The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2011

The Multinational Arabidopsis Steering Committee May 2011

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The Multinational Arabidopsis Steering Committee-May 2011

Cover Design
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Cover Image: Root xylem vessels are patterned by mobile microRNA 165/6 and HD-ZIP III transcription factors.
Left image is the expression of the sensor GFP that is targeted by miR165/6. Low GFP intensity indicates high levels of miR165/6. Right image shows xylem vessels in wild type roots.

Courtesy of:
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Foreword to the Report

This is the 2010/2011 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 that initiated 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. This aimed 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 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 centres; 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 therefore 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.

Following the success of the Multinational *Arabidopsis thaliana* Genome Research Project that led to completion of the sequencing of the reference Arabidopsis genome in 2000, the ambitious goal to determine the function of every Arabidopsis gene by the year 2010 was set by a new Project, the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. Numerous laboratories internationally have taken part in this project and very large datasets and resources have been 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 this organism, 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 programmes. 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' have been unprecedented. Studies originally conducted in Arabidopsis are increasingly being translated in the development of biotechnological tools that will help meet global challenges such as food security. 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 for projects that link basic and applied approaches. Given the increasingly important role that Plant Science will play in all of our futures, future support mechanisms for Arabidopsis resources should be identified. For example, in 2010 MASC and NAASC hosted two workshops to consider how the very large amount of data arising from Arabidopsis research can be managed (and funded) in a coordinated manner internationally. This is essential in order to fully leverage the impressive gains obtained thus far through Arabidopsis research and to maintain cutting edge research in plant biology. Following these workshops the creation of an international consortium for Arabidopsis informatics funded by a variety of sources was proposed (IAIC, (2010) An International Bioinformatics Infrastructure to Underpin the Arabidopsis Community. Plant Cell (22): 2530-2536) and the community is currently making its first steps to establish it.

Building upon its well established tradition for international cooperation MASC is currently preparing a road map for the next decade, which we hope 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
May 2011

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 nuclear 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 and the intent has always been that the knowledge gained from this reference species would serve to advance understanding about other organisms, particularly crop species. It can be expected that Arabidopsis research will translate into new and improved plant products and contribute to agricultural productivity. The transfer of knowledge from Arabidopsis is accelerating due to the efforts of a vibrant research community and the leveraging of advances and resources made over the last 15 years or more. Arabidopsis has shifted from model to reference organism - the plant in which the fundamentals 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 levels and resources currently available and under development will allow rapid experimentation to answer existing and future challenging questions. However, the utility of Arabidopsis 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, are 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) as of May 10th 2011 there were 21,771 Arabidopsis researchers in 8,465 laboratories worldwide, with 9,378 people and 4,866 laboratories updated in the last five years. It is interesting to note that the number of people and laboratories updated in the past five years continues to increase (9,168 and 4,065 respectively in 2010), 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.

Highligths in Arabidopsis research

The past year continued to be strong for Arabidopsis publications. 3,423 Arabidopsis peer-reviewed research papers were published in 2010, an 8.5-fold rate increase over 1994 (when 402 peer-reviewed papers were published; Fig. 1, page 11), and an increase of 50-fold in the last 20 years. This report includes summaries of just a few research highlights in the past year (pages 11-16) including:

- Discovery of the plant sugar transporters targeted by pathogens
- Technology advancement to isolate cell type specific RNA
- Insight into local adptation on serpentine soils through natural variation studies in *Arabidopsis lyrata*
- Discovery of NINJA, the missing link of the jasmonate signaling pahway
- Discovery of microRNA signalling across cells
- Insight into Casparian Strips and their possible tight junction-like role
- Sequencing advancement and generation of large scale collection of knockdowns for Arabidopsis miRNA families

Examples of applications arising from Arabidopsis research

The knowledge gained from studies in Arabidopsis serves to advance our understanding of other plant species, particularly 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 increase: in 2010 there were 1,137 utility patents referencing Arabidopsis compared to 23 in 1994, a nearly 50-fold increase (See Fig. 2, page 20). In the same timeframe, a 35- and a 5.6-fold increase have been recorded for European and world's published applications (i.e. patents) referencing Arabidopsis (See Fig.3 and Fig.4, page 21). 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 (pages 21-24):

- Easier and cheaper mechanism to extract sugars from plant material developed in Arabidopsis to meet biofuel demands
- A master regulator of plant root hair growth acting as the nutrient mining machinery to enhance the plant root system
- Extraction of petroleum precursors from plants to produce green

plastic
- Discovery of an Arabidopsis gene that confers resistance in Brassica
- Insight into chromosome imbalances and predictable plant defects
- An Arabidopsis gene employed by Monsanto to improve soybean yields

New initiatives announced this year
- **Israel**- Formal international agreements for collaborations and student exchanges have been formalized between the The Center for Plant Cell Biology at the University of California at Riverside (USA) and the Manna Center for Plant Biosciences (Tel Aviv University, Israel) and the Department of Plant Sciences (Weizmann Institute of Science, Israel).
- **Japan**- New Arabidopsis initiatives started in 2010, including two 5-year projects and a 2.7 billion yen project that aims to realize a low carbon sosciety.
- **UK**- BBSRC in partnership with the Bill and Melinda Gates Foundation, the UK Department for International Development and the Indian Department of Biotechnology, BBSRC launched a £20M/$32 major international research initiative to improve food security for the developing countries. In partnership with the US National Science Foundation, BBSRC awarded funding totaling £6.11M/$10.3M to four transatlantic research teams to improve photosynthesis with a view of increasing the yield of important crops for food production or sustainable bioenergy.

MASC Subcommittees

The MASC Subcommittees promote international cooperation in a number of areas of functional genomics research:
- Bioinformatics - Following the Bioinformatics workshops (April 2010 in Nottingham, UK and May 2010 in Washington DC, USA sponsored by BBSRC and NSF) hosted by MASC and NAASC respectively, the creation of the International Arabidopsis Informatics Consortium (IAIC) was proposed. IAIC envisions a distributed system of data, tools and resources for Arabidopsis and related species, accessed via a single portal and funded via a variety of sources.
- Metabolomics - In the light of the growing –omics integration, the subcommittee redefined its goals in 2010. A subcommittee website was launched at www.masc-metabolomics.org and subcommittee members have participated to several plant and non-plant specific metabolomics meetings
- Natural Variation and Comparative Genomics - Great progress has been made on the 1001 Genomes Project. It is expected that the goal of 1001 sequenced accessions will be surpassed in 2012.
- Phenomics - Subcommittee members continue to track progress by the various phenomics efforts underway worldwide including artifical target mimics, very rapid mapping of mutants, insertion lines, phenotyping platforms and facilities, databases, phenomics meetings, and community events including the participation to European and Internation Plant Phenotyping Networks.
- Proteomics - Subcommittee members continued to develop resources for the community including the development of the first biological proteomics aggregation portal (MASCP Gator). Subcommittee members initiated a discussion with the Human Proteomics Organization and participated in two workgroups of Model organism Proteome (September 2010; April 2011) to examine practices and standards in model systems. An open and well attended subcommittee workshop focussing on protein phosphorylation was held at ICAR, Yokohama, 7th June 2010.
- Systems Biology - The subcommittee aims to increase community action on standards and accessibility (of data, models and software tools), on training, and communicating to the public to build on the opportunities that this presents. Advancing these aims should promote a growing breadth and sophistication of Systems Biology approaches in Arabidopsis.

MASC recommendations and goals for the next year

In addition to recommendations previously listed in the 2009 and 2010 MASC reports four new recommendations are outlined below for the years ahead.
1. Systems approach for the understanding of complex regulatory systems in plant growth, development and environmental adaptation.
2. Development of bioinformatics infrastructure including useful tools and databases for the promotion of systems and computational biology in plants.
3. Development of genomics and biological resources for the understanding of adaptation to environmental changes based on natural variation.
4. Translational research based on Arabidopsis basic knowledge for the application to crops and trees in the fields, which contributes to solve global problems such as foods, energy and environment.

Analysis and Recommendations

As the first plant to have its entire nuclear genome sequenced, *Arabidopsis thaliana* has become the most important model system for plant biology (Koornneef and Meinke, 2010). Arabidopsis research has increasingly impacted on our understanding of other plants with the intent of utilizing the knowledge accrued from this reference plant to advance our understanding in crops and trees. The Arabidopsis 2010 Project has come to an end with amazing progress in basic plant science and functional genomics. Ten years after the completion of the sequencing of its nuclear genome in 2000, Arabidopsis has become the most important model system not only for the promotion of plant science but also for the understanding of complex systems in multicellular organisms. Most plant scientists agree that the year of 2010 was a year of commemoration and celebration of the success of the international coordinated Arabidopsis 2010 project as well as a year for the development of the next stage of plant science and crop biotechnology.

The Arabidopsis 2010 project has played a central role in understanding various functions of coding and noncoding plant genes and their regulatory networks. In the United States, the National Science Foundation (NSF) has supported this large project for 10 years, which has been successful in the establishment of research resources and informatics platforms. Similar functional genomics projects in Europe, Japan and other parts of the world also have provided resources and databases for the promotion of Arabidopsis functional genomics. In the international coordinated 2010 project, various genomic and mutant resources have been developed and deposited in resource centers including the Arabidopsis Biological Resource Center (ABRC), the Nottingham Arabidopsis Stock Centre (NASC) and RIKEN BioResource Center (BRC). Plant and crop scientists have been using these important resources for the functional analyses of their target genes. Numerous bioinformatics tools and databases have been developed in these projects and integrated by advanced IT technologies and bioinformatics. The Arabidopsis Information Resource (TAIR) is an important hub for genome information, various databases, resources, and other useful information for Arabidopsis researchers.

Arabidopsis provides a unique system to address biological questions that range from the molecular to the ecosystem level. Arabidopsis resources allow rapid experimentation to answer existing and future challenging questions. The MASC 2011 Report illustrates a number of research outputs on basic knowledge of plant gene function and the possible transfer of this knowledge to biotechnology and agriculture. Target research areas include the regulatory networks of phytohormone signaling from perception, complex functions, synthesis and transport for their functions. In addition, novel functions of peptide hormones have been extensively analyzed. Amazing advances have been reported on various functions of noncoding RNAs, including siRNA, miRNA and so on, which are involved in the epigenetic regulation of plant genomes (Pages 11–16).

Technology development in DNA sequencers and mass spectrometry has extended functional genomics for the integration of different 'omics' for the systematic analyses of gene expression, protein profiling and modification, and metabolite profiling. New DNA sequencing technologies are providing powerful tools for the analysis of natural variation in Arabidopsis ecotypes with the aim to understand the environmental effects on plant genome functions (Page 13). The Arabidopsis 1001 genomes project is providing basic data for the analysis of biodiversity and SNPs of ecotypes in various environmental conditions. In addition, high-throughput DNA sequencing technology is generating a number of genome sequences of various plants and crops. The collected genome information will be invaluable for comparative and evolution plant biology in the future. Development of imaging technologies using fluorescent tags is also providing us with powerful tools for the analysis of cellular regulation of various molecules. Bioresources and information resources have become more and more important for the promotion of systems biology and evolutional biology.

According to TAIR, the number of people and laboratories updated in the past five years continues to increase. The increasing number of researchers and laboratories registered at TAIR represents an increase in active users. Peer-reviewed research papers of Arabidopsis published in 2010 increased 8.5-fold compared to those in 1994, and an increase of 50-fold in the last 20 years (Page 11). Many plant scientists have used Arabidopsis for the functional analysis of their research targets as an important reference. Moreover, many crop scientists have also used Arabidopsis resources for the functional analysis of their target genes. This may be the reason why the users of Arabidopsis mutants and genomic and information resources have seen such an increase.

Following the concerns regarding the future of Arabidopsis bioinformatics infrastructure, five companies and one research institution are supporting TAIR in its current funding period to mantain a number of its activities including literature curation. At the same time three bioinformatics workshops in which the MASC Bioinformatics subcommittee played a key were held. Following these discussions the development of an International Arabidopsis Informatics Consortium (IAIC) envisaging a distributed model with a central portal funded by a variety of sources was proposed (Page 29).

Numerous Arabidopsis genomics and mutant resources have been developed during the Multinational Coordinated Arabidopsis projects over the past 20 years. Resources include chemically generated mutants, homozygous T-DNA insertion mutant lines, RNAi suppressor resources and the recently-developed artificial microRNAs, cDNA and ORF clones, large-scale microarray data, and RILs and other mapping populations. Resource centers have played an important role in collecting, preserving and distributing these

resources to researchers. ABRC and NASC have been in place since 1991. In Japan, RIKEN opened the BioResource Center (BRC) in 2001, which provides resources mainly developed in Japan. The activities of resource centers are reported on Pages 17-19.

Numerous basic Arabidopsis research outputs can be translated into new crop products contributing to an increased agricultural productivity and to the production of biomaterials and biofuels.The knowledge gained from studies in Arabidopsis is utilized to advance our understanding of crops and trees, and thus translate into increasing their productivities. This transfer of basic knowledge is accelerating thanks to the efforts of research communities including both the public and private sectors. The filing of patents is one measure of potential commercial activity. US utility patents referencing Arabidopsis patents increased nearly 50-fold from 1994, which is one evidence of the translation of Arabidopsis knowledge as shown in Pages 20-21.

Due to the increasingly important role that plant science will play in all of our futures for the realization of a sustainable society (i.e. food and biofuel production) more scientists will need to be trained in plant sciences and Arabidopsis represents an ideal teaching and training system. As the global demand for food and renewable energy supplies increases, several governments across the world are allocating more money from their financial budget to plant science compared to previous years. In particular, food crop research with immediate applications is being encouraged. However, for the development of innovative technology, basic research becomes more important. Recently, the Howard Hughes Medical Institute and the Gordon and Betty Moore foundations (USA) decided to fund basic plant science to contribute solving global problems such as food availability, environment and energy problems. Founders agree that basic plant science will contribute to solving global problems of the 21st century.

In addition to recommendations previously listed in the 2009 and 2010 MASC reports four new recommendations are outlined below for the years ahead.

1. Systems approach for the understanding of complex regulatory systems in plant growth, development and environmental adaptation.
2. Development of bioinformatics infrastructure including useful tools and databases for the promotion of systems and computational biology in plants.
3. Development of genomics and biological resources for the understanding of adaptation to environmental changes based on natural variation.
4. Translational research based on Arabidopsis basic knowledge for the application to crops and trees in the fields, which contributes to solve global problems such as foods, energy and environment.

Koornneef M, Meinke, D (2010) The development of Arabidopsis as a model plant. Plant J. (61): 909-921.

Progress and Activities of Multinational Arabidopsis Steering Committee

Progress and activities of MASC in 2010/2011

In 2010, Kazuo Shinozaki (RIKEN, Japan) succeeded Prof Keith Lindsey (Durham University, UK) to become the MASC Chair and Mark Estelle (UC San Diego, USA) became Co-chair. Prof Estelle will become the new MASC chair when Prof Shinozaki steps down following the annual International Conference on Arabidopsis Research (ICAR) in June 2011. Dr Irene Lavagi (University of Warwick, UK) is the MASC Coordinator.

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. For the 2008 ICAR, 336 of 628 submitted abstracts contributed 3,060 total distinct AGI codes, including 926 loci that were not already associated to the literature in TAIR at that time. In 2009, 645 of 646 abstracts were linked to 1,634 distinct AGI codes, including 25 loci that were not already associated to literature in TAIR. In 2010, 391 of 922 abstracts were linked to 754 distinct AGI codes, including 7 loci that were not already associated to the litetature in TAIR.

Google Analytics were employed beginning June, 2007 to track the usage of MASC webpages at TAIR which are maintained by the MASC Coordinator. The community regularly visits the MASC pages: in the 1 year period between March 1, 2010 and March 1, 2011, 46 different MASC pages were viewed 9,239 times, an average of about 770 views a month. The top-viewed page (2,623 views) contains information on projects funded through the US 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 Coordinator's Journal page (www.arabidopsis.org/portals/masc/journal.jsp) and the MASC Report page (www.arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp), which received 996, 698 and 571 views respectively over the last year. The International Arabidopsis Informatics Consortium (IAIC) page was set up in September 2010 to inform the wider community of the bioinformatics infrastructure developments. In the same timeframe this page (www.arabidopsis.org/portals/masc/IAIC.jsp) has received 226 visits and views are expected to increase in the summer as the next steps towards the establishment of an international bioinformatics consortium will be made.

MASC subcommittees, proposed in 2002, were established to help track the progress and advances made by the international Arabidopsis community. In the last 8 years, 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 reorganisation 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 6 of the 7 current subcommittees: Bioinformatics, Metabolomics, Phenomics, Proteomics, Natural Variation and Comparative Genomics and Systems Biology. A special MASC Subcommittees workshop will be held at ICAR 2011 in Madison, USA, to showcase activities of the subcommittees to the wider community.

