January 2011).

GARNet organised two workshops in 2012. *Making Data Accessible to All* focussed on open science and the issues associated with making plant science data open access. The New Technologies for Plant Research aimed to encourage plant scientists to explore next generation sequencing (NGS) technologies by showcasing the many ways NGS is currently being applied in plant research.

GARNet can be found online at www.garnetcommunity.org.uk/. In 2012 the GARNet blog (http://blog.garnetcommunity.org.uk) and GARNet Twitter accounts (@garnetweets; @weedinggems) were launched.

UK Plant Science Federation

The UK Plant Sciences Federation (UKPSF; www.plantsci.org.uk) was established in late 2011 to provide 'one voice for UK Plant Science'. It is now a special interest group of the Society of Biology, and is managed by Executive Officer Mimi Tanimoto who took on the position in June 2012. Ruth Bastow was awarded the Society of Biology President's Award for her work toward setting up the UKPSF and is now its Scientific Advisor. The UKPSF includes representatives of a number of stakeholders, including plant research communities, learned societies, industrial groupings and plant science educationalists.

The inaugural conference of the UKPSF, PlantSci 2012, was a success. Over 200 people attended the conference in Norwich, UK, to hear speakers including Professor Sir John Beddington present their work on all areas of plant science, from molecular biology to education and outreach.

The UKPSF has been working with Sense About Science to set up a panel of plant science experts who will answer questions about plant biotechnology and agriculture from the public. The first event, held in October 2012, was a successful online Q&A about the future of organic and GM agriculture systems.

The UKPSF operates with financial support from the Society for Experimental Botany and the Gatsby Charitable Foundation. UKPSF Member Organisations are listed online http://www.societyofbiology.org/aboutus/special-interest-groups/ukpsf/ukpsfmembers

Conferences and Meetings

Past meetings:

- 4th New Phytologist Workshop: Synthetic Biology, 6-8 June 2012, University of Bristol
- Making Data Accessible to All, 12-13 July 2012, University of Exeter. Organised by the Social Sciences ESRC genomics centre at the University of Exeter and GARNet.
- New Technologies in Plant Research, 26 November 2012, University of Liverpool. Organised by GARNet.
- Centre for Plant Integrative Biology Study Groups: opportunities throughout the year for plant biologists and mathematicians to mathematically model plant biological processes.

Upcoming meetings:

- UK PlantSci 2013: the second UK Plant Science conference will be held on 16-17 April 2013 in Dundee, Scotland.
- Synthetic Biology Workshop: GARNet is hosting its first workshop of 2013 in Nottingham, UK, on 21-22 May 2013.
- Centre for Integrative Plant Biology (University of Nottingham) Study group: 25-28 March 2013

Selected Publications

Sherstnev A, Duc C, Cole C, Zacharaki V et al. (2012) Direct sequencing of Arabidopsis thaliana RNA reveals patterns of cleavage and polyadenylation. Nature Structural & Molecular Biology (19): 845–852.

Federici F, Dupuy L, Laplaze L, Heisler M & Haseloff J (2012) Integrated genetic and computation methods for in planta cytometry. Nature Methods (9): 483–485.

Péret B, Li G, Zhao J, Band LR et al. (2012) Auxin regulates aquaporin function to facilitate lateral root emergence. Nature Cell Biology (14): 991–998.

Liu F, Bakht S, Dean C (2012) Cotranscriptional Role for Arabidopsis DICER-LIKE 4 in Transcription Termination. Science (335): 1621-1623.

Coustham V, Li P, Strange A, Lister C et al. (2012) Quantitative Modulation of Polycomb Silencing Underlies Natural Variation in Vernalization. Science (337): 584-587.

Ling Q, Huang W, Baldwin W, and Paul Jarvis (2012) Chloroplast Biogenesis Is Regulated by Direct Action of the Ubiquitin-Proteasome System. Science (338): 655-659.