New countries have joined MASC and submitted a report including Czech Republic (Viktor Zarsky, Charles University, Prague), Finland (Ykä Helariutta. University of Helsinki, Helskinki), Ireland (Charles Spillane, National University of Ireland, Galway), Sweden (Maria Eriksson, Umea University, Umea) and Switzerland (Wilhelm Gruissem, ETH, Zurich).

Due to the evolving needs of the scientific community and the increasing importance of management of very large data sets, the Bioinformatics MASC subcommittee played a central role at the MASC and NAASC Bioinformatics workshops. The first MASC Bioinformatics workshop was held in Nottingham, UK (15-16 April 2010) and the second took place in Washington DC, USA (10-11 May 2010). In addition, a Bioinformatics workshop organised by Nicholas Provart (Chair of Bioinformatics) and other members of MASC was held at ICAR 2010 in Yokohama, Japan, to report on the MASC Bioinformatics workshops and develop further discussions. Following these discussions the development of an International Arabidopsis Informatics Consortium (IAIC) envisaging a distributed model with a central portal funded by a variety of sources was proposed. This has been described in a Plant Cell publication (IAIC, (2010) An International Bioinformatics Infrastructure to Underpin the Arabidopsis Community. Plant Cell (22): 2530-2536) by workshop attendees. An IAIC page hosted at TAIR has been developed to inform the wider community of the current and future developments (www.arabidopsis.org/portals/masc/IAIC.jsp) of Arabidopsis bioinformatics and a workshop was held at the Plant and Animal Genomes Conference in San Diego, January 2011.

The Metabolomics subcommittee has launched a subcommittee website, and is assiduously participating to metabolomics-related meetings to promote a continuous dialogue

among subcommittee members and the wider community.

Members of the Natural Variation and Comparative Genomics have made great progress on the 1001 Genomes Project. It is expected that the goal of 1001 sequenced accessions will be surpassed in 2012.

Members of the Phenomics subcommittee continued to monitor the development of phenomics-based resources and were involved in a number of community events to promote international collaboration and outreach.

The MASC Proteomics subcommittee (MASCP) organized a workshop focused on protein phosphorylation on the 7th June at ICAR 2010, Yokohama, Japan.

The Systems Biology subcommittee set the aim to increase community action on standards and accessibility (of data, models and software tools), on training, and communicating to the public to build on the opportunities that this presents. Advancing these aims should promote a growing breadth and sophistication of Systems Biology approaches in Arabidopsis.

A full-time MASC Coordinator position, established in 2002, has been previously supported by the NSF (US) for 6 years and by DFG (Germany) for one year. The current Coordinator's position is UK-based and will be supported by BBSRC (UK) from 2009-2012. MASC webpages are hosted at TAIR (http://www.arabidopsis.org/portals/masc/index.jsp) and are regularly updated. 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 organisation 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 centres, and (5) maintaining and 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.

Scientific Highlights of the Past Year

Following a one year plateau, the annual number of publications involving Arabidopsis research has increased again. The number of peer-reviewed articles in 2010 in rice was slightly lower to that of Arabidopsis but appeared to follow the same trend. Evidencing the impact that Arabidopsis has had in the plant community and benefiting from the recently sequenced genomes, articles involving research on rice/oryza and corn/maize have also increased. 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 and the recently-developed artificial microRNAs; cDNA and ORF clones; large-scale microarray data; and 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 put forth by the many worldwide Arabidopsis research groups. 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.

As the global demand for food and renewable energy supplies increases, some governments are placing a greater emphasis on plant science research. In particular, food crop research with immediate applications is being encouraged. 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).

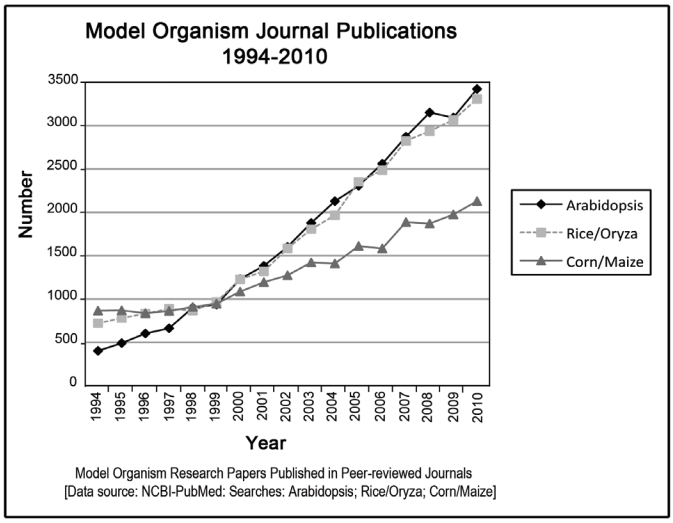

Figure 1: Model Organism Journal Publications (1994-2010)

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 the reference plant. Between 1994 and 2010, the number of peer-reviewed Arabidopsis publications increased 8.5-fold, while rice and corn publications increased about 4.6-fold and 2.5-fold, respectively (Figure 1). Over 3,400 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.

Host sweet host
By: Irene Lavagi, MASC Coordinator

Export of sugar from cells is key to many cellular processes across kingdoms, including maintenance of blood sugar levels in animals and sweetening of nectar in plants. Despite the crucial role of this process, the identity of the molecular players involved in glucose export has not been described until recently.

A family of sugar transporters, SWEETs, responsible for transporting sugar between cells in both plants and animals, has been recently described (1). Most importantly, pathogenic fungi and bacteria that exploit sugar from living plants have been shown to selectively target SWEETs. Pathogenic microorganisms are therefore able to manipulate the expression of sugar transporters and to divert the flow of glucose into the spaces between plant cells where the microorganisms can use this sugar as a souce of energy to rapidly grow and reproduce. This ability to divert a sugar for their own use may be pivotal to disease induction by microbes that proliferate in living host tissue.

The elegant experimental method used by Chen and co-workers employed a novel glucose nanosensor capable of measuring small changes in glucose concentration in living cells. *In silico* analysis of the Arabidopsis membrane protein database identified candidate sugar transporters, which were then expressed in cultured human embryonic kidney cells together with the nanosensor. The protein nanosensor was engineered for fluorescence resonance energy transfer (FRET) studies. Binding of the ligand glucose caused a conformational change in the protein that resulted in the emission of fluorescence proportional to the amount of glucose present. Therefore, a high level of glucose corresponded to a high level of fluorescence. Using this approach the AtSWEET1 protein in Arabidopsis was identified. AtSWEET1 is a novel type of glucose efflux transporter as it can transport sugar across plasma membranes or between subcellular compartments. Modelling studies predicted the 7 helices of SWEET proteins form a single pore for transporting sugar across the membrane. The Arabidopsis SWEET family comprises 17 members, whereas 21 are predicted in rice. The SWEET family also occurs in animals, with 7 members in nematodes and one in humans, suggesting a widespread role in sugar export both in animals and plants. The high levels of expression of *AtSWEET1* in Arabidopsis petals and stamens suggest that it is involved in supplying sugar to nectaries.

Analysis of *AtSWEET* transcript levels by qPCR and microarray data revealed that the expression of these genes is induced by inoculation with the bacterium *Pseudomonas syringae*, powdery mildew fungus *G. cichoracearum* and *Botrytis cinerea* in Arabidopsis leaves and that distinct sets of *AtSWEET* genes are induced by different pathogens.

Altering the activity of SWEET efflux transporters could therefore be a mechanism used by invading pathogens to divert glucose towards them. For example a mutation in the promoter sequence of *OsSWEET11* has been reported to confer resistance to the bacterium *Xanthomonas oryzae* (2). This mutation of the *OsSWEET11* promoter impedes its targeting and increased expression by the *Xanthomonas oryzae* transcriptional-activator-like (TAL) effector protein, PthXo1. Resistance to *Xanthomonas oryzae* is therefore acquired by blocking its ability to acquire sugar form the host plant. Similarly, *OsSWEET14*, another glucose-efflux transporter gene, is activated by another *X. oryzae* TAL effector, AvrXa7, indicating that the targeting of SWEETs is a common pathogenic mechanism.

The identification of SWEETs represents an important milestone both in plant and animal biology. In plants, this discovery opens up new exciting avenues of research for developing disease-control strategies. In animals, the identification of SWEET proteins gives the opportunity to study sugar efflux in physiological processes such as lactation and glucose homeostasis.

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(2) Yang,B Sugio, A, White FF (2006) Os8N3 is a host disease-susceptibility gene for bacterial blight of rice. Proc.NatlAcad.Sci.USA (103): 10503–10508

Arabidopsis-based technology to isolate cell type specific RNA
By: Irene Lavagi, MASC Coordinator

Multicellular organisms would not exist without the ability to produce specialized cell types that make up tissues and organs (e.g. liver cells in animals, roots in plants). These types of specialised cells are formed from progenitor/stem cells via the expression of specific set(s) of genes that define the cell in question. Such transcriptional programmes are often determined and maintained by epigenetic regulation such as gene silencing and histone modification.

Despite the importance of specialised cells types in the evolution of eukaryotes, little is known about how developmental programmes of cell lineages are defined. This is in part due to the difficulty in isolating single cell types for analysis.

A new approach developed by Steven Henikoff and Roger Deal addresses the requirement for abundant cell-type-specific RNA and chromatin from specific cell types. Their elegant strategy removes the need for physical separation and costly equipment. Instead nuclei from specific cell types are transgenically tagged and then separated out via affinity purification. Using a fusion protein system consisting of nuclear targeting sequence, GFP and biotin ligase recognition peptide (BLRP), which is the substrate used by *E.coli* biotin ligase (BirA) to generate biotin, biotinylated nuclei are generated and then isolated via the strong affinity between biotin and streptavidin. The system is known as INTACT, Isolation of Nuclei TAgged in specific Cell Types. The simplicity of the approach and methodology applied by Henikoff and Deal to tackle this problem will have a major impact on future developmental studies of single cells in plants and animals.

The authors chose *Arabidopsis thaliana* root epidermal hair and non-hair cell types as a model to develop and test their technique as a result of the wealth of available data at the genetic, cell biology and trancriptomal level on these two cell types.

Researchers introduced the fusion protein driven either by the *ACTIN DEPOLYMERIZING FACTOR 8* (*ADF8*) promoter (that is specific for hair cells) into one transgenic line of Arabidopsis, or driven by the *GLABRA2* (*GL2*) promoter specific for non-hair cells in another line. Each transgenic also contained BirA under the control of the constitutive *Actin 2* (*ACT2*) promoter giving rise to fluorescent nuclei in the hair cells of the ADF8 line and in the non hair cells of the GL2 line, which could be isolated via streptavidin purification.

Subsequent gene profiling of isolated hair and non-hair cells was performed to assess the efficiency of the newly established method and compare it with previously described methods. Microarray analysis identified 946 genes enriched in hair cells and 118 genes enriched in non-hair cells (a gene was defined as preferentially expressed in a given cell type if it showed >1.3 increase between cell types). In addition 19 out of 24 genes previously confirmed to be hair cell specific via reporter studies where found to be enriched in the isolated hair cells indicating that this technology was sufficient to identify most cell type specific genes. Interestingly, when compared to FACS only 20% of previously reported cell-type specific genes were found by INTACT. This finding may be due to the difference in purity of nuclei achieved with each of the methods. INTACT was shown to achieve a purity of 93% and 95% for hair and non hair cell type respectively, whereas the authors were unable to achieve a purity higher than 50% for hair and non –hair cell protoplasts by using FACS. It should also be noted that INTACT only isolated the nuclear RNA, whereas the total cellular RNA is isolated by FACS. Gene ontology (GO) analysis for each set of genes reinforced the gene profiling results, showing a strong correlation between function of the overexpressed genes and cell-type.

Chromatin profiling was also undertaken on the hair and non hair cell nuclei for the presence of the transcriptionally active associated histone modification of trimethylation of H3 lysine 4 (H3K4me3) and transcriptionally silent associated histone modification tri methylation of H3 lysine 27 (H3K27me3). The authors noted that the genes that exhibited the largest expression differences between hair and non-hair cells in expression profiling also showed differences between cell types in the trimethylation of H3K4me3 and H3K27me3. Chromatin differences between cell types can therefore easily be distinguished using this method, opening up many new avenues to chromatin analysis.

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Lessons from Arabidopsis lyrata on local adaptation

By: Irene Lavagi, MASC Coordinator

The discovery of the genetic and molecular basis of plant local adaptations will be crucial to ensure plant growth and future food production in a constantly changing environment.

One of the long-standing goals of plant biology has been to link the variations that can be observed in natural/wild populations to the underlying genotypic variation, with the aim of exploiting this variation to engineer beneficial traits into plants of agricultural and commercial importance. Arabidopsis has proven to be the most efficient plant model for the genetic analyses of natural variation because of the ease of manipulation, wealth of understanding of genetic and biochemical pathways and most importantly its abundance of natural variation.

A joint effort by researchers from the USA, Austria and the UK has led to the discovery of polymorphism in heavy metal detoxification and calcium and magnesium transport loci in *Arabidopsis lyrata* plants growing on serpentine soils (1).

Serpentine soils are characterized by low calcium to magnesium ratio, the lack of essential nutrients (i.e. nitrogen, potassium and phosphorus) and high concentrations of heavy metals. Plants growing on serpentine soils are typically tolerant of the extreme conditions imposed by the soil composition, making them an excellent model to identify alleles responsible for the molecular adaptations required to thrive in these soils.

In this study, an association of allele frequency with environmental conditions was performed. DNA pooled from individual *Arabidopsis lyrata* plants from US serpentine soils and nonserpentine soils was sequenced to identify the polymorphisms responsible for the adaptation of *Arabidopsis lyrata* to serpentine soil. Pooling DNA from natural populations provides an excellent measure to work out the frequencies of each polymorphism within a given population and between populations on a genome-wide scale. The team found that among the 8.4 million detected polymorphisms, 96 had allele differences of greater than 80% between soil types. Interestingly, the polymorphisms that were found to be most strongly associated with soil type were highest in heavy metal detoxification and calcium and magnesium transport loci, providing excellent candidates for serpentine adaptation. 12.5% of the metal ion transmembrane transporters were the most differentiated loci between soils in this study. For example, the *MRS2-2* gene contained the third most strongly soil-associated polymorphism in the genome, represented by a single base pair insertion and deletion (indel) in the 3' UTR. To add further scope to the study this locus was sequenced in a serpentine and non serpentine population of the Scottish subspecies of *A. lyrata*, *A. lyrata petraea*. Whilst a few of the polymorphisms identified in the US *A. lyrata* populations were also found in Scottish populations of *A. lyrata petraea*, four unique polymorphisms completely differentiated in serpentine and non serpentine soil populations were found in the Scottish populations. Among these were a SNP and 13-base pair indel in the 3'UTR of the *MRS2-2* locus. Other polymorphic sites were found to be strongly associated with soil type, as in the case of the pore domain of the voltage-gated calcium channel *Calcium channel 1* gene, but little differentiation at linked sites. At this locus the only linked polymorphism with a significant allele frequency difference between soil types was found to be a shared polymorphism with *Arabidopsis thaliana*. This polymorphism (a valine to glycine substitution) could be an old variant maintained by spatially varying selection between soils with different calcium content. In fact, in plants from the Scottish subspecies this locus showed that glycine was fixed in the serpentine population, whereas valine was fixed in the non serpentine population, supporting the hypothesis that this mutation is locally adaptive to serpentine soils.

A third locus, the intergenic region between the heavy metal detoxification genes *Metallothionein 1a* and *1c* displayed a clear difference depending on soil type in the US populations. However, in the Scottish populations this region did not display

the polymorphism found in the US populations differentiating soil type. Nevertheless, other polymorphisms were found in this region of the genome of the Scottish *A. lyrata* populations.

Overall, this study showed that sequencing three candidate loci in the European populations of *A. lyrata* indicated parallel differentiation of the same polymorphism at one locus, confirming ecological adaptation, and different polymorphisms at two other loci, indicating convergent evolution.

The availability of next generation sequencing is increasingly allowing researchers to study allele frequency across the genome. By combining this data with functional knowledge of loci/gene annotation it is now feasible for plant researchers to study the basis of adaption alongside the effects of environmental conditions. By combining the power of emerging technologies with the extensive knowledge base that has been built up in previous decades, the Arabidopsis community is perfectly poised to lead the way in the utilization of natural variation to understand how sequence variation affects biological and evolutionary processes.

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Jasmonate signaling: Is NINJA the missing link?

By: Irene Lavagi, MASC Coordinator

A new player of the jasmonate signaling pathway has been recently identified (1). Jasmonates (JAs) are plant hormones that regulate diverse processes in plants, including response to wounding and pathogens, pollen development and root growth. Jasmonates are derived from fatty acids, biosynthesized from linolenic acid. Jasmonates include jasmonic acid and its esters such as methyl jasmonate (MeJa), originally isolated from the jasmine oil of *Jasminum grandiflorum*, which led to the discovery of the molecular structure of jasmonates. The level of JA in plants varies depending on tissue function, cell type, developmental stage, and as a response to several different environmental stimuli. High levels of JA are found in flowers and pericarp tissues of developing reproductive structures and in the chloroplasts of illuminated plants; JA levels also increase rapidly in response to mechanical perturbations such as tendril coiling and in response to wounding.