Major Funding Sources

- The Biotechnology and Biological Science Research Council (BBSRC; www.bbsrc.ac.uk) is the major funder of Arabidopsis research in the UK. Its Strategic Plan for 2010-15 lays out research priorities including food security and crop science, bioenergy, systems approaches to the biosciences, and synthetic biology. The UK plant science research community is ideally placed to contribute to these priorities.
- The BBSRC is funding a wheat transformation service at NIAB. Half of the funded fifty transformations are reserved for researchers working on model organisms.
- Publications containing research funded by UK Research Councils must now be free for anyone to access. There is a ring-fenced sum of money available for gold open access publishing.
- The ERA-Net for Coordinating Action in the Plant Sciences (ERA-CAPS; www.era-caps.org) launched its first joint call for proposal on November 19th 2012. The call closed on 15th February 2013, and its total budget is around €20M. The call, "Expanding the European Research Area in Molecular Plant Sciences", covers all areas of molecular plant science.
- The Gatsby Foundation funded the development and running costs of a new plant science research institute, the Sainsbury Laboratory University of Cambridge. The building, designed by architect Stanton Williams, won the Stirling Prize for architecture in 2012.

United States

http://arabidopsis.org/portals/masc/countries/United_States.jsp
Contact: Blake Meyers (Meyers@dbi.udel.edu) University of Delaware, NAASC President (2012-2013); Dominique Bergmann (Bergmann@stanford.edu) Stanford University, NAASC President-elect (2013-2014); Joanna Friesner (jdfriesner@ucdavis.edu) NAASC Coordinator

General Activities

North American Arabidopsis Steering Committee (NAASC)

NAASC is an elected body composed primarily of U.S. researchers that provides North American representation to MASC and serves as the main organizing and fundraising body for the International Conference on Arabidopsis Research (ICAR) when it is held in North America (e.g. ICAR 2014-University of British Columbia, Vancouver, Canada.) NAASC's community service efforts include: (1) fundraising to support ICARs including participation by young scientists and under-represented scientists, (2) serving on relevant advisory committees and boards, (3) acting as leaders and participants for community-related initiatives, and (4) acting as liaison between researchers, funders, and other relevant groups such as ABRC. http://arabidopsis.org/portals/masc/countries/NAASC_Info.jsp

- NAASC members serve four-year terms with two of eight members rotating off annually. Xinnian Dong (Duke University) and Blake Meyers (University of Delaware) conclude their terms in fall 2013 after the next election at which time Dominique Bergmann will become NAASC president and representative to MASC for 2013-2014. Continuing members include: Wolf Frommer (Carnegie Institution for Science), Dominique Bergmann (Stanford University), Nick Provart (University of Toronto), Jose Alonso (NC State University), and, newly elected in fall 2012: Siobhan Brady (University of California, Davis) and Keiko Torii (University of Washington).
- Community funding support obtained in the past year for participation by early career scientists, under-represented minorities, faculty at HBCUs and MSIs, and several invited early career or special session speakers: Dominique Bergmann secured an NSF grant in support of ICAR 2012 and Jose Alonso secured an NSF grant in support of ICAR 2013. Jose's ICAR 2013 grant also includes funding to support a special 'Simon Chan Memorial Symposium' to honor a promising and talented young researcher and faculty member at the University of California, Davis who tragically passed away last summer (see 'In Memoriam' section below for more information.)
- Joanna Friesner, NAASC Coordinator, supports all NAASC efforts including, among other duties, acting as lead conference organizer for North American ICARs and assistance with NAASC-led community initiatives such as the IAIC (see below).

- NAASC Honors, Awards, and Distinctions: (1) May 2012: Elected to the National Academy of Sciences: Xinnian Dong; (2) October 2012: Elected as Fellows of the American Association for the Advancement of Science: Blake Meyers, Keiko Torii; (3) ASPB Awards 2012: Lawrence Bogorad Award for Excellence in Plant Biology Research: Wolf Frommer.
- Committee service: Jose Alonso, Nick Provart, and Blake Meyers serve on the Arabidopsis Biological Resource Center (ABRC) advisory committee. Jose Alonso and Nick Provart are the conference organizing committee co-chairs for ICAR 2014 (see below). Blake Meyers is the Interim Director for the International Arabidopsis Informatics Consortium (IAIC, details below) and leads the IAIC Steering Committee. Nick Provart also is member of the IAIC Steering Committee.

What's happening with TAIR

The Arabidopsis Information Resource (TAIR) has been the primary global public database for Arabidopsis information, including housing and maintaining the 'gold-standard' Arabidopsis genome data. Funding for TAIR has primarily come from the U.S. National Science Foundation (NSF); the official end of the TAIR funding period is August 2013. Since 2009, members of NAASC and MASC, and others in the international Arabidopsis community, have been working to ensure the vital resources and information provided by TAIR will remain accessible and updated. The current status of these community efforts is summarized in the TAIR section of the MASC report.

The International Arabidopsis Informatics Consortium (IAIC)

The IAIC is a community-led consortium initiated in 2010 in response to growth in the size and complexity of Arabidopsis data, combined with an expected reduction in funding for TAIR, the primary Arabidopsis information database. The goal of the IAIC is to develop a novel, integrated, international framework with which to address the informatics needs of the Arabidopsis community, while providing a smooth transition from the current TAIR-based central database structure to this stable, long-term structure. In the past year, the focus of the IAIC has been to facilitate progress on the effort to secure funding for a new Arabidopsis Information Portal (AIP). IAIC leaders and others from the North American and Multinational Arabidopsis Steering Committees facilitated the formation of an expert team to develop a funding proposal to establish the AIP. Chris Town of the J. Craig Venter Institute and Matt Vaughn of the iPlant Collaborative emerged as leaders in the proposal effort, along with colleagues Konstantinos Krampis (JCVI), and Gos Micklem (University of Cambridge).

Updates on IAIC

- September 2012: Proposal for funding to develop the Arabidopsis Informatics Portal (AIP) submitted to the U.S. National Science Foundation (NSF) by PI Chris Town (JCVI) and co-PIs Matt Vaughn (iPlant Collaborative), Konstantinos Krampis (JCVI) and Gos Micklem (University of Cambridge)
- March 2013: the NSF has responded to the AIP proposal with a request for a detailed AIP implementation plan.
- March 15, 2013: TAIR-to-iPlant Collaborative transition-most TAIR software has been installed at iPC. The TAIR interface will continue to be available at the same URL (http://arabidopsis.org) after the migration is complete, but the URL will direct traffic to the TAIR software running on iPC servers. See TAIR section of this report for more information.
- July 2013: The Steering Committee (SC), established in June 2010, concludes their formal service at ICAR 2013. SC members: Blake Meyers (Interim IAIC Director), Ruth Bastow, Jim Beynon, Volker Brendel, Rion Dooley, Erich Grotewold, Nick Provart, Dan Stanzione, and Doreen Ware. Dr. Meyers will continue supporting the IAIC in his role for the duration of the NSF grant that supports IAIC activities (NSF Award #1062348). IAIC activities: (1) platform talk by Interim Director Blake Meyers and workshop at 2012 ICAR in Vienna, Austria, (2) community workshop at PAG 2013 in San Diego, CA; (3) community workshop at ICAR 2013 in Sydney, Australia.
- February 2012: Scientific Advisory Board (SAB) initial members appointed:

  Gloria Coruzzi- USA
  Kazuki Saito- Japan
  Magnus Nordborg- Austria
  Mark Estelle- USA, Committee Chair
  Mark Forster- UK
  Paul Kersey- UK
  Xuemei Chen- USA

- Community website: www.arabidopsisinformatics.org/

Rationale for development of the IAIC

Arabidopsis informatics needs are growing quickly with new data types and a rapidly increasing rate of data generation. Individual investigators are devising new data handling and visualization tools that have broad utility. The Arabidopsis community is global, yet most of the current informatics support is funded on a national level. The community needs to determine the best way(s) to internationalize Arabidopsis informatics efforts, integrate new tools, maintain long-term database stability, address the needs of users, and do this in a way that enhances the position of Arabidopsis in the top tier of model organisms.