In the absence of the endogenous bioactive hormone JA-Ile, the transcriptional repressor protein JAZ1 binds and inactivates MYC2 (a transcriptional activator of jasmonate response genes). Whilst in the presence of JA-Ile, the JAZ1 protein is degraded by the proteasome via the E3 ubiquitin ligase CORONATINE INSENSITIVE 1 (COI1). Degradation of JAZ1 relieves the transcriptional repression on MYC2 allowing it to activate expression of jasmonate response genes and induce the jasmonate signaling pathway.

Tandem affinity purification (TAP) tagged JAZ1 was expressed in Arabidopsis cells in the presence or absence of JA-Ile. In addition to the proteins that had previously been identified as candidate interactors of JAZ1, a novel protein, NINJA, was identified. Interestingly NINJA is related to the ABI-FIVE BINDING PROTEIN (AFP) family. Abscisic acid induces the expression of AFP genes in Arabidopsis seedlings, whereas MeJA induces the expression of NINJA.

A yeast-2-hybrid assay using JAZ2 and JAZ3 as baits identified NINJA as a direct interactor. NINJA was found to interact with most other JAZ proteins but did not interact with members of the AFP family, showing specificity of the JAZ interaction for NINJA. JAZ proteins have a TIFY motif and a C-terminus conserved "Jas" domain, the latter interacts with COI1 and MYC2. A yeast-2-hybrid screen with a deletion series of the JAZ1 protein as bait, showed that the TIFY motif is essential for NINJA binding to JAZ1. A similar experiment with deletion series of NINJA showed that the C-domain is necessary and sufficient for JAZ protein interaction and that a 39 amino acid fragment within the JAZ TIFY motif interacts with the C-domain of NINJA.

Overexpression and knockdown of NINJA by RNAi suggested that NINJA acts as a negative regulator of jasmonate signaling; NINJA overexpression significantly decreased JA sensitivity, observed as an impaired inhibition of root growth, whereas microarray analysis of NINJA RNAi lines showed an increased expression of many known early jasmonate-responsive genes even in the absence of JA, indicating a derepressed response.

TAP experiments using NINJA as a bait found NINJA in complex with TOPLESS (TPL) and its homologues TPR2 and TPR3 independently of JA elicitation. TPL interacts with the N-terminal EAR motif of AUX/IAA protein IAAI2 and the EAR motif is found is most AUX/IAA proteins. Yeast-2-hybrid and fluorescence based complementation experiments showed that the EAR motif of NINJA mediates the NINJA-TPL interaction. Indeed, if the EAR motif of NINJA is deleted NINJA cannot interact with TPL. A similar effect is achieved when mutating the conserved Leu into Ala in the EAR motif. The EAR domain is sufficient for NINJA interaction with TPL. Phenotypic analysis of *tpl-1* mutants revealed hypersensisetivity to JA, supporting the idea that NINJA connects JAZ proteins with TPL co- repressors.

Although parallels between the auxin and jasmonate pathways have become recently apparent, for example FBox targeted proteasome degradation, this study highlights the difference between the two pathways; the EAR motif in the jasmonate pathway exists as separate protein (NINJA) rather than being part of the proteasome targeted repressor as observed in the auxin pathway. The presence of this additional subunit may allow cross talk with other signaling pathways and fine-tuning of the jasmonate response.

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MicroRNA communicates across cells to control root development

By: Irene Lavagi, MASC Coordinator

A key question in developmental biology is how cells exchange positional information to achieve tissue specification and differentiation and thereby proper patterning during organ development. Plant roots display a highly conserved radial tissue organization with a central vascular cylinder in which two water conducting cell types, protoxylem and metaxylem, form from xylem precursors and are arranged in a circular pattern around

the centre, centripetally. The strong evolutionary conservation of xylem patterning across plant species suggests the presence of common molecular mechanisms that constrain its organization.

An international team of scientists recently discovered the mechanism that orchestrates the radial patterning in the root, which involves the movement of microRNAs across cells (1). The transcription factors SHORT ROOT (SHR) and SCARECROW (SCR) are central to the specification of cell types in root. SHR is normally produced in the vascular cylinder and moves into the endodermis to activate SCR. In *shr* and *scr* mutants the asymmetric cell divisions that form the endodermis, and cortex, do not occour and the quiescent centre (that provides the root stem cells) is not maintained causing these mutants to have short roots with only one ground tissue layer. In addition the metaxylem in *shr* and *scr* mutants differentiates ectopically in the place of protoxylem indicating that *shr* and *scr* affect stele development in a non-cell autonomous manner. To understand whether SHR and SCR activities are required for xylem patterning, they were individually expressed exclusively in the stele or in the ground tissue of *shr scr* mutants. The observations indicated that the presence in endodermis of both SHR and SCR is required for xylem patterning. Together these transcription factors activate MIR165a and MIR166b. Endodermally produced microRNA165/6 then acts to degrade its target mRNAs encoding class III homeodomain-leucine zipper (HD-ZIPIII) transcription factors in the endodermis and stele periphery. The resulting differential distribution of target mRNA in the vascular cylinder determines xylem cell types in a dosage-dependent manner.

In a screen for altered vascular development in *Arabidopsis thaliana*, a mutant showing similar phenotypes to *shr*, short root and frequent differentiation of metaxylem in place of protoxylem was identified. This mutant was found to be a point mutation in the miRNA165/6 target site in HD-ZIPIII PHABULOSA (PHB). This gain of function mutant form of *PHB* is resistant to mRNA degradation. RNA *in situ* hybridazation in wild type showed that PHB localizes primarily to the metaxylem precursors, whereas the mRNA of mutant *phb* was found to expand throughout and outside the stele. These findings indicated that miR165/6 post transcriptionally restricts PHB within the root meristem to the stele centre for proper xylem patterning and SHR regulates this process by promoting miR165/6 activity in the stele periphery and endodermis.

This study originally conducted in Arabidopsis showed that microRNA operate across cells as well as within cells and this is very likely to have implications for many areas of biology. For example this work is likely to have implications in the medical sphere, as a number of cancers are linked to the over proliferations of cells that have escaped their normal developmental programme (ontogeny). It may therefore be possible to use microRNA communication between cells to repress genes that have become overactive.

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Are Casparian strips the plant's tight junctions?

By: Irene Lavagi, MASC Coordinator

In animal systems extracellular structures known as tight junctions, which hold together the closely associated areas of two cells via their membranes, have been known about for a long time. Tight junctions act as the glue that holds cells together and form diffusion barriers that enable the maintenance of polarity, thus playing a vital role in an organism's physiology and development.

Recent work in Arabidopsis roots showed that Casparian strips play a similar role to the tight junctions in animals (1). Casparian strips are localized cell wall depositions that surround the cell like a belt sealing the extracellular space. Casparian strips are found in the endodermis, which in a plant root is the cell layer found between the cortex, the outer layer in contact with soil, and the stele, the central part of the root. The endodermis performs a key role in creating a diffusion barrier between the extracellular space of root cortex, soil, and the vascular system, which connects the root to other organs. Therefore two opposite sides of the endodermis plasma membrane face two separate compartments, the cortex and the stele, which in turn perform different nutrient transport functions, nutrient uptake and nutrient load respectively.

The development mechanisms that regulate tissue specification of the endodermis are known to involve the SHR transcription factor. However, the timing of the initial specification and the mechanisms that translate it into differentiated endodermis remained undiscovered until now.

Recent work performed by Niko Geldner and collaborators established molecular markers for the analysis of endodermal polarity and the Casparian strip formation in Arabidopsis. A quantitative imaging analysis assay to describe the development sequence of events leading to a differentiated endodermal cell was set up. In these assays the timing of differentiation events were counted as the number of cells after onset of elongation. The team showed that the endodermal polarity present in meristems, is established early in embryogenesis and is independent of the Casparian strip domain, the plasma membrane domain underlying the Casparian strip. The establishment of the apoplastic diffusion barrier between the cortex and the vascular cylinder is a key feature of endodermal function. Studies involving the fluorescent apoplastic marker propidium iodide showed that the apoplastic barrier is established when xylem vessels start to appear, at 14.4 cells after onset of elongation, as the marker only penetrates in the outer half of the endodermis after this time. Similarly, penetration of the lipid tracer FM4-64 only occurs up to the presumptive position of the Casparian strip domain, indicating the absence of lateral diffusion into the stele-facing plasma membrane domain of the endodermis. Observations of the autofluorescence of the Casparian strip, composed of suberin and lignin-like compounds, showed that the first localized cell wall deposition occurred at 11.7 cells, coinciding with membrane attachment and preceding the apoplastic barrier, suggesting that the Casparian strip plays a role in membrane adhesion like tight junctions do in animal cells.

Since the inner (stele-facing) and outer (cortex-facing) plasma membranes of the endodermis perform different functions in nutrient transport, the group investigated whether the distribution of nutrient transporters in the endodermis is localized. Two boron transporters, NIP5;1 and BOR1, displayed a clear polar localization

to inner and outer domains of the plasma membrane, reflecting their function in uptake and xylem loading respectively. Interestingly, it was observed that although less restricted, this polar distribution of boron transporters is also present in meristematic proendodermal cells and in the quiescent centre, indicating that the Casparian strip is not necessary for the establishment of polarity, but rather to refine and separate already existing partially overlapping polar domains. It is possible that the polarity of these boron transporters does not follow global coordinates but rather orientate toward or away from the centre of the root. Indeed, signals from the stele may act as polarizing cues for more peripheral tissue. Experiments on cellular trafficking confirmed that the polarity of boron transporters is achieved via a mechanism that differs from that used by PIN proteins.

In addition to revealing that endodermal cells of the meristem are able to define three different polar distributions of plasma membrane proteins, towards the centre (stele), toward the periphery (cortex) and toward the base of the plant, this work provides the first line of evidence for a strict diffusion block between polar domains in plants. Although further studies on endodermal transporter polarity will greatly increase our understanding of plant nutrition and stress tolerance in roots, this work provides an excellent basis on which to move forward.

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Beware, it's a mimic: put the protein down!

By: Irene Lavagi, MASC Coordinator

MicroRNAs (miRNAs) are a class of small RNA (sRNA) molecules that are key regulators of gene activity. In plants, many targets of miRNAs are thought to have significant roles in plant physiology and development.

In plants, miRNAs are derived from larger precursors (pri-mRNAs), a cutting process carried out by DICER-LIKE1 (DCL1) which occurs predominantly in the nucleus. The sRNA duplex is methylated and translocated to the cytoplasm where it docks with an RNA-induced silencing complex (RISC) and a catalytic component from the ARGONAUTE (AGO) family. RISC recognises mRNAs with sequences complementary to the miRNA.

Spatio-temporal expression patterns of miRNAs are largely regulated at the transcriptional level, and different members of a miRNA family can have distinct, specialised expression domains. In addition a further regulatory mechanism was discovered to be involved in the phosphate starvation response. *Induced by phosphate starvation 1* (*IPS1*) encodes a non-coding RNA with a short motif highly complementary to miR399 (Franco-Zorrilla *et al*., 2007 (1)), which is also involved in phosphate starvation. *IPS1* has a three-nucleotide insertion enabling it to act as a target mimic to miR399, thus preventing normal miRNA guided cleavage taking place, which in turn leads to sequestration of RISCmi399 and reduced miR399 activity.

It has often been difficult to assess miRNA function as plant miRNAs are typically encoded by medium-size gene families. However, with the aid of artificial miRNA target mimics, based on the example of endogenous mimicry mechanism highlighted above, it has been possible to generate a large scale collection of knockdowns for Arabidopsis miRNA families. Studies of this collection of knock downs show that extremely conserved miRNAs tend to have a strong impact on growth. In several cases plants expressing target mimics directed against miRNAs involved in development gave rise to phentoypes consistent with previous reports using plants expressing miRNA-resistant forms of individual target genes. Interestingly the less conserved miRNAs rarely give rise to obvious effects on plant morphology which in turn indicates that most do not affect key aspects of development or are even dispensable. The work from Todesco *et al*., 2010 (2) provides insights into the modes of miRNA action as well as providing a toolkit for other researchers; the collection of artificial target mimics generated in this research is available from NASC and ABRC.

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Whole genome sequencing to identify mutations

By: Irene Lavagi, MASC Coordinator

Short read sequencing technologies are being exploited for rapid mapping and identification of both spontaneous and chemically induced mutations in the Arabidopsis reference genome Col-0.

Recent work by the Weigel group has demonstrated that the short read sequencing technologies can be utilised for the analysis of new mutations in a nonreference inbred accession that differs from the reference genome in approximately 0.5% of all positions (1). The utilisation of this technology led to the development of the SHOREmap pipeline, which supports the mapping of mutations after sequencing bulked segregates along with the identification of newly induced mutations in the mapping interval (2). For example, the F2 populations of the two Arabidopsis accessions, Krotzenburg and Anholt, were small purplish, non flowering plants. Conventional mapping identified a 530 kb interval linked to the dwarf phenotype.

With the aid of short-read sequencing in addition to other data sets detailed in Laitinen *et al*., 2010 (1) the group were able to identify the responsible 1bp deletion in the seventh exon of At1g58440. The phenotype of their F2 cross of Krotzenburg and Anholt matched that of a T-DNA insertion knockout in Col-0. The study provides the proof of concept for the identification of mutations in a background other than a reference genome using direct whole genome sequencing.

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Community Arabidopsis Projects and Resources

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

By: Eva Huala, TAIR Director

TAIR usage statistics:

Usage of TAIR continued to increase in 2010, with an average of 43,000 unique visitors to the TAIR website each month, an increase of 14% over the number of visitors in 2009. The number of registered TAIR users also continued to grow: as of May 10, 2011 there were 21,771 registered TAIR users (including 9378 that have been added or updated in the past 5 years) and 8465 labs (including 4866 that have been added or updated in the past 5 years).

Curation of gene function data:

Gene function annotations added to TAIR in the past year were based on experimental results reported in 558 published research articles, representing 30% of all articles with curatable data published during this period. These annotations were generated in part by TAIR's in-house article curation efforts and in part from TAIR's collaboration with several of the top journals publishing plant biology research articles (see Journal Collaboration section below). To maximize the impact of our limited curation resources, articles describing the function of previously uncharacterized genes were given highest priority in our internal curation pipeline. As a result of the combined efforts of TAIR curators and community data submitters, in the past year TAIR has added 3584 new gene function annotations based on experimental data to 1796 Arabidopsis genes. Of these, 639 genes had no previous annotations based on experimental data. As of March 22, 2011 a total of 9663 Arabidopsis genes have been annotated with Gene Ontology terms based on direct experimental data. If experimental data on gene expression patterns is also included, 20,574 genes (71% of all TAIR10 genes excluding transposon genes and pseudogenes) now have experimental annotations in TAIR.

TAIR Journal Collaboration Program

TAIR's ongoing journal collaboration program aims to gather Arabidopsis gene function data, including subcellular localization and interaction partners as well as biological process and molecular function, directly from authors whose articles have just been accepted for publication. The program was launched in early 2008 with the journal Plant Physiology and recently expanded to include a total of 11 journals:

Journals included in TAIR Program	Publisher	Collaboration Start Date
Plant Physiology	ASPB	2/2008
The Plant Journal	Wiley-Blackwell	8/2009
Plant, Cell and Environment	Wiley-Blackwell	7/2010
Journal of Integrative Plant Biology	Wiley-Blackwell	7/2010
Plant Science	Elsevier	7/2010
Environmental Botany	Elsevier	7/2010
Plant Physiology and Biochemistry	Elsevier	7/2010
Journal of Experimental Botany	Elsevier	8/2010
Plant Cell	ASPB	9/2010
Molecular Plant	Oxford Journals	9/2010
Frontiers in Plant Genetics and Genomics	Frontiers	pending

Since the start of the program in early 2008 TAIR has received author data submissions for 204 Plant Physiology articles and 73 articles in other journals. A new interactive web form for community gene function data submission was released in May 2010. To access the form, click on the TAIR 'Submit' menu and choose "Online Submission for Authors and Others" or go directly to http://arabidopsis.org/doc/submit/ functional_annotation/123. An improved pipeline for reviewing and loading community annotations has also been developed, allowing TAIR to efficiently process submissions made through the new interface.

Curation of gene structures and genome assembly:

The most recent genome release, TAIR10, was made public on November 17, 2010. The TAIR10 release builds upon the gene structures of the previous TAIR9 release, drawing mainly on RNA-seq and proteomics datasets to improve Arabidopsis gene structures. As with previous releases we also incorporated missing genes and made corrections to gene structures based on experimental evidence provided directly to us by researchers. The TAIR10 release contains 27,416 protein coding genes, 924 pseudogenes, 3903 transposable element genes and 1359 ncRNAs (33,602 genes in all, 41,671 gene models). A total of 126 new loci and 2099 new gene models were added. A full description of the TAIR10 release can be found on the TAIR Genome Snapshot page (http://arabidopsis.org/portals/ genAnnotation/ genome_snapshot.jsp) or on the TAIR news page (http://arabidopsis.org/doc/news/ breaking_news/140). Genome release files can be downloaded from ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR10_genome_release/. No changes to the underlying assembly were made for TAIR10.

TAIR funding and new TAIR Sponsorship program:

TAIR is in the second year of its current four year funding period (Sept 1 2009 – Aug 31 2013). Although we originally planned to phase out TAIR's literature curation effort by September 2010 due to the steep funding cuts in our current budget, we have been able to extend it with funding from the new TAIR sponsorship program. Five companies, including Syngenta, Dow Agro, Monsanto, GrassRoots Biotechnology, Pioneer Hi-Bred and one research institution, the Gregor Mendel Institute in Vienna, have become TAIR sponsors. We are extremely grateful for the support of our sponsors and we hope that additional companies and research institutions will consider following their example to ensure that TAIR will be able to continue to add new Arabidopsis gene structure and function data over the next couple of years while a longer term funding solution is worked out. Please see http://arabidopsis.org/doc/about/ tair_sponsorship/412 for information on how to join the program and http://arabidopsis.org/ doc/about/tair_sponsors/413 for a list of our current sponsors.

The Arabidopsis Biological Resource Center (ABRC, http://abrc.osu.edu/)

By: Erich Grotewold, ABRC Director and Jelena Brkljacic

The Arabidopsis Biological Resource Center (ABRC) continues to acquire, maintain, propagate and distribute various resources of Arabidopsis and related species for research and teaching. The current collection is comprised of almost one million accessions. The existing ABRC seed stock holdings include insertion lines covering 28,397 genes (24,561 protein coding genes); the 11,000+ lines of the Arabidopsis TILLING service; 1,400 distinct natural accessions, some of which are grouped into "core 360" set representing genetically fingerprinted variants, the Weigel set of 80 and the Ecker set of 200 accessions, sequenced by the 1001 Genomes Project; 29 recombinant inbred populations; a set of near-isogenic lines; new GABI-Kat T-DNA lines; new mutation accumulation lines from R. Shaw; RNAi lines; transgenic lines; 50+ accessions of the genus Brassica; and approximately 70 accessions of other closely related species, including several recently sequenced accessions (e.g. *Thellungiella halophila*, *Arabidopsis lyrata* and *Capsella rubella*). 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. The collection has expanded recently to include T87 cell culture and protein resources. Education resources represent our newest addition to the collection and include seeds, DNA and written materials. A number of these are suitable for K-12 classes and some represent education resources developed at ABRC, the details of which can be found at the ABRC Education website (abrc.osu.edu/Education.html). The distribution of all resources combined reached almost 90,000 samples in 2010.

As a result of previous, successfully conducted, donation campaigns, our collection of characterized mutant and transgenic lines has increased to almost 4,000. This core collection represents one of the most valuable and highly utilized seed resources. Both types of resources will remain a top priority for our next donation campaign. In addition, we will primarily seek donations of seed resources targeting loci for which no resources are available. We are also currently seeking high-value Brassica genetic resources, including segregating populations for molecular marker analysis, BAC and EST clones and libraries etc. Donations of other seed stocks as well as clones continue to be welcome.

ABRC continues to focus on functional genomics. The J. Ecker laboratory (Salk Institute, http://signal.salk.edu/gabout.html) is genetically purifying to homozygosity two T-DNA insertion knockout lines for each of the 24,500 protein-coding genes in Arabidopsis genome. To date, 42,315 of these lines have been received. The stocks being utilized for this project include the J. Ecker (SALK) population, plus lines from Syngenta (SAIL), B. Weisshaar (GABI-Kat) and P. Krysan/R. Amasino/M. Sussman (Wisconsin Ds-Lox). So far 36,058 lines have been made available and are ready for distribution. The majority of confirmed lines have been grouped into sets for forward screening, the third installment of which was made available during 2010. Receipt and distribution of Entry and Expression full length/ORFeome clones remain a priority. ORF clones lacking a stop codon continue to be received from members of the Arabidopsis Membrane Interactome Project, with 2,706 received to date, and from The AGRON-OMICS Consortium, with 620 received this year. Expression ORF collections have been received from various donors, with 28,550 of these currently in-house. This includes 12,069 HaloTag® (Promega) clones designed for expression in wheat germ lysate or rabbit reticulocyte systems. ABRC also received in 2010 3,649 amiRNA clones targeting gene families. We are pleased to report that 14,941 loci are now represented by clones in a GatewayTM entry vector, and 12,266 by clones in the pUNI51 vector. More than 10,000 different loci are represented by a clone in both a GatewayTM entry vector and the pUNI51 vector.

Twenty years after it was established, ABRC continues to be strongly supported by the NSF. The most recent renewal of the grant secured ~$1.8 million for the Center. Combined with strong community support, this guarantees the financial sustainability of the ABRC for the next five years.

The Nottingham Arabidopsis Stock Centre (NASC, http://arabidopsis.org.uk)

By: Sean May, NASC Director, Zoe Phillips & Marcos Castellanos Uribe.

By the time this article is published NASC will already have seen its 21st birthday; have passed the 130,000 stocks sent per annum point for this sending year; and will be nearing the curation of our one millionth stock. That said, donations of new seed stocks as well as clones continue to be very welcome and this year we have seen the expansion of both existing populations and new high value stocks (please see our web pages for specific details and ordering instructions).

Since our last MASC report we have happily received continuation funding from the UK's Biotechnology and Biological Sciences Research Council (BBSRC) for NASC's stock catalogue, resource databases and bioinformatics services despite the current economic environment (for which we are very grateful and relieved). This year we will be asking for a five-year continuation of our physical seed handling resources to complement our successful cost recovery structures.

For yet another year, the distribution figures have increased for physical resources (seed distribution has doubled since 2009/2010 which is the largest single jump in our history); and our Affymetrix throughput has increased once again to over 1,000 chips per annum. As always, all Arabidopsis GeneChip data is made public within a short period from hybridisation and we now have arrangements with the brassica, brachypodium and tobacco communities to perform the same public oriented service with GeneChips for those species.

As part of the current bioinformatics grant, we have committed to reducing costs for Arabidopsis and Human GeneChip users whilst increasing throughput. We have therefore acquired an ultra-high-throughput GeneTitan system from Affymetrix and are assisting them in developing a new, cheaper Arabidopsis GeneChip based on TAIR10 with superior gene coverage and whole transcript, multi-exon capabilities. This should be available during the second half of 2011 for £250 (~$400) including all consumables and will enable processing of up to 96 chips simultaneously - please see http://affy.arabidopsis.info.

RIKEN BioResource Center
(RIKEN BRC, www.brc.riken.jp/lab/epd/Eng/) and National BioResource Project of Japan (NBRP, www.nbrp.jp/index.jsp)

By: Masatomo Kobayashi, RIKEN BRC Coordinator

RIKEN BioResource Center (RIKEN BRC) promotes resource projects on experimental animal (mouse), experimental plant, mammal cells and DNA (including human origin), and microbes. The experimental Plant Division collects, preserves and distributes seed, DNA material and cultured cell of Arabidopsis and other model plants. Seed stocks of Arabidopsis include transposon-tagged lines (RATM line; insertion site information available; 15,000+), activation(T-DNA)-tagged lines (for phenotype screening; 36,000+), FOX lines (Arabidopsis plants that over-express Arabidopsis full-length cDNA; for phenotype screening; 6,000), natural accessions (SASSC stock) and individual mutants and transgenic lines generated in Japan. In addition, homozygous insertion has been confirmed for 2,700 transposon-tagged lines that are available from RIKEN BRC. The DNA resource includes full-length cDNA clones from various plant species such as Arabidopsis (RAFL clone; 250,000+), *Physcomitrella patens* (140,000+), poplar (20,000+), cassava (19,000+), tobacco (3,000+) and *Thellungiella halophila* (19,000+). The plant cultured cell resource includes well-known cell lines such as Tobacco BY-2 and Arabidopsis T87. The total number of plant resources in RIKEN BRC exceeds half a million and we have provided plant materials to 1,441 laboratories across the globe (up to the end of January 2011).

In 2011, RIKEN BRC will start distributing Rice FOX lines (Arabidopsis plants that over-express rice full-length cDNA) for screening. Full-length cDNA clones of Chinese cabbage and ORF clones of Arabidopsis transcription factors will be available by the end of 2011.

Quality control of resources is one of the most important tasks of resource centers. Before shipment from RIKEN BRC, we examine the quality of resources by characterizing insertion site (for transposon-tagged line) or end-sequence (for full-length cDNA clone). Arabidopsis T87 cells are maintained with the conditions originally used by the developer to prevent any change in their character. Cryopreservation technology is going to be applied for long term storage of the cell lines. RIKEN BRC has opened SABRE (Systematic consolidation of Arabidopsis and other Botanical REsource) database for providing organized information about plant resources of RIKEN BRC. In SABRE, most of the cDNA resources preserved in RIKEN BRC are linked with Arabidopsis genes by the similarity of nucleotide/deduced amino acid sequences. (http://saber.epd.brc.riken.jp/sabre/SABRE0101.cgi) Prompt response is another important feature of RIKEN BRC. Most DNA resources are shipped within a few weeks from the arrival of order, while preparation of shipment for insertion mutant usually takes three to four weeks. RIKEN BRC has distributed 36,910 materials since 2002. The destination of the materials extends to 1,441 laboratories in 41 countries including Japan.

RIKEN BRC participates in the National BioResource Project (NBRP) which is conducted by Japanese government. NBRP covers mammal and plant resources as well as microbes, and the total number of materials preserved by NBRP is 5.6 million. The plant resources within NBRP include Arabidopsis, rice, wheat, barley, Lotus/Glycine, tomato, morning glory, Chrysanthemum and algae. Distribution of each resource requires acceptance of a MTA and payment of handling and shipping fee.

Broader Impacts of Arabidopsis Research

Impacts on Industry

Arabidopsis research has increasingly impacted the study of other plants. The knowledge gained from this reference plant serves to advance our understanding of other plant species, particularly 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, many of which take place within private companies. This division of labour between the public and private sector is successful due to their complementary approaches; publicly funded basic research, typically performed in universities, benefits from relative freedom to explore a broad range of hypotheses and to develop novel tools and approaches. This curiosity-driven approach facilitates discoveries that can be leveraged by private companies whose research programs are more focused on applications with commercial value. In this system, basic research thrives on open exchange of information and resources while private companies are structured to maintain confidentiality. Companies commonly make their findings publicly known only during later stages of the commercialization process and such disclosures may contain few details unless they are conveyed through peer-reviewed publications. This presents a predicament to Arabidopsis research supporters who want to understand the usefulness of basic research to commercial applications. Compounding challenges include the relatively long time from discovery to application and the pervasive reality that commercial products are often not explicitly defined by the contributions derived from Arabidopsis studies.

When evaluating the success of Arabidopsis as a means of advancing applied research, it is important to keep the realities of public vs. private research and relatively long timeframe from discovery to product in mind. Similarly, it can take a bit of sleuthing to uncover the ways in which Arabidopsis research plays important roles in the success of commercial products, or any research project that in the end, focuses on another species. Importantly, while the recent advances in Arabidopsis research have been phenomenal, it is worth remembering that it is still a fairly new model organism. According to the National Center for Biotechnology Information (1), 25 years ago there were 263 and 465 publications citing rice or corn, respectively, but only 5 citing Arabidopsis. Similarly, the US Patent and Trade Office (2) listed 545 patents referencing rice and 1,491 referencing corn at that time. In comparison, the first U.S. utility patent referencing Arabidopsis was filed in 1989, six years later.

An indication of what we might expect from translating basic Arabidopsis research into crop species and commercial products in the next decade is informed by the rapid increase in publication rate and patent filing in the last 15 years, the timeframe in which Arabidopsis became established among other classic model organisms such as rice and corn. Between 1994 and 2010, the number of peer-reviewed Arabidopsis publications increased by 8.5-fold, while rice and corn publications increased roughly 4.6-fold and 2.5-fold, respectively (Fig. 1, page 11). In that same timeframe, while the number of U.S. patents referencing rice and corn increased 3 and 2.6 fold respectively, the number of patents citing Arabidopsis increased almost 50-fold (Figure 2, Page 20).

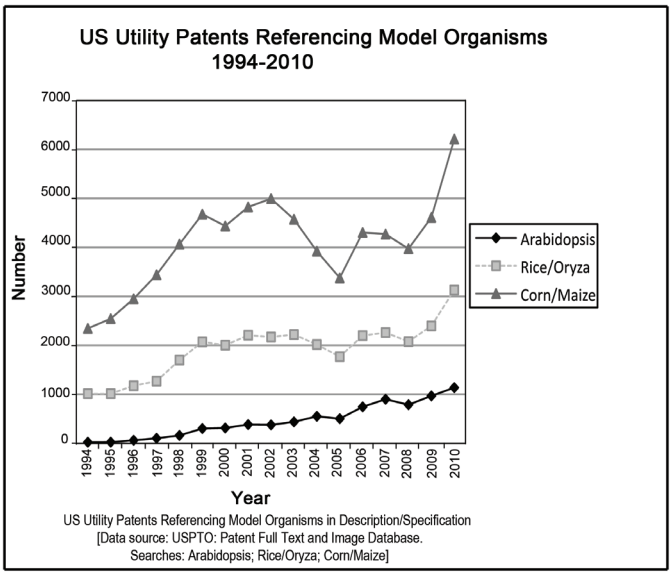

Figure 2: US Utility Patents Referncing Model Organisms 1994-2009

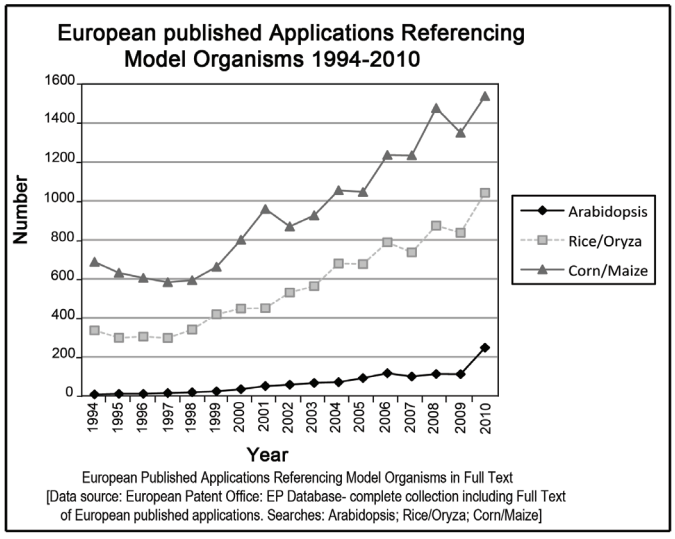

Figure 3: European published Applications Referencing Model Organisms 1994-2010

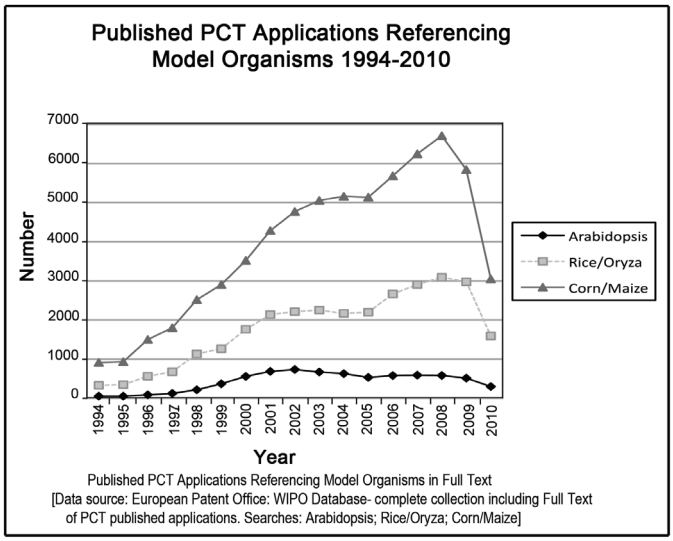

Figure 4: Published PCT Applications Referencing Model Organisms 1994-2010

The number of European and world's published applications also increased in the period between 1994 and 2010. Interestingly, a 35-fold increased was registered for European published applications referencing Arabidopsis, whereas a 3 and a 2.2 fold increase occurred for rice and corn respectively. From a world's perspective (or PCT perspective), published applications referencing Arabidopsis increased by 5.6-fold, whereas rice and corn registered a 4.8- and 3.3 fold increase respectively. The absolute number of patents citing rice and corn exceed those citing Arabidopsis. This reflects how access to a reference sequence enables both applied and basic research and illustrates how strong funding of Arabidopsis as a model organism by numerous funding bodies has been central to developing Arabidopsis as a reference for plant biology, and for leveraging the knowledge gained in Arabidopsis for studies in other plant species. It is also interesting to note that European published Applications referencing Arabidopsis, rice and corn followed the same increasing trend, whilst the published PCT applications followed the same decreasing trend in 2010, perhaps reflecting that most patents are filed for the USA and Europe.