Notable Awards and Honors for US Researchers Using Arabidopsis

- Elected to the National Academy of Sciences, May 2012: Xinnian Dong (NAASC), Harry Klee, Sabeeha Merchant, Natasha Raikhel
- Elected as Fellows of the American Association for the Advancement of Science, October 2012: Nick Carpita, Vitaly Citovsky, Luca Comai, Xing Wang Deng (former NAASC), Kathleen Donohue, Joe Ecker (former NAASC), Steve Henikoff, Georg Jander, Alan Jones, Dan Klessig, Elena Kramer, Jianming Li, Sheng Luan, Blake Meyers (NAASC), Joseph Noel, Thomas Peterson, Eran Pichersky, Danny Schnell, Keiko Torii (NAASC), Geoff Wasteneys (Canada), Shuqun Zhang
- ASPB 2012: Martin Gibbs Medal: Steve Kay (former NAASC); Dennis R. Hoagland Award: Mary Lou Guerinot (former NAASC); Lawrence Bogorad Award for Excellence in Plant Biology Research: Wolf Frommer (NAASC); Excellence in Education Award: Peggy Lemaux; Early Career Award: Michael Nodine

Conferences and Meetings

NAASC will organize the 2014 ICAR, which is scheduled for the University of British Columbia in Vancouver (July 28 – August 1). This is the second Canadian ICAR; NAASC previously organized ICAR 2008 in Montreal. ICAR 2014 conference organizing committee co-chairs are Jose Alonso and Nick Provart, with Joanna Friesner, NAASC Coordinator, serving as lead organizer. NAASC members fill out the core organizing committee with UBC faculty comprising a local organizing committee. As in previous years, NAASC members will seek funding to support conference participants. Additionally, the committee is considering several new sessions and activities, in part to support early-career and under-represented minority researchers. NAASC will conduct a community survey this summer to solicit input for ICAR 2014.

In Memoriam

Simon Chan, University of California-Davis (1974 – 2012)

The Department of Plant Biology invites friends and colleagues to leave messages in memoriam here: http://www.plb.ucdavis.edu/labs/srchan/

Recent community recognition: (1) The Simon Chan Memorial Symposium, co-chaired by Siobhan Brady and Luca Comai (UC Davis) at the 2013 International Conference on Arabidopsis Research (ICAR), June 24-28, Sydney, Australia; (2) The Simon Chan Memorial Symposium on Chromosomal Biology, chaired by William Lucas (UC Davis) at the 2013 ASPB annual meeting, July 20-24, Rhode Island, USA.

Simon Chan, an associate professor of plant biology at the University of California, Davis, whose work on plant breeding promised to help some of the world's poorest people, died Aug. 22, 2012. He was 38. Chan had been suffering from primary sclerosing cholangitis, an autoimmune disorder, and developed complications while awaiting a liver transplant. "Simon was an incredible scientist, superb mentor and a great friend," said James Hildreth, dean of the College of Biological Sciences at UC Davis. "His brilliant work could fundamentally change how new crop plants are generated and may shed light on how new plant species are formed." Professor Bill Lucas, chair of the Department of Plant Biology, described Chan as "one of a kind." "His enthusiasm for his science was contagious and his passion for teaching and mentoring his students served as a true role model for us all. Words cannot express our deep sorrow at losing such a talented and wonderful human being," Lucas said. Working with the model plant Arabidopsis, Chan's laboratory discovered a way to breed plants with genes from only one parent, making it possible to "breed true" without generations of inbreeding. In June 2011, Chan was one of two UC Davis scientists selected for the first-ever class of HHMI-GBMF Investigators, funded jointly by the Howard Hughes Medical Institute and the Gordon and Betty Moore Foundation to support promising research in plant sciences. Chan planned to use the HHMI-GBMF award to expand his work to crop plants such as tomatoes and Chinese cabbage. Chan was also working with plant breeders in Colombia, Tanzania and Kenya to find new ways to breed bananas, plantain and cassava, staple foods for millions of the world's poorest people. That project was supported by a grant from the NSF-BREAD (Basic Research to Enable Agricultural Development) program, a joint initiative of the Bill & Melinda Gates Foundation and the National Science Foundation. Chan was born in 1974 in Auckland, New Zealand, and earned his bachelor's degree in biochemistry from the University of Auckland in 1996. From there he went to UCSF, where he worked with Professor Elizabeth Blackburn, winner of the 2009 Nobel Prize in physiology or medicine, and was awarded his doctoral degree in cell biology in 2002. Chan carried out postdoctoral research at UCLA, where he began working on plants with Professor Steven Jacobsen in the Department of Molecular, Cell and Developmental Biology. Chan joined the faculty at UC Davis in 2006 as an assistant professor. In June 2012 he had been granted tenure and promoted to associate professor. Friends and colleagues recalled that Chan loved music, especially jazz. He played bass guitar and saxophone. As a teenager he dreamed of being a professional musician, but settled on science instead. "We will all miss Simon so much," wrote Neelima Sinha, professor of plant biology at UC Davis. "He was a wonderful colleague, a rare intellect, and such a great friend. Will miss his enthusiasm for science, life, music, movies, food, people and the world in general." Wrote Keith Bradnam, a project scientist at the UC Davis Genome Center, via Twitter: "It sounds a cliché, but I don't think there is anyone who would have a bad word to say about Simon. He was respected and loved by all who knew him." Chan is survived by his parents, Avril and Robert Chan, his sister, Caron Chan, and her husband and two children.