Explanation of patent searches

The European Patent Office database esp@cenet (3) currently allows the searching of three databases to gather information on the existing patents across the world: 1) EP-complete collection including full text of European published applications 2) Worldwide- full collection of worldwide published applications from 80+ countries 3) WIPO complete collection including full text of PCT published applications. In the U.S. the correct term for a patent is 'utility patent', whereas in Europe they are referred to as 'published applications'. Most of the world's countries are signatories to the Patent Cooperation Treaty (PCT). The PCT is an international patent law treaty (London, 1970) that provides a unified procedure for filing patent applications and protects inventions in each of its contracting states. As of January 2011, there were 142 contracting states to the PCT. A patent application filed under the PCT is called an international application, or a PCT application. The number of European published applications (i.e. patents) and PCT published applications referencing model organisms have been included, searching for the keyword of interest in the full-text option, as it corresponds more closely to the US Description/Specification field (Figure 3 and 4).

(1) http://www.ncbi.nlm.nih.gov/sites/entrez?db=PubMed
(2) http://patft.uspto.gov/netahtml/PTO/search-adv.htm
(3) http://ep.espacenet.com:80/advancedSearch?locale=en_EP

Examples of Translation Research Using Arabidopsis

The importance of basic Arabidopsis research cannot be understated and it is clearly an invaluable reference to applied research efforts. The upcoming decade will likely yield a number of commercial advances based on Arabidopsis studies. In this report, we have chosen just a few recent examples of discoveries that demonstrate the importance of basic Arabidopsis research to applied research, and how knowledge gained in this reference organism can be translated into real-world applications.

Biofuels: A sweet solution from wood
By: Irene Lavagi, MASC Coordinator

In response to an increasing and wealthier world population, cheaper and renewable energy sources need to be found. The availability of the energy sources that we currently use most, oil, is decreasing and will not be sufficient to sustain us in the future. The production of greener energy from plants, and in particular from non-food crops, would allow a reduction in the use of fossil fuels and contribute to minimizing the competition between land for food and fuel. One of the current challenges in the production of biofuels is the extraction of sugars from plants in an economically sustainable manner. The complex and interwoven nature of the plant cell wall polysaccharides make it hard to release sugars that could be subsequently fermented into biofuel. In a recent study in Arabidopsis a simpler and more easily extractable version of plant sugars was created (1), which could help overcome this problem.

In wood tissue, vast amounts of energy are stored in the form of lignocellulose, which provides plant strength and rigidity. Lignocellulose is mainly composed of xylan, a polysaccharide with a long thin and complex structure composed of a linear β(1,4)-linked backbone of xylosyl residues substituted by glucuronic acid, 4-O-methylglucuronic acid or arabinose depending on the plant species and cell types. These decorations have major influences on the properties of the polysaccharide. For example, xylan in wood and straw could account for up to a third of the available sugar for bioethanol production, but the current problem in extracting this sugar limits the release of energy from lignocellulose and the production of fuels from non food crops.

Researchers at the University of Cambridge, UK, have discovered two key Golgi-localized glycosyltransferases. GlucUronic acid substitution of xylan (GUX)-1 and GUX2 are required for the addition of both glucuronic acid and 4-O-methylglucuronic acid branches to xylan in Arabidopsis stem cell walls. T-DNA insertions in the *GUX1* and *2* loci were used to generate single and double mutant lines. The single *gux1* and *2* mutants both exhibited loss of xylan

glucoronyltransferase and reduced acid substitution of the xylan backbone, whilst the double mutant (*gux1 gux2*) showed undetectable xylan substitution. Xylan from double mutant plants showed improved extractability from the cell wall as a result of its composition of single monosaccharides that required fewer enzymes for complete hydrolysis. Further studies of the double mutants revealed that the xylan in these plants did not display a reduced xylan backbone quantity, indicating that backbone synthesis and substitution can be uncoupled. Despite possessing a simplified version of xylan, *gux1gux2* mutants displayed a normal growth phenotype, although the stems showed slightly decreased strength in bending assays. These results demonstrate the potential for manipulating and simplifying the structure of xylan to improve the properties of lignocellulose allowing cheaper sugar extraction for bioenergy and other uses.

The xylan machinery in Arabidopsis was chosen for initial studies due to its biological similarities with willow. The group therefore plans to work with colleagues studying willow and miscanthus grass to transfer Arabidopsis-discovered technology into non-food crops in order to develop more sustainable processes for generating fuels from crop residues.

(1) Mortimer, JC Miles, GP Brown, DM Zhanga, Z Segura, MP Weimar, T Yua, X Seffen, KA Stephens, E Turner, SR Dupreee, P (2010) Absence of branches from xylan in Arabidopsis gux mutants reveals potential for simplification of lignocellulosic biomass. PNAS (107): 17409-14

Grow your hair to grab more nutrients

By: Irene Lavagi, MASC Coordinator

In the face of an increasing demand for food production, improving land use efficiency will be crucial to supply adequate food and resources to a growing population. The availability of nutrients in the soil is a major limiting factor that currently constraints the accessibility of arable land. Most soils in Australia, sub-Saharan Africa and up to 30% of China's territory cannot be productively used because of the limited phosphate and iron availability.

A team of researchers from Oxford University and the John Innes Centre, led by Prof Liam Dolan, has discovered a master regulator of plant root hair growth in Arabidopsis (1) that plays a major role in promoting plant growth on poor soils. The gene in question is the basic helix-loop-helix transcription factor *RSL4* (*ROOT HAIR DEFECTIVE 6-LIKE 4*) that acts like a switch; root hairs elongate when the gene is switched on, and stop growing when it is off.

Although it had long been known that when crops such as barley and wheat grown are grown in poor soils, plants with longer root hairs give higher yields compared to plants with shorter root hairs. The genetic and molecular mechanism for this difference had remained undiscovered until now. The team of UK researchers, led by Liam Dolan, noted that loss of RSL4 function in Arabidopsis resulted in the development of very short root hairs, whereas constitutive expression led to the formation of very long root hairs. In addition, hair-cell growth signals such as auxin and low phosphate availability modulated root hair cell extension by regulating *RSL4* at the transcriptional and translational level. In fact, by growing plants in phosphate-poor soils RSL4 expression was activated and plants grew very long root hairs. In field conditions these longer root hairs would be able to burrow deeper and further into the soil environment to scavenge for nutrients and release chemicals that would be able to crack rocky minerals releasing important plant growth nutrients such as phosphate and iron. *RSL4* has therefore been identified as the driver behind this nutrient mining machine of plants.

Liam Dolan's team worked on genes that play a vital role in anchorage, water use and nutrient uptake in plants. These genes are highly conserved in plants and have already been proved to enhance root systems in transgenic plants of major crops. In November 2010 an exclusive commercial license agreement for technology that enhances the root system of plants and with important implications for crop improvement was licensed to Dow AgroSciences.

This technology was discovered as a result of basic research undertaken to answer fundamental biological questions, such as how organisms control the size of their cells, and has resulted in the discovery of a tool that could have an important impact on world agriculture.

(1) Yi, K Menand, B Bell, E Dolan, L (2010) A basic helix-loop-helix transcription factor controls cell growth and size in root hairs. Nature Genetics (42): 264-9

Green bottles

By: Irene Lavagi, MASC Coordinator

Currently, we largely rely on petroleum as a source of energy and for the production of widely used chemicals and materials such as plastics. The ability to produce these materials from different sources will be key for their future sustainable production. Plants are well suited to serve this purpose as they are capable of producing oils that could be engineered to generate the building blocks we currently obtain from petroleum-based chemicals. However the major challenge in the development of plants as green factories producing relevant compounds for the production of materials such as plastics is the ability to accumulate the desired compounds to sufficiently high levels that make its extraction and processing economically viable. To address this problem, researchers at the US Department of Energy's Brookhaven National Laboratory and Dow AgroSciences have metabolically engineering a fatty acids pathway in Arabidopsis to maximize the accumulation of precursors that can be converted into plastics (1).

The authors focused their attention on the production of particular fatty acid, ω-7 fatty acids which is rather unique as it contains carbon atoms that are double bonded to adjacent carbons and can be used as a feedstock for the generation of octane, a highly demanded industrial product. Although some plants, such as cat's claw vine (*Doxantha unguis-cati*) naturally produce oils containing ω-7 fatty acids (palmitoleic 16:1D and cis-vaccenic 18:1D), but the low yields and poor agronomic properties of these plants are not suitable for commerical production. So the team decided to work on modifying existing pathways in the model plant Arabidopsis via the introduction of desaturase enzymes which remove hydrogen atoms from fatty acid chains to form carbon-carbon double bonds.

To begin with, naturally occurring variant desaturases with the desired specificities were engineered to work faster and with greater specificities than then natural plant enzymes. A plastidial 16:0-ACP (acyl carrier protein) desaturase was engineered to convert C16 fatty acids (16:0) to a C16 fatty acid with an additional double

bond (16:1D) with a specificity more 100-fold higher than that of naturally occurring paralog of *Doxantha unguis-cati*. Expression of this engineered enzyme led to an increase of ω-7 fatty acids from 2% to 14% in Arabidopsis but this increase is not sufficient for commercial use. To further increase the accumulation of ω-7 fatty acids a number of additional modifications were introduced to the plant's metabolic pathway, such as the downregulation of another enzyme, β-ketoacyl-ACP synthase II 16:0 elongase, which competes for the introduced enzyme's fatty acid substrate. This resulted in a further increase of ω -7 fatty acids to 56%. In addition, desaturases capable of intercepting substrate that had escaped the first desaturase enzyme as it progressed through the oil-accumulation pathway were also introduced. The level of 16:0 exiting the plastid without desaturation also increased to 21%. Coexpression of a pair of fungal 16:0 desaturases in the cytosol reduced the 16:0 level to 11%. By combining all these modifications Arabidopsis plants with an increase of ω -7 fatty acids up to 71% were produced. These levels are much higher than the ω -7 fatty acid levels in milkweed, and equivalent to those observed in cat's claw vine.

Although further technology needs to be developed to convert the fatty acid into the chemical building block of plastics, this research showed that it is possible to synthesize industrially relevant compounds in plants at levels sufficient for commercial exploitation.

(1) Nguyen, HT Mishra, G Whittle, E Bevan, SA Owens Merlo, A Walsh, TA Shanklin, J (2010) Metabolic Engineering of Seeds Can Achieve Levels of ω-7 Fatty Acids Comparable with the Highest Levels Found in Natural Plant Sources. Plant Phys (154): 1897–1904

WRR4 confers resistance in Brassica

By: Irene Lavagi, MASC Coordinator

Recently a group of researchers were able to directly show the applicability of Arabidopsis research to Brassica crops (1). A disease resistance gene, *WRR4*, from Arabidopsis was shown to confer resistance in transgenic Brassica to a major pathogen of oilseed production in India and North America.

White blister rust caused by the oomycete *Albugo candida* (Pers.) Kuntze is a common and often devastating disease of oilseed and vegetable brassica crops worldwide. Notable examples include a major group of physiological races that are destructive in different vegetable or oilseed crops. For example *Brassica juncea* (*A. candida* race 2), *B. rapa* (race 7), or *B. oleracea* (race 9); alternatively this pathogen can be parasitic on wild crucifers such as *Capsella bursa-pastoris* (race 4).

Arabidopsis thaliana is naturally immune to these *A. candida* races in the wild, but several Arabidopsis accessions (e.g. Ws-3) allow varying degrees of white rust development after inoculation with *A. candida* races 2, 4, and 7. Borhan and colleagues utilised the partial suceptibility of Ws-3 to map base clone the first white rust resistance (*WRR*) gene, *WRR4*. *WRR4* was found to encode for a cytoplasmic toll-interleukin receptor-like nucleotide-binding leucine-rich repeat receptor-like protein. Transgenic expression of the *Arabidopsis thaliana* Columbia allele was found to confer dominant broad spectrum white rust resistance to the *A. candida* races 2,4, 7 and 9 in the Arabidopsis sensitive ecotype Ws-3 (2).

Not only could WRR4 confer resistance in Arabidopsis, more importantly expression of the Arabidopsis gene *WRR4* conferred full resistance resistance to *A. candida* in transgenic *B. napus* (race 7) and *B. juncea* (race 3). This study established the transgenic testing of the first gene of a complex trait in brassicas, and recommended the cloning of the underlying genes as an approach for capturing the full and potentially durable source of white rust resistance (1).

(1) Borham, MH Holub, EB Kindrachuk, C Omidi, M Bozorgmanesh-Frad, G Rimmer, SR (2010) WRR4, a broad-spectrum TIR-NB-LRR gene from Arabidopsis thaliana that confers white rust resistance in transgenic oilseed brassica crops. Mol Plant Pathology (11): 283-91

(2) Borham, MH Gunn, N Cooper, A Gulden, S Tor, M Rimmer SR and Holub, EB (2008) WRR4 encodes a TIR-NB-LRR protein that confers broad-spectrum white rust resistance in Arabidopsis thaliana to four physiological races of Albugo candida. Mol Plant-Microbe Interact (21): 757-68

Chromosome imbalances lead to predictable plant defects

By: Irene Lavagi, MASC Coordinator

The ability to manipulate plant traits will be key to ensuring increased crop yields in the future. For example genetic variation in cultivated wheat has been greatly diminished as a result of the selection of pure breed lines for agricultural purposes. The introduction of desirable characters into wheat will therefore require the selection and insertion of useful genes from wild relatives . However just 'adding' in a gene of interest does not always generate the desired outcome. In the simplest description of gene expression and dosage, if the expression of one gene on one chromosome has a desirable effect then it would seem logical to conclude that by adding an extra copy of that chromosome would amplify this positive effect.

However, this is often not the case and organisms have evolved mechanisms to maintain gene dosage. For example, in theory having two copies of the X chromosome in women should result in double the expression of the genes located on this chromosome compared to men (XY). But the expression of these genes is suppressed in women to ensure correct gene dosage. Failure of this mechanism would lead to imbalances. One of the most studied examples of aneuploidy (abnormal number of chromosomes) in humans is Down Syndrome, also known as trisomy 21. The addition of an extra chromosome generates a number of phenotypes that are believed to be related to gene dosage. By understanding the rules that regulate chromosome imbalances, it would be possible to predict the outcome of adding or deleting a gene from an organism.

Plants are very tolerant to aneuploidy, aneuploid plants can easily be obtained from triploid individuals, providing a powerful system for a genome-wide study of aneuploid syndrome that would not be possible in animal systems. For example Brian Dilke's team at Purdue University in the USA utilized the model plant *Arabidopsis thaliana* as the organism of choice for the study of chromosome imbalance. In a recent publication they phenotyped a population of Arabidopsis aneuploid individuals and demonstrated that certain traits are strongly associated with the dosage of specific chromosome types and that chromosomal effects can be additive (1). Easily measured characteristics such as stem diameter, rosette size and other physical features were found to vary depending on imbalances of specific chromosomes. Plants with excess of both

chromosome 1 and deficiency of chromosome 3 displayed a stem diameter as predicted. Most intriguingly, chromosomal imbalances in parent plants were found to result in abnormal traits expressed in the offspring despite the offspring having a normal number of chromosomes indicating that long-term phenotypic consequences of aneuploidy can persist after chromosomal balance has been restored. Trans-generational phenotypic effects may be due to epigenetic modifications passed from aneuploid parents to the diploid progeny.

The team hope that future research on chromosome imbalances in crop plants such as corn will help us to understand how the excess or deficiency of a gene leads to a particular phenotypic characteristic in the field. The findings of the Purdue team clearly illustrates that genes are sensitive to their dose relative to the rest of the genome and shed light on how addition or deletion of genes and the organization of the genome affects growth and development.

Insight into the mechanisms that regulate the translation of chromosome imbalances into certain characteristics could open up new avenues of research aimed at correcting these defects in plants as well as animals and humans.

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Monsanto: How an Arabidopsis gene can be used to improve soybean yields

By: Irene Lavagi, MASC Coordinator

It has been argued that doubling crop yields by 2030 could be possible through the integration of improvements in breeding and agronomy with reduced economical impacts. The Arabidopsis *Bbx32* gene was presented by Robb Fraley, Monsanto, at the Plant and Animal Genome Conference (PAG) in 2010 as a potentially valuable gene for increasing plant growth through providing more nodes and increasing grain yield (1). *Bbx32* encodes for a protein induced by phytochrome mediated light signals and is a member of the Zn-finger protein family, believed to have transcriptional factor activity (2). The gene has been shown to be active in soybean. At PAG in 2011, Monsanto presented a study on *Bbx32* in soybean, showing that its overexpression significantly improved broad acre yield compared to wild type soybeans plants. *AtBBX32* overexpressing soybean plants were also observed to be taller, have more nodes, pods, and flowers. Soybean lines overexpressing the Arabidopsis *AtBBX32* gene displayed altered gene expression profiles. The expression levels of *GmTOC1* and *GmLHY*, both core components of the plant's circadian clock were altered and some physiological changes, such as the levels of starch and soluble sugars in the leaves were observed.

It was also reported that an overexpression of the orthologous gene from soybean, Glycine max BBX32 gave similar results, whilst GmBBX32-RNAi lines showed decreased yields (3).

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(3) Petracke, ME Preuss, S McClerren, A Weihe, J Xu, J Zhu, J Urwin, CP Meister, R Anil Shiri, V Ruff, TG (2011) Overexpression Of The Arabidoipsis Bbx32 Gene In Soybean Leads To Improved Broad Acre Yield. PAG Abstracts

Reports of the MASC Subcommittees

Bioinformatics

Prepared by Nicholas Provart (Chair, nicholas.provart@utoronto.ca) with input from MASC Bioinformatics Subcommittee members Sébastian Aubourg (aubourg@evry.inra.fr), Yves Van de Peer (yvdp@psb.ugent.be) Eva Huala (huala@acoma.stanford.edu), Tetsuro Toyoda (toyoda@base.riken.jp)

The past year saw the release of some exciting new data sets and tools for Arabidopsis. TAIR released the TAIR10 Arabidopsis Genome Release, adding 126 new loci, updates to 1184 gene structures, and 2099 new gene models. Genome sequences and polymorphisms for more than 80 natural accessions were released by the Weigel Lab and collaborators, as part of the 1001 Genomes Project (1001genomes.org; (1)). A comprehensive chloroplast proteome database with subplastidial localization and curated information on envelope proteins was published (2), accessible through the AT_CHLORO tool (http://www.grenoble.prabi.fr/at_chloro/). A phosphoproteome data set was generated for both Arabidopsis and rice (3): both these and other proteomic data sets are conveniently searchable through a newly released aggregating proteomics portal of the MASC Proteomics Subcommittee, MASCPGator (4).

In terms of other tools, TAIR released its N-Browse tool for exploring literature-documented protein-protein interactions. The Arabidopsis community is eagerly anticipating data sets on Arabidopsis membrane protein-protein interactions from the Frommer lab, and a comprehensive all-by-all interactome from the Braun and Vidal labs at Harvard. In addition, two groups published Arabidopsis gene function prediction tools, AraNet (5) and GeneMANIA (6), both of which use several large data sets (expression profiles, protein domain information, protein-protein interactions etc.) to predict gene function for both annotated and unknown genes in Arabidopsis. CATdb (http://urgv.evry.inra.fr/CATdb) added to its repository of gene expression data for Arabidopsis produced with the CATMA microarray, now encompassing 11,200 hybridized samples. Also under the broad category of gene expression analysis, AtCAST was released, which permits the identification of gene expression similarities between expression profiling experiments (7). ePlant ((8); http://BAR.utoronto.ca/eplant/) taps into the BAR's large repository of published data from the kilometer (sequence variation) to nanometer (protein structure) scales, and presents these in a seamless 3D framework.

Several tools aimed to expand the organismal reach of Arabidopsis by providing comparisons to other species. The Narcisse browser (http://narcisse.toulouse.inra.fr) enables exploration of the extent of synteny and sequence conservation between 26 plant genomes. GreenPhylDB ((9); http://greenphyl.cirad.fr) provides a set of web tools to support comparative and functional genomics in 16 fully-sequenced plant species including Arabidopsis, with genes grouped into clusters or gene families. FLAGdb++ ((10); 2011; http://urgv.evry.inra.fr/FLAGdb) continued adding new data to facilitate translational efforts between Arabidopsis and crops. PLAZA 2.0 from the Vandepoele lab, released in September 2010, integrates structural and functional annotation from 23 plants covering eleven dicots, five monocots, two mosses, and five algae.

The announcement in 2009 of cuts to TAIR's funding caused a flurry of activity this year. On the one hand, TAIR was able to maintain its literature curation efforts beyond September 2010 through sponsorship money from several large plant biotechnology companies, and cuts to staff have thus been less than they would have been. Second, two sets of workshops in the spring of 2010 on the future of Arabidopsis bioinformatics, hosted by MASC and NAASC, and funded by the BBSRC and NSF respectively, saw the creation of the International Arabidopsis Informatics Consortium (11), which envisions a globally distributed system of data, tools, and resources for Arabidopsis and related species, accessed via a single information portal and funded by a variety of sources. It is hoped the efforts like the iPlant Collaborative (iplantcollaborative.org) and webservices provided by groups worldwide will enable a robust cyberinfrastructure that can be used for this portal. The IAIC will be an integral part of MASC's next 10 year vision for Arabidopsis, where in this humble but very well researched plant will become a platform for systems biology modeling from "molecules to fields".

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Metabolomics

Prepared by Kazuki Saito (Chair, ksaito@psc.riken.jp) and Wolfram Weckwerth (Co-chair, wolfram.weckwerth@univie.ac.at)

Aims

Since metabolomics is an important component of Arabidopsis '-omics', a continuous major goal of this subcommittee will be to promote metabolomics research in 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 (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 aims 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 form for data integration.

To achieve these goals, we aimed to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. The MASCM (Multinational Arabidopsis Steering Committee Metabolomics) webpage has been recently launched at www.masc-metabolomics.org. Subcommittee discussions will not be limited to an annual meeting at ICAR, a continuous dialogue among subcommittee members will be encouraged through the participation in numerous other metabolomics-related meetings.

Recent meetings:

- The Metabolomics 2010 meeting www.metabolomics2010.com Amsterdam, The Netherlands, June 27 – July 1, 2010 has be organized by Robert Hall to join forces to organize the first integrated conference of The Metabolomics Society, The Plant Metabolomics Platform, The Metabolic Profiling Forum and a number of additional groups involved in metabolomics research.
- The joint NSF (US) and JST (Japan) workshop for 'Identifying Potential Collaborative Research Opportunities in Metabolomics' was held May 6-7, 2010, at the University of California, Davis, California, US, with Lloyd Sumner, Kazuki Saito and Oliver Fiehn as the organizers. This workshop has successfully led to the establishment of a joint research program between NSF (http://nsf.gov/pubs/2011/nsf11527/nsf11527.htm) and JST (http://www.jst.go.jp/sicp/announce_usjoint.html).
- At Pacifichem 2010 (http://www.pacifichem.org/) in December 15-20, 2010, in Hawaii, US, the symposium on 'Metabolomics for Fundamental and Applied Plant Sciences' was organized by Kazuki Saito, Ute Roessner and Basil Nikolau.

Updates

- An Arabidopsis metabolome expression database 'AtMetExpress development' has been established (1) at http://prime.psc.riken.jp/.
- A web portal of Arabidopsis Metabolomics Consortium at www.plantmetabolomics.org that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants has been launched (2).
- Mass spectral databases, MassBank (http://www.massbank.jp/index.html?lang=en) (3) and ReSpect for Phytochemicals (http://spectra.psc.riken.jp/) are publicly available.
- 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. 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

Report text provided by Detlef Weigel (Member, weigel@tuebingen.mpg.de). Subcommittee Co-chairs Brian Dilkes (bdilkes@purdue.edu) and Chris Pires (piresjc@missouri.edu)

Genetic and epigenetic resources for natural variation

- In the 1001 Genomes Project (http://1001genomes.org), almost 500 accessions have been sequenced. Polymorphisms for 80 of these, which have been sequenced at the Max Planck Institute (Tübingen, Germany), have been released last year, and the seeds are available from the stock centers. About 200 additional accessions each have been sequenced at the Gregor Mendel Institute (Vienna, Austria) and the Salk Institute (La Jolla, US), and the data will be released in 2011. For the latter two sets, transcriptome and methylome data have been generated as well. Commitments for additional accessions exist, and it is likely that the goal of 1001 sequenced accessions will be surpassed in 2012. Recently, the spontaneous mutation rate and spectrum in *A. thaliana* has been directly determined (1), providing an important resource for interpreting the polymorphisms observed in natural accessions.
- A 250k SNP chip has been used by a University of Chicago/ University of Southern California consortium to genotype over 1,000 natural accessions. Several proof-of-principle papers that demonstrate the power of this data set for genome-wide association studies (GWAS) have been published (2-6), and we can expect that this field will follow a similar trajectory as GWAS in humans, with soon dozens, if not hundreds of studies being conducted. Web tools for on-the-fly GWAS analyses are being developed at the Gregor Mendel Institute, enabling also those without a deep knowledge of GWAS to make use of this elegant approach.
- Progress has also been made in understanding the population history of *Arabidopsis thaliana* on both a local and global scale (7,8). Although predominantly selfing, the species outcrosses surprisingly often in certain environments, which has important implications for selection studies conducted in natural environments. Furthermore, with the exception of North America and Great Britain, much of the world-wide diversity is often captured by relatively few local accessions, with identical multi-locus genotypes being generally only found in single patches of plants.

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Phenomics

Prepared by Bob Furbank (Co-chair, robert.furbank@csiro.au) and Uli Schurr (Co-chair,u.schurr@fz-juelich.de)

New mutant resources

A collection of artificial target mimics, which block miRNA action, has been produced and is available from the stock center (1). This resource allows systematic study of miRNA action on a genome-wide scale.

Short read sequencing is being exploited for rapid mapping and identification of induced and spontaneous mutants. The Max Planck Institute (Tübingen, Germany) developed the SHOREmap pipeline, which supports mapping of mutations after sequencing bulked segregants along with the identification of newly induced mutations in the mapping interval (2). Originally designed for mapping mutations induced in the Col-0 reference accession, this approach has been extended to spontaneous mutations arising in non-reference accessions as well (3). Mapping of induced mutations can now be achieved in a matter of one or two weeks, with sequencing costs of 1,000 US dollar or less.

High throughput phenotyping projects

Australian Plant Phenomics Facility: Commissioning of Infrastructure

All systems are now fully operational at The Plant Accelerator,

Australian Plant Phenomics Facility Adelaide node, including growth cabinets and growth rooms for growth and analysis of Arabidopsis using the Lemnatec platform. At the High Resolution centre in Canberra, 3 novel instruments for high throughput analysis of Arabidopsis have been designed, two of these have been commissioned and one has been tested and will be commissioned in June 2011. A newly built CabScan, a robotic arm which integrates into the light banks of growth chambers, allows in cabinet monitoring of plant growth in trays by both projected leaf area and stereovision (using infrared detection so that night time measurements of growth are possible) is now available. Additional cameras for far infrared can also be mounted. CabScan is compatible with the multitier Conviron Flex cabinets and other common formats. PlantScan is now operational and is designed to give full 3-D reconstruction of plant architecture (in single pots rather than trays) in data cubes which include colour, texture and a high resolution FIR temperature map of the plant. Throughput is approximately 1000 plants per day at high resolution and the associated software carries out feature recognition for plant parts and quantification of features, areas, volumes and temperature matrices. In June, TrayScan, a dedicated 20 by 20 plant tray imaging system for pulse modulated chlorophyll fluorescence, FIR rosette temperature and 3-camera view pseudo-3D will be commissioned, capable of imaging 3000 plants per day. This system will enable high throughput measurements of stress response, photosynthetic response, screening of mutants in stomatal function and digital growth analysis.

Juelich Plant Phenotyping Center (JPPC)

Significant extensions of the capacities and the parameters that can be quantified have been developed in 2010. Two specific phenotyping growth chambers have been integrated to allow for fast changes in environmental conditions and the automated analysis of growth and photosynthesis responses in high-throughput. New and high-capacity root phenotyping facilities for analysis of root system properties in agar-based and soil-based systems have been designed and are presently implemented.

JPPC is involved in a number of projects including Arabidopsis phenotyping with 1001-Genomes, breeders and molecular biologists with respect to abiotic and biotic responses of growth, photosynthesis and plant structure of Arabidopsis in the vegetative stage.

JPPC coordinates the National German Plant Phenotyping Network (DPPN) and the European Plant Phenotyping Network (EPPN). Both projects integrate significant phenotyping activities, provide access to infrastructures and develop novel and targeted soft- and hardware for plant phenotyping in general. JPPC organizes the 2nd International Plant Phenotyping Conference 5-7 September 2011 at Jülich Research Center (Germany) https://www.congressa.de/phenosymp2011/

RIKEN:

RIKEN Arabidopsis Activation Tag lines, Ac/Ds transposon lines and FOX lines are available from RIKEN BioResource Center (http://www.brc.riken.jp/lab/epd/Eng/catalog/seed.shtml). RIKEN Plant Functional Genomics Group increased Arabidopsis FOX (Full-length cDNA over-eXpressor) lines to 25,000 lines in total and 6,000 lines are available through RIKEN BRC. A Hub Database SciNetS (https://database.riken.jp) has been developed by Tetsuro Toyoda to provide an integrated access point for RIKEN data. Through this database phenotype information of Activation tag lines, Ac/Ds transposon lines and FOX lines are available. Activation tag lines; http://amber.gsc.riken.jp/act/top.php or Ac/Ds transposon lines; http://rapid.psc.database.riken.jp Arabidopsis FOX lines; under construction Rice FOX lines; http://amber.gsc.riken.jp/ricefox/index.php RIKEN Plant Functional Genomics Group generated inducible 500 independent transcription factor lines to observe phenotype. A review paper for mutant resources and phenome approaches is as follows Kuromori T, Takahashi S, Kondou Y, Shinozaki K, and Matsui M (2009) Phenome analysis in plant species using loss-of-function and gain-of-function mutants. Plant and Cell Physiology (50): 1215-1231 The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast) provides easy access to the phenotype and segregation data of Arabidopsis Ds/Spm or T-DNA-tagged mutants for nuclear-encoded chloroplast proteins, which includes over 200 mutants with abnormal phenotypes (Kazuo Shinozaki and Fumiyoshi Myouga).

Development of the European Plant Phenotyping Network (EPPN)

Standardization of Phenotyping Techniques, Growth Conditions and Protocols

Lead by the Jülich Plant Phenotyping Center (JPPC) a major infrastructure proposal for the establishment of a European Plant Phenotyping Network (EPPN) was developed and positively evaluated (final decision of granting is pending). According to the rues of the EC the EPPN will build on existing infrastructure and make it available transnationally. The participating phenotyping centres will provide, through a joint access procedure, their facilities to the scientific community. The EPPN transnational access will also provide options for the Arabidopsis community.

EPPN will also contribute to standardization of techniques for growing and phenotyping (incl. Arabidopsis) in controlled environments to allow meaningful database of genotype to phenotype to be assembled. This will allow a coordinated multinational effort to be made to phenotype genetic stocks for key traits (in much the same way as genome sequencing was divided up internationally, phenotyping could also be carried out across national research centers). Toward these ends, Massonet *et al* (4) recently highlighted the importance of establishing uniform growth conditions for HTP experiments and that the concept of a standardized environment is a slippery one in the case of this comparison of results from 10 different laboratories. This study will soon be extended in a multi-partner “ring experiment” to ascertain how best to obtain comparable phenotypic results across laboratories.

International Plant Phenotyping Network (IPPN)

The subcommittee aims to expand the International Plant Phenomics Network (IPPN) and the website http://www.plantphenomics.com as a venue for discussion and comparison of such data and protocols, subject to funding of this activity.

Phenotyping of Arabidopsis Genetic Resource Stocks and Phenoype to Genotype Databases

Developing a database of phenotypes for Arabidopsis genetic resources, mapped to genetic information such as insertion sites or genomic re-sequence data is a priority for improving the utility of Arabidopsis functional genomics information. Toward these ends, Chloroplast 2010 is nearly complete, with >5000 insertion mutants tested. The data are available to the community and two papers were published this year, one describing the LIMS and database and a use case (5) and another on the strengths and weaknesses of large reverse genetics projects and a variety of examples of what were discovered (Ajjawi et al DOI 10.1104/pp.109.148494).

A collaboration has been established between the High Resolution Plant Phenomics Centre (HRPPC) in Canberra Australia and Max Planck Institute for Developmental Biology, Tubingen, Germany, to produce a baseline phenotypic data set from ecotypes re-sequenced in the 1001 Genomes Project (7) encompassing growth rate and mathematical descriptions plant architecture using the digital imaging systems at HRPPC. These data will be lodged in PODD, the Phenomics Ontology Driven Database which is now in operation at the Australian Plant Phenomics Facility and linked to the TAIR databasesin the near future. (http://www.plantphenomics.org.au/PODDProject).