Adapted from the article: http://news.ucdavis.edu/search/news_detail.lasso?id=10312)

Members of the MASC Subcommittees

Bioinformatics

Nicholas Provart
(Chair)
University of Toronto, Canada
nicholas.provart@utoronto.

Tetsuro Toyoda
RIKEN BASE, Japan
toyoda@base.riken.jp

Yves van den Peer
VIB / Ghent University, Belgium
yvdp@psb.UGent.be

Klaus Mayer
Helmholtz Zentrum München, Germany
Kmayer@gsf.de

Sean May
University of Nottingham, U.K.
sean@arabidopsis.info

Sébastien Aubourg
INRA, Evry, France
aubourg@evry.inra.fr

Yasukazu Nakamura
Kazusa DNA Research Institute, Japan
yn@kazusa.or.jp

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

—

Clone-Based Functional Genomics Resources (ORFeomics)

Motoaki Seki
(Chair)
RIKEN PSC, Japan
mseki@psc.riken.jp

Joe Ecker
(Co-chair)
The Salk Institute for Biological Studies, U.S.
ecker@salk.edu

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

Chris Town
The J. Craig Venter Institute, U.S.
cdtown@jcvi.org

—

Metabolomics

Kazuki Saito
(Chair)
RIKEN PSC, Japan
ksaito@psc.riken.jp

Wolfram Weckwerth
(Co-chair)
University of Vienna, Austria
wolfram.weckwerth@univie.ac.at

Mike Beale
Rothamsted Research, U.K.
mike.beale@rothamsted.ac.uk

Alisdair Fernie
Max Planck Institute for Molecular Plant Physiology, Germany
Fernie@mpimp-golm.mpg.de

Oliver Fiehn
University of California, U.S.
ofeihn@ucdavis.edu

Tony Larson
University of York, U.K.
trl1@york.ac.uk

Rob Last
Michigan State University, U.S.
lastr@msu.edu

Basil Nikolau
Iowa State University, U.S.
dimmas@iastate.edu

Ute Roessner
The University of Melbourne, Australia
u.roessner@unimelb.edu.au

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Natural Variation and Comparative Genomics

Brian Dilkes
(Co-chair)
Purdue University, U.S.
bdilkes@purdue.edu

J. Chris Pires
(Co-chair)
University of Missoury, U.S.
piresjc@missouri.edu

Natural Variation

Carlos Alonso-Blanco
CSIC, Madrid, Spain
calonso@cnb.csic.es

Thomas Altmann
IPK Gatersleben, Germany
altmann@ipk-gatersleben.de

Ian Bancroft
John Innes Centre Norwich U.K.
ian.bancroft@bbsrc.ac.uk

Joy Bergelson
University of Chicago, U.S.
jbergels@uchicago.edu

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

Kathleen Donohue
University of Chicago, U.S.
k.donohue@duke.edu

Matthias Hoffmann
University of Halle, Germany
matthias.hoffmann@botanik.uni-halle.de