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Proteomics

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The MASC Proteomics subcommittee (MASCP) has spent the past year continuing its efforts with the promotion of plant proteomics and reaching out to various groups and research communities. The group recently developed one of the first biological data aggregation portals (MASCP Gator) with a specific focus on bringing together and summarizing diverse Arabidopsis proteomic information. Since members of MASCP have been responsible for development of many of the Arabidopsis proteomics resources it was possible to coordinate a standardized communication process that has enabled data to be retrieved upon request, ensuring that displayed information at the MASCP Gator is always up to date. This approach has the advantage of maintaining the specialities and expertise of distributed data resources while providing an integrated overview. MASCP has recently contacted the Human Proteomics Organization (HUPO) who had initiated a Model Organism Proteome workgroup (iMOP) to stimulate scientific exchange and to examine practices and standards in model systems as a driver for future proteomic systems. The iMOP program HUPO initiative was approved at their annual meeting in Sydney in September 2010 (http://www.hupo.org/research/iMOP). A number of MASCP members are currently serving as Arabidopsis representatives on this initiative and MASCP members are also participating in iMOP meeting in April 2011 (MASCP iMOP delegates: Steve Briggs, Klaas van Wijk, Katja Baerenfaller and Alex Jones). With the addition of two new Arabidopsis resources (RiPP-DB and AT_CHLORO) and the expansion of other Arabidopsis proteomics resources it is again interesting to examine the current experimental evidence for Arabidopsis gene models (Table 1).

Database	Number of Proteins	Unique Proteins
SUBA	6,346	192
pep2pro	14,582	1,795
PPDB	6,172	1,245
ProMEX	~1000	ND
AtPeptide	16,769	3,557
PhosPhAt	4,859	502
AT_CHLORO	1,323	0
RiPP-DB	2,244	78
	Total Unique	7,369
	Total (shared)	14,208
	Total (non-redundant)	21,577

Table 1. Number of identified proteins collated in online Arabidopsis databases by proteomics studies against TAIR10 as of March 2011

Collectively these data provide evidence for the translation of 21,577 proteins and comprise 61% of potential proteins and 72% of gene models from the recent Arabidopsis genome release

(TAIR10). This represents a ~10% increase in the total number of proteins experimentally identified in the Arabidopsis proteome.

Recent activities:

- Meetings and the organization of proteomics workshops have been established on a regular basis at the International Conference on Arabidopsis Research. There was a well attended workshop held last year at ICAR 2010 in Yokohama. The workshop was held over lunch on Monday 7th June and focused on protein phosphorylation. A discussion during the workshop produced interesting feed-back and has enabled MASCP to better understand questions and demands from the scientific community concerning plant proteomics. The workshop was organized by MASCP members Joshua Heazlewood, Alex Jones and Hiro Nakagami with Scott Peck also in attendance. We appreciate the efforts made by Hiro Nakagami and the ICAR 2010 organizers in making the facilities available for this workshop at such short notice.
- Upcoming workshops being organized by MASCP members include a subcommittee workshop at ICAR 2011 (Madison, Wisconsin, USA) and a proteomics workshop at the XV International Congress on Molecular Plant-Microbe Interactions (Kyoto, Japan).
- The MASCP Gator (Arabidopsis proteomics aggregator) has been released (http://gator.masc-proteomics.org/). This web service summarizes publicly available proteomics data from an array of Arabidopsis proteomics resources to provide a snapshot of proteomics information for an Arabidopsis protein. The visual aggregation utility displays live information from a series of eight online Arabidopsis proteomics resources (PPDB, SUBA, AtPeptide, pep2pro, AT_CHLORO, RiPP-DB, PhosPhAt and ProMEX) to create a proteomics summary of phosphorylation, spectral coverage, organ evidence and subcellular localization.
- Three new members were invited to join MASCP in the past year: Steve Briggs (UC San Diego, USA), Norbert Rolland (CEA, Grenoble, France) and Stefanie Wienkoop (University of Vienna, Austria).
- The MASC Proteomics Subcommittee (MASCP) website (http://www.masc-proteomics.org/) has been updated and expanded also in response to feed-back from the scientific community. It now contains further information on potential funding sources to promote the exchange of researchers interested in undertaking proteomics projects at MASCP member laboratories. The website also contains many useful resources for the Arabidopsis proteomics community including guidelines and standards for data interpretation, recommendations on where raw and processed mass spectrometry data should be submitted, an updated catalogue of Arabidopsis proteomic resources, meeting and workshop information and links to contact MASCP members.
- The MASCP members have continued to maintain and establish major online Arabidopsis proteomics resources. While the MASCP Gator unified much of the basic information through a single web portal, more detailed protein information can be obtained from the specific resources. The AtProteome proteogenomic resource has been significantly updated and relaunched as pep2pro with a series of new and updated analyses of the Arabidopsis proteome (http://www.pep2pro.ethz.ch/). The newly developed AT_CHLORO database contains information on the sub-proteomes of Arabidopsis chloroplasts (http://prabi2.inrialpes.fr/at_chloro/). The RiPP-DB resource houses a new and extensive phosphoproteomic analysis of Arabidopsis (http://phosphoproteome.psc.database.riken.jp/). Significant updates to proteomics data (~30% increase) in the SUBA resource (http://suba.plantenergy.uwa.edu.au/) also occurred.
- MASCP members have made significant contributions during 2010 / 2011 to two special issues initiated in refereed journals showcasing plant proteomics – one in Phytochemistry and the other in Proteomics.

There were a number of significant papers published in the past year (2010-2011) that advanced proteomics in Arabidopsis and include:

- Joshi HJ, Hirsch-Hoffmann M, Baerenfaller K, Gruissem W, Baginsky S, Schmidt R, Schulze WX, Sun Q, van Wijk K, Egelhofer V, Wienkoop S, Weckwerth W, Bruley C, Rolland R, Toyoda T, Nakagam H, Jones A, Briggs SP, Castleden I, Tanz S, Millar AH and Heazlewood JL. (2011) MASCP Gator: An aggregation portal for the visualization of Arabidopsis proteomics data. Plant Physiology (155): 259-270. *The creation of an Arabidopsis proteomics portal (MASCP Gator) by MASCP members that provides a visual overview of proteomics information of an AGI.*
- Nakagami H, Sugiyama N, Mochida K, Daudi A, Yoshida Y, Toyoda T, Tomita M, Ishihama Y, Shirasu K (2010) Large-scale comparative phosphoproteomics identifies conserved phosphorylation sites in plants. Plant Physiology (153): 1161-1174. *Arabidopsis and rice phosphoproteomic study which examined the conservation of phosphorylation sites between the two species and the construction of the RiPP-DB phosphorylation resource.*
- Baerenfaller K, Hirsch-Hoffmann M, Svozil J, Hull R, Russenberger D, Bischof S, Lu Q, Gruissem W, Baginsky S (2011) pep2pro: a new tool for comprehensive proteome data analysis to reveal information about organ-specific proteomes in Arabidopsis thaliana. Integrative Biology (3): 225-237. *pep2pro was released as a proteome data analysis tool and the data resource updates the previous proteomics analysis of Arabidopsis organs with expanded quantitative protein information and proteogenomic visualization of data.*
- Olinares PDB, Ponnala L, van Wijk KJ (2010) Megadalton complexes in the chloroplast stroma of Arabidopsis thaliana characterized by size exclusion chromatography, mass spectrometry and hierarchical clustering. Molecular & Cellular Proteomics (9):1594-1615. *Identification of many previously unobserved proteins mostly involved in plastid gene expression and mRNA metabolism, as well as ribosome biogenesis factors*
- Ito J, Batth TS, Petzold CJ, Redding-Johanson AM, Mukhopadhyay A, Verboom RE, Meyer EH, Millar AH, Heazlewood JL (2011) Analysis of the Arabidopsis cytosolic

proteome highlights subcellular partitioning of central plant metabolism. Journal of Proteome Research (in press). *The first in-depth characterization of a plant cytosol with over 1000 identified proteins demonstrates partitioning of plant metabolism.*

- Lee CP, Eubel H, Millar AH (2010) Diurnal changes in mitochondrial function reveal daily optimisation of light and dark respiratory metabolism in Arabidopsis. (2010) Molecular & Cellular Proteomics (9):2125-2139. *Evidence of diurnal rhythms in the mitochondrial proteome in plants modulating respiration at night by translational and post-translational processes.*

Systems Biology

Prepared by Rodrigo A. Gutiérrez (Co-Chair, rgutierrez@uc.cl) & Andrew Millar (Co-Chair, Andrew.Millar@ed.ac.uk)

Systems biology approaches in Arabidopsis research continued to flourish during the past year. Systems biology can be defined as the exercise of integrating the existing knowledge about biological components, building a formal model of the system as a whole and extracting the unifying organizational principles that explain the form and function of living organisms. More practically speaking, a systems approach to understand biology can be described as an iterative process that includes (1) experimentation at a global level, (2) data collection and integration, (3) system modeling and (4) generation of new hypotheses to initiate a new cycle of experimentation at a global level.

Given the limitations of global assays for many biological processes, Systems Biology research often focuses on subsystems and aims to test all components of the subsystem, often across spatial scales. The promise of systems biology is that by using this global integrative and iterative approach we will greatly increase our understanding of biological systems, both by broadening the scope of understanding to include more biological components, and by deepening understanding of systems that are complex enough to limit research progress that is unaided by models.

A primary goal of the Systems Biology Subcommittee is to further the use of Systems Biology among Arabidopsis researchers to elucidate the structure, dynamics, and organizational principles of the regulatory and metabolic networks that support living cells. Development in different areas is needed in order to fully adopt a systems perspective across the field:

1. Component description and measurements. To identify the primary structure of components and their location and to obtain quantitative measurements of components with spatial resolution.
2. Component relationships or connections. To determine functional associations of components in pathways, networks, multinetworks in the cell, tissues, organs, individual in population and species in ecosystems.
3. Dynamics over space and time. To determine component measurements and relationships at different time scales for biochemical and intramolecular processes (sub-second), biosynthetic and signalling timescales (seconds to hours), rapid environmental responses (seconds to days), plastic/ developmental dynamics within individual (days to months), daily and seasonal cycles as well as over evolutionary time scales.
4. Public Infrastructure. To construct model repositories, data repositories, software tools and standards for experimental data and corresponding metadata (for samples, for experimental methods, for tools and for conclusions).

Arabidopsis-focused scientists are leading high-profile Centres and Projects in Systems Biology, such as the CSBE and CPIB in Edinburgh and Nottingham (UK), the IGSP at Duke (USA) and the SystemsX.ch project PGCE (Switzerland). Important training opportunities for students are also in place, such as the IGERT training program in Plant Systems Biology at the Salk Institute and University of California, San Diego. Increased community action on standards and accessibility (of data, models and software tools), on training, and communicating to the public will be important to build on the opportunities that this presents. We welcome the input and contribution of the Arabidopsis community to further these aims. Advancing these aims should promote a growing breadth and sophistication of Systems Biology approaches in Arabidopsis.

The International Arabidopsis Functional Genomics Community

Country Highlights

Argentina

Arabidopsis plants were used as an efficient vector to study abiotic stress resistance conferred by the sunflower gene *HaHB1*. This technology, developed by Raquel Chan, has been transferred to Plant Bioscience Litmited (UK).

Australia and New Zealand

- The Canberra and Adelaide phenotyping facilities were officially opened in 2009 and the Adelaide node is now fully operational, International collaborations are encouraged.
- XVIII International Botanical Congress, Melbourne 23-30 July 2011.
- Arabidopsis 2013 – The 24th International Conference on Arabidopsis research will be held in Sydney, Australia, 24th-28th June.

Austria

- New research networks: "RNA Regulation of the transcriptome" -GMI and Max F. Perutz Labs; "MeioSys-Systematic analysis of factors controlling meiotic recombination in higher plants" - EU FP7 with partners from Austria, France, Italy, Netherlands, Spain and UK; "Ecological and evolutionary plant epigenetics" - ESF EEFG project, Netherlands, Germany, Switzerland and Austria.
- Arabidopsis 2012 – The 24th International Conference on Arabidopsis research will be held at the Hofburg Palace in Vienna, 3-7 July 2012.

China

- A new centre for plant research, the Institute of Plant Science was opened in Shanghai in December 2010.
- The web-based software GOEAST-Gene Ontology Enrichment Analysis Software Toolkit that provides an user friendly visualization resouce for gene ontology analysis for high-throughput data was developed.

Czech Republic

- Czech Republic joined MASC in September 2010 with Viktor Zarsky (Charles University, Prague) as its representative.
- An online tool to access and analyze trancriptomic data has been developed (Arabidopsis Gene Family Profiler).
- It is hoped that major EU investments in the Czech Republic scientific infrastructure will positively affect plant science in the coming years.

Finland

- Finland joined MASC individually in the spring of 2011 with Ykä Helariutta (University of Helsinki, Helsinki) as its representative.
- Finnish universities are organized in biocentres to avoid unnecessary duplication of equipment. The umbrella organization Biocenter Finland comprises six Finnish universities and provides funding for nationwide technology services for the benefit of the entire community.

Ireland

Ireland 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. www.plantresearchireland.org/

Israel

- BARD announced that no more than 25% of awards could go to "proposals whose outcomes are expected to have application in more than seven years", making it very unlikely for Arabidopsis research to be funded via this channel.
- The Manna Center for Plant Biosciences, growth and analyses facility, Tel Aviv University, is now fully operational
- Formal international agreements for collaborations and student exchanges between the Center for Plant Cell Biology at the University of California at Riverside, the Manna Center in Tel Aviv and the Weizmann Institue have been reached.

Italy

- No new Arabidopsis-related large initiatives have been initiated this year.
- S. Sabatini (Sapienza University, Rome) received a European starting grant for the study of the root meristem.

Japan

- Japan hosted the 21st International Conference on Arabidopsis Research (ICAR2010, http://arabidopsis2010.psc.riken.jp/) on June 6-10, 2010 in Pacifico Yokohama, Yokohama, Japan. ICAR 2010 highlighted recent advances in Arabidopsis research and its translation into research in crops and trees. Approximately 1,300 scientists (including 700 overseas) attended the meeting.
- New Arabidopsis initiatives started in 2010, including two 5-year projects and a 2.7 billion yen project that aims to realize a low carbon society.

The Netherlands

Notable published highlights: Schlereth et al. (2010); Kaufmann *et al*, Science 2010.

Sweden

- Sweden joined MASC as an individual country in Spring 2010 with Maria Eriksson (Umea University, Finland) as its representative.
- Swedish published highlights include: Boutté, Y *et al*. (2010) EMBO Journal (29): 546-558; Eklund, M *et al*. (2010) Plant Cell (22): 349-353; Weinhofer, I *et al*. (2010) PLoS Genet (6): e1001152; Sjögren, LL *et al.* (2011) Plant Cell (23): 322-332; Carlsbecker *et al*. (2010) Nature (465): 316-321; Zhao, Z *et al*. (2010) Nature (465): 1089-1092.

Switzerland

- Switzerland joined MASC in Spring 2010 with Wilhelm Gruissem (ETH, Zurich) as its representative.
- The AGRON-OMICS consortium developed the AGRONOMICS1 Arabidopsis genome tilling array in colaboration with Affymetrix., which has been made available to the Arabidopsis community in 2010.
- The Plant Swiss Network was created in 2010 and the Swiss Plant Science Web was established to coordinate educational, training and research activities of plant scientists in Switzerland.
- The 8th Tri-National Arabidopsis Meeting (TNAM, Austria-Germany-Switzerland) in 2012 will be hosted by Switzerland at the University of Lausanne.

United Kingdom

- In January 2011 in partnership with the Bill and Melinda Gates Foundation, the UK Department for International Development, the Indian Department of Biotechnology, BBSRC launched a £20M/$32M major international research initiative to improve food security for the developing countries.
- In 2011 BBSRC invested £26M into the Norwich Research Park, where the prestigious plant research institute the John Innes Centre and the Genome and Analysis Centre (TGAC) are based.
- GARNet, the UK Arabidopsis Researchers Network, updated its website (www.garnetcommunity.org.uk).
- GARNet facilitated discussions with other UK plant science communities to establish UK Plant Science (UKPS), a Federation of UK plant scientists.
- The UK "PlantSci" website was launched in December 2010 (www.plantsci.org.uk) to provide information relevant to UK plant scientists all in one place, including funding, news, and a database of UK plant scientists.

United States

- The two newly elected members of the North American Arabidopsis Steering Committee (NAASC) are Jose Alonso (North Carolina State University, USA) and Nicholas Provart (University of Toronto, Canada). Joanna Friesner is the NAASC Coordinator and Scott Poethig (University of Pennsylvania, Philadelphia) served as the NAASC Chair in the past year.
- The creation of the International Arabidopsis Information Consortium (IAIC) has been proposed following the MASC/NAASC workshops in 2010. Blake Meyers (University of Delaware) together with Erich Grotewold (ABRC, Ohio University) submitted a grant to NSF to support the creation of the IAIC. Nominations and elections for the Scientific Advisory Board are expected to take place through summer 2011.