Daniel Kliebenstein
University of California, U.S.
kliebenstein@ucdavis.edu

Olivier Loudet
INRA, France
loudet@versailles.inra.fr

Annie Schmitt
Brown University, U.S.
Johanna_Schmitt@brown.edu

Daniel Kliebenstein
University of California, U.S.
kliebenstein@ucdavis.edu

Comparative Genomics

David Baum
University of Wisconsin, U.S.
dbaum@wisc.edu

Hans Bohnert
University of Illinois, U.S.
bohnerth@life.uiuc.edu

Sean Cutler
University of California Riverside, U.S.
Sean.cutler@ucr.edu

Graham King
Southern Cross University, Australia
graham.king@scu.edu.au

Marcus Koch
University of Heidelberg, Germany
marcus.koch@urz.uni-heidelberg.de

Martin Lysak
Masaryk University, Czech Republic
lysak@sci-muni.cz

Ray Ming
University of Illinois, U.S.
rming@life.uiuc.edu

Detlef Weigel
Max Planck Institute for Developmental Biology, Germany
weigel@tuebingen.mpg.de

—

Phenomics

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

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

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

John Doonan
Aberystwyth University, UK
john.doonan@aber.ac.uk

Joe Ecker
Salk Institute, U.S.
ecker@salk.edu

Christine Granier
INRA-SUPAGRO, France
granier@supagro.inra.fr

Jeremy Harbinson
Wageningen University, The Netherlands
Jeremy.Harbinson@wur.nl

Maarten Korneef
Max Planck Institute for Plant Breeding Research, Germany
koornnee@mpiz-koeln.mpg.de

Rob Last
Michigan State University, U.S.
lastr@msu.edu

Minami Matsui
RIKEN PSC, Japan
minami@riken.jp

Xavier Sirault
CSIRO Plant Industry, Australia
Xavier.sirault@csiro.au

Detlef Weigel
Max Planck Institute for Developmental Biology, Tübingen, Germany
weigel@tue.mpg.de

Proteomics

Joshua Heazlewood
(Co-chair)
Lawrence Berkeley National Laboratory, U.S.
jlheazlewood@lbl.gov

Alexandra Jones
(Co-chair)
The Sainsbury Laboratory, U.K.
alex.jones@sainsbury-laboratory.ac.uk

Katja Baerenfaller
ETH -Zurich, Switzerland
bkatja@ethz.ch

Sacha Baginsky
Martin-Luther-Universität Halle-Wittenberg, Germany
sacha.baginsky@biochemtech.uni-halle.de

Hans-Peter Braun
Leibniz Universität Hannover, Germany
braun@genetik.uni-hannover.de

Steve Briggs
University of California, San Diego, USA
sbriggs@ad.ucsd.edu

Geert De Jaeger
VIB Ghent University, Belgium
gejae@psb.vib-ugent.be

Hans-Peter Mock
Institute for Plant Genetics and Crop Plant Research, Germany
mock@ipk-gatersleben.de

Harvey Millar
The University of Western Australia, Australia harvey.millar@uwa.edu.au

Hirofumi Nakagami
RIKEN PSC, Japan
hironakagami@psc.riken.jp

Scott Peck
University of Missouri, U.S.
pecks@missouri.edu

Loïc Rajjou
AgroParisTech, France
loic.rajjou@versailles.inra.fr

Waltraud Schulze
Max Planck Institute of Molecular Plant Physiology, Germany
schulze@mpimp-golm.mpg.de

Sigrun Reumann
University of Stavanger, Norway
sigrun.reumann@uis.no

Norbert Rolland
CEA, France
norbert.rolland@cea.fr

Michel Rossignol
INRA, France
rossign@supagro.inra.fr

Nicolas Taylor
The University of Western Australia, Australia
ntaylor@cyllene.uwa.edu.au

Jay Thelen
University of Missouri, U.S.
thelenj@missouri.edu

Klaas van Wijk
Cornell University, U.S.
kv35@cornell.edu

Wolfram Weckwerth
University of Vienna, Austria
wolfram.weckwerth@univie.ac.at

Julian Whitelegge
University of California, Los Angeles, U.S.
jpw@chem.ucla.edu

Stefanie Wienkoop
University of Vienna, Austria
stefanie.wienkoop@univie.ac.at

Systems Biology

Malcolm Bennett
(Co-chair)
University of Nottingham, U.K.
malcolm.bennett@nottingham.ac.uk

Siobhan Brady
(Co-chair)
University of California, U.S.
sbrady@ucdavis.edu

Rodrigo Gutierrez
Pontificia Universidad Catolica de Chile, Chile
rodrigo.gutierrez@gmail.com

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

Members of the Multinational Arabidopsis Steering Committee

Wolfram Weckwerth
wolfram.weckwerth@univie.ac.at
University of Vienna, Austria
(Chair, Representing Austria)

Barry Pogson
barry.pogson@anu.edu.au
The Australian National University Canberra, Australia
(Co-chair, Representing Australia and New Zealand)

Luise H. Brand
luise.brand@uni-tuebingen.de
University of Tuebingen, Germany
(MASC coordinator)

Thomas Altmann
altmann@ipk-gatersleben.de
IPK-Gatersleben, Germany
(Representing Germany)

Ruth Bastow
ruth@garnetcommunity.org.uk
University of Warwick, U.K.
(Representing U.K.)

Dominique Bergmann
Bergmann@stanford.edu
Stanford University, U.S.
(Representing U.S.)

Jim Beynon
jim.beynon@warwick.ac.uk
University of Warwick, U.K.
(Representing U.K.)

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

Jorge J. Casal
casal@ifeva.edu.ar
IFEVA/University of Buenos Aires, Argentina
(Representing Argentina)

Charis Cook
charis@garnetcommunity.org.uk
University of Warwick, U.K.
(Representing U.K.)

Maria E. Eriksson
maria.erikson@plantphys.umu.se
Umea Plant Science Centre, Sweden
(Representing Sweden)

Joanna Friesner
jdfriesner@ucdavis.edu
University of California, U.S.
(Representing U.S., IAIC coordinator)

Wilhelm Gruissem
wgruissem@ethz.ch
ETH Zurich, Switzerland
(Representing Switzerland)

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

Heribert Hirt
hirt@evry.inra.fr
URGV, Evry, France
(Representing France)

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

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

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

Minami Matsui
minami@riken.jp
RIKEN BRC, Japan
(Representing Japan)

Sean May
sean@arabidopsis.org.uk
NASC, Loughborough, UK
(Representing U.K., NASC director)

Blake Meyers
meyers@dbi.udel.edu
University of Delaware, U.S.
(Representing U.S., IAIC director)

Javier Paz-Ares
jpazares@cnb.csic.es
Nacional de Biotechnoligia-CSIC, Madrid, Spain
(Representing Spain)

Ben Scheres
b.scheres@uu.nl
University of Utrecht, The Netherlands
(Representing The Netherlands)

Giovanna Serino
giovanna.serino@uniroma1.it
University of Rome, Italy
(Representing Italy)

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

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

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

Lieven De Veylder
lieven.deveylder@psb.vib-ugent.be
VIB Ghent Universtity, Belgium
(Representing Belgium)

Sacco de Vries
sacco.devries@wur.nl
Wageningen University, The Netherlands
(Representing the Netherlands)

Shaul Yalovsky
ShaulY@tauex.tau.ac.il
Tel Aviv University, Israel
(Representing Israel)

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

Viktor Zarsky
viktor@natur.cuni.cz
Charles University and Academy of Sciences of the Czech Republic, Prague, Czech Republic
(Representing Czech Republic)

Jelena Brkljacic
brkljacic.1@osu.edu
ABRC, Columbus, U.S.
(ABRC associate director)

Erich Grotewold
grotewold.1@osu.edu
ABRC, Columbus, U.S.
(ABRC director)

Eva Huala
huala@acoma.stanford.edu
TAIR, Stanford, U.S.
(TAIR director)

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


MASC