Argentina

http://www.arabidopsis.org/info/2010_projects/Argentina.jsp
Contact: Jorge J. Casal
IFEVA, Faculty of Agronomy, University of Buenos Aires
Email address casal@ifeva.edu.ar

New Grants from the National Research Council of Argentina (CONICET), which support Arabidopsis research:

- 11420100100200. DC1-domain proteins in development and defense in *Arabidopsis thaliana*. Fiol, Diego Fernando. Instituto de Investigaciones Biológicas, Universidad de Mar del Plata.
- 11220100100102. Retrograde mitochondrial signals in *Arabidopsis thaliana*. Martín, Mariana Laura. Instituto de Investigaciones Biológicas, Universidad de Mar del Plata.
- 11220100100395. Polyamines in the *Arabidopsis thaliana*-*Botrytis cinerea* system. Pieckenstain, Fernando Luis. Instituto Tecnológico de Chascomús (IIB-Intech), Chascomús.
- 11220100100018. Mismatch repair systems and genomic stability in *Arabidopsis thaliana*. Spampinato, Claudia Patricia. Centro de Estudios Fotosintéticos y Bioquímicos (CONICET - Fund. M. Lillo) Universidad Nacional de Rosario.

Noteworthy breakthroughs published in 2010:
A search of the published literature yields 39 articles published by research investigators from Argentina where *Arabidopsis thaliana* is mentioned in the title or abstract. We have selected the following three to highlight:

- Sanchez, SE Petrillo, E Beckwith, EJ Zhang, X Rugnone, ML Hernando, CE Cuevas, JC Godoy Herz, MA Depetris-Chauvin, A Simpson, CG Brown, JWS Cerdán, PD Borevitz, JO Mas, P Ceriani, MF Kornblihtt, AR Yanovsky, MJ (2010) A methyl transferase links the circadian clock to the regulation of alternative splicing. Nature (468): 112-116
- Mateos, JL Bologna, NG Chorostecki, U Palatnik, JF (2010) Identification of MicroRNA Processing Determinants by Random Mutagenesis of Arabidopsis MIR172a Precursor. Current Biology (20): 49-54
- Strasser, B Sánchez-Lamas, M Yanovsky, MJ Casal, JJ Cerdán, PD (2010) Arabidopsis thaliana life without phytochromes. PNAS(107): 4776-4781

Using Arabidopsis as a test tube to find functions of genes of other species

The characterization of Arabidopsis genes has been and continues to be the most efficient road to investigate plant gene function. In addition, the knowledge and facilities offered by Arabidopsis makes it an excellent heterologous system to test the function of genes of other species. Dr Raquel Chan, leader of a CONICET-funded laboratory at Universidad Nacional del Litoral in Santa Fe-Argentina, has discovered that the *HaHB1* gene from sunflower confers impressive resistance to a diverse range of abiotic stresses, including freezing at temperatures as low as -8°C, chilling for several days at temperatures just above freezing, and prolonged drought. The experiments were performed in transgenic Arabidopsis plants bearing the constructs in which the *HaHB1* gene under the control of either its own promoter or a constitutive promoter. This technology has been transferred to Plant Bioscience Limited (UK).

Australia & New Zealand

http://www.arabidopsis.org/info/2010_projects/Australia.jsp
Contact: Barry Pogson
The Australian National University, Canberra
http://www.anu.edu.au/bambi/people/academic/pogson.php
Email: barry.pogson@anu.edu.au

Major areas of Arabidopsis research and functional genomics are Canberra, Melbourne 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) Centre of Excellence in Plant Energy Biology (www.plantenergy.uwa.edu.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.

Key technology and informatics platforms:

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) or Mark Tester (mark.tester@acpfg.com.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.

Upcoming Conferences

- **XVIII International Botanical Congress**, Melbourne 23rd-30th July 2011. See http://www.ibc2011.com/

- **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. Contact the Chair or a member of the organizing committee for more details and to make suggestions for symposia and speakers. **Chair**: Barry Pogson (barry.pogson@anu.edu.au). **Local Organising Committee**: Bernie Carroll, Chris Cazzonelli, David Smyth, Suresh Balasubramanian, Gonzalo Estavillo, Jean Finnegan, Harvey Millar, Ian Small, Iain Searle, Jim Whelan, Joanna Putterill, Auckland, John Bowman, Josh Mylne, Liz Dennis, Mark Tester, Mary Byrne, Peter Waterhouse, Richard Macknight, and Tony Millar.

Austria

http://www.arabidopsis.org/info/2010_projects/Austria.jsp
Contacts: Marie-Theres Hauser, BOKU-University of Natural Resources & Applied Life Science, Vienna
Ortrun Mittelsten Scheid, GMI-Gregor Mendel Institute of Molecular Plant Biology
Email: marie-theres.hauser@boku.ac.at
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Arabidopsis projects are undertaken at five institutions (BOKU-University of Natural Resources & Applied Life Science Vienna, GMI-Gregor Mendel Institute of Molecular Plant Biology, Faculty of Life Sciences, MFPL-Max F. Perutz Laboratories of the University Vienna and the Medical University Vienna, University of Salzburg, University of Graz) on:

Population genetics:

- Magnus Nordborg: (www.gmi.oeaw.ac.at/research-groups/magnus-nordborg). Scientific Director of the GMI since 2009

Systems biology:

- Wolfram Weckwerth (www.univie.ac.at/mosys/wolfram_weckwerth.html). Austrian representative for the COST European plant proteomics consortium, Chair of the MASCP (proteomics subcommittee), the largest proteomics database resource for *Arabidopsis thaliana*

Chromosome biology:

- Karel Riha (www.gmi.oeaw.ac.at/research-groups/karel-riha): telomeres and genome stability
- Peter Schlögelhofer (www.mfpl.ac.at/index.php?cid=54): meiotic recombination

Development, hormones and stress responses:

- Lindy Abas (www.dagz.boku.ac.at/11133.html): membrane proteins, hormone transport
- Andreas Bachmair: (www.mfpl.ac.at/index.php?cid=702): ubiquitination and sumoylation
- Wolfgang Busch (www.gmi.oeaw.ac.at/research-groups/wolfgang-busch): regulatory networks of root development
- Thomas Greb (www.gmi.oeaw.ac.at/research-groups/thomas-greb): vascular tissue development
- Marie-Theres Hauser (www.dagz.boku.ac.at/11135.html?&L=1): development, stress
- Claudia Jonak (www.gmi.oeaw.ac.at/research-groups/claudia-jonak): stress signalling and adaptation
- Jürgen Kleine Vehn (www.dagz.boku.ac.at/dagz.html?&L=1): phytohormonal crosstalk and differential growth regulation
- Christian Luschnig (www.dagz.boku.ac.at/7968.html?&L=1): auxin, chromatin
- Irute Meskiene (www.mfpl.ac.at/index.php?cid=53): PP2Cs in stress and development
- Thomas Roitsch (www.uni-graz.at/botanik/): carbohydrate metabolism, hormone action, biotic and abiotic stress responses, reproduction
- Markus Teige (www.mfpl.ac.at/ index.php?cid=55): Targets of calcium-dependent protein kinases
- Andrea Pitzschke (www.dagz.boku.ac.at/dagz.html?&L=1): Early signaling events in the plant stress response
- Eric van der Graaff (www.uni-graz.at/botanik/): molecular genetics of stress responses

Epigenetics:

- Antonius and Marjori Matzke (www.gmi.oeaw.ac.at/research-groups/antonius-marjori-matzke): RdDM, nuclear architecture
- Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/research-groups/ortrun-mittelsten-scheid): genetic and epigenetic changes in polyploids and upon abiotic stress
- Hisashi Tamaru (www.gmi.oeaw.ac.at/research-groups/hisashi-tamaru): chromatin during pollen development

Glycobiology:

- Lukas Mach (www.dagz.boku.ac.at/7967.html): glycosylation enzymes, proteinases, vacuolar proteins
- Georg Seifert (www.dapp.boku.ac.at/2238.html?&L=1): arabinogalactan proteins and PCD
- Richard Strasser (www.dagz.boku.ac.at/12349.html?&L=1): N-glycosylation
- Raimund Tenhaken (www.uni-salzburg.at/zbio/tenhaken): biosynthesis of nucleotide sugar for cell wall polymers, PCD

Plant pathogen interactions:

- Gerhard Adam (www.dagz.boku.ac.at/11137.html?&L=1): role of mycotoxins in plant-pathogen interactions
- Holger Bohlmann (/www.dapp.boku.ac.at/2238.html?&L=1): MIOX gene in nematode induced syncytia
- Julia Hofmann (www.dapp.boku.ac.at/h953_einheit.html?&L=1): Molecular pathophysiology

RNA metabolism:

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

Current Research Consortia

- "Chromosome dynamics - unravelling the functions of chromosomal domains" is a multiorganismal project (Arabidopsis represented by Peter Schlögelhofer) (www.mfpl.ac.at/index.php?cid=647).
- "From regulatory complexity to biological function: Metabolic adjustment of plant development by regulatory bZIP factor networks" (www.zmbp.uni-tuebingen.de/PlantPhysiology/bzip/) a cooperative International Project funded by the German DFG, the Austrian FWF, the Dutch NWO, and the Spanish MEC.

- "Chloroplast Signals, COSI" (www.univie.ac.at/cosi) EC-funded Marie-Curie Initial Training Network (ITN) investigating chloroplast signals and metabolic regulation in a network of 10 European Institutions including BayerBioScience as industrial partner.
- "Signalling to plant immunity responses" (PathoNet) is an ERANet PG project coordinated by Irute Meskiene with members from Austria, Germany and United Kingdom (www.erapg.org/everyone/16790/18613/19533/19539)
- "Calcium Regulation of Plant Productivity" (CROPP) is an ERANet PG project with members from Austria, Germany, Israel and United Kingdom (www.erapg.org/everyone/16790/18613/19533/19537)
- "Alternative Splicing and Abiotic Stress" (PASAS) is an ERANet PG project with members from Austria, Israel and United Kingdom(www.erapg.org/everyone/16790/ 18613/19533/19538)
- "Fusarium Metabolites and Detoxification Reactions" SFB 37-Project coordinated by Gerhard Adam from the BOKU-University of Natural Resources & Life Sciences, Vienna (www.dagz.boku.ac.at/sfbf37fusarium.html)
- "RNA Regulation of the transcriptome" SFB 43, coordinated by Renee Schroeder, Max F Perutz Labs, project leaders include: Marjorie Matzke, GMI and Andrea Barta, Max F. Perutz Labs.
- "MeioSys-Systematic analysis of factors controlling meiotic recombination in higher plants", a collaborative project funded by the EU (FP7) with partners from Austria (Peter Schlögelhofer), France, Italy, Netherlands, Spain and the UK.
- "Ecological and evolutionary plant epigenetics" (EpiCOL): ESF EEFG project with members from the Netherlands, Germany, Switzerland and Austria.
- "Trans-national Infrastructure for Plant Genomic Science" (transPLANT) EU project, spearheaded by EBI with partners from Austria (Magnus Nordborg), Germany, France, Poland, UK, Spain, Netherlands

Conferences:

- 30th International Symposium of the European Society of Nematologists (ESN), 19-23 September 2010, Vienna; www.esn-online.org/esn-2010-vienna
- **Arabidopsis 2012** – The 23th International Conference on Arabidopsis research will be held at the Hofburg Palace in Vienna, 3-7 July 2012. The local organising committee is: Magnus Nordborg, Marie-Theres Hauser and Wolfram Weckwerth.

Public Relations- Education:

- GEN-AU Summer School: educational program for high school students (www.gen-au.at/artikel.jsp?id=761&base=vermitteln&lang=en)
- "Dialog Gentechnik": 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/index.php?lang=en)
- Vienna Biocenter International PhD Programmes:international competitive program offer up to 4 years Arabidopsis research projects. www.univie.ac.at/vbc/PhD/
- Max F. Perutz International PhD Program: since 2009, two calls per year, several plant research groups are recruiting.www.projects.mfpl.ac.at/mfpl-phd-selection/
- University Meets Public: Information on genetically modified plants for the general public
- VBC Summer School is a ten week reseach and teaching programme for undergraduates from around the world (www.vbcsummerschool.at)

Major funding sources

(government/public/private) for Arabidopsis functional genomics

- Basic and translational research: FWF (www.fwf.ac.at)
- Vienna region: WWTF (www.wwtf.at)
- Specific programs (GEN-AU) (www.gen-au.at/index.jsp?lang=en)
- Austrian Research Promotion Agency (FFG) (www.fff.co.at)

Awards:

Magnus Nordborg received an Advanced ERC grant to support his work on the genetic architecture of adaptive natural variation (www.gmi.oeaw.ac.at/news/magnus-nordborg-awarded-erc-grant).

China

http://www.arabidopsis.org/info/2010_projects/China.jsp
Contact: Wei-Cai Yang
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences
Email: wcyang@genetics.ac.cn

The current funding for Arabidopsis research by the National Science Foundation of China (NSFC) supports development, sexual plant reproduction, hormone, stem cell, and plant-microbe interactions. The funding for Arabidopsis research will continue to benefit from the rapid increase in NSFC budget in 2011. Two more projects with each of 25-30m RMB on seed development and fatty acid biosynthesis respectively, will most likely be funded in 2011 by the Ministry of Science and Technology of China (MOST).

Current Major Projects:

- The eight-year program on phytohormones continues to support research projects in Arabidopsis. In the year 2010, 30m RMB was invested in projects on the biology of hormone metabolism and modification, hormonal regulation of organogenesis and abiotic stress, and technology on quantification of phytohormones.
- NSFC also supported three key projects on plant-virus interaction. In addition, two new projects with about 25m each mainly on Arabidopsis research were funded in 2010. One on meiosis headed by Dr. Hong Ma of Fudan University and the other on protein modification and degradation headed by Dr. Qi Xie of IGDB respectively, were supported by the "Reproduction and Development Initiative" and "Proteomics 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.

New Institute:

The Institute of Plant Science, a new centre for plant research headed by its deputy director Dr. Hongquan Yang, was inaugurated in Shanghai Jiaotong University on December 3, 2010. The newly established institute will focus on molecular mechanisms controlling plant development, disease and insect resistance, secondary metabolism, genetic engineering, molecular breeding, and plant physiology.

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://www.arabidopsis.org/info/2010_projects/Czech Republic.jsp
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Department of Experimental Plant Biology, Charles University and IEB ASCR Prague
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All the labs working with Arabidopsis in Czech Republic have formal as well as informal collaborations and contacts with the colleagues abroad, however in respect to Arabidopsis functional genomics no specific major collaborative project was proposed.

Funding sources

- There is no specific focus of Arabidopsis research funding in the Czech Republic. However, both major grant/funding agencies for basic research – 1. Czech Science Foundation (GACR) Prague (http://www.gacr.cz) and 2. Ministry of Education, Youth and Sports of Czech Republic, Prague (http://www.msmt.cz/research-and-development-1)– regularly support projects based on the use of Arabidopsis as a model plant.
- Smaller agencies - e.g. Grant Agency of the Academy of Sciences or universities grant agencies – support Arabidopsis based projects.
- The Grant Agency of the Ministry of Agriculture supports more applied research but Arabidopsis may be included as a knowledge template for applications.
- Recently, the Technological Grant Agency (TACR) for applied research was established and it has to be seen how far this agency will support research based on Arabidopsis model.

Arabidopsis research activities:

Arabidopsis research in Czech Republic is mainly carried out at universities and institutes of the Academy of Sciences of the Czech Republic (ASCR):

- Charles University, Prague, Department of Experimental Plant Biology (http://kfrserver.natur.cuni.cz/english/index.html)
- Masaryk University, Brno, Institute of Experimental Biology (http://www.sci.muni.cz/main.php?stranka=314010&podtext=20&jazyk=EN)
- Mendel University of Agriculture and Forestry, Brno, Department of Molecular Biology and Radiology (http://umbr.af.mendelu.cz/en?lang=en)
- Palacky University, Olomouc, Section of Biology (http://www.upol.cz/en/faculties/faculty-of-science/departments-institutions/)
- South Bohemian University, Ceske Budejovice, Faculty of Science, Department of Plant Physiology (http://kfr.prf.jcu.cz/download/english_info.pdf)
- Institute of Experimental Botany ASCR, Prague and Olomouc (http://www.ueb.cas.cz/en)
- Institute of Biophysics ASCR, Brno (http://www.ibp.cz/cs/)
- Institute of Molecular Plant Biology ASCR, Ceske Budejovice (http://www.umbr.cas.cz/)
- The major Arabidopsis research activity over the last years was concentrated in the three Research Centers comprising researchers from all above summarized laboratories.
- Research Centers “SIDROS” (Signaling in Plant Development and Growth) and “REMOROST” (The regulation of plant morphogenesis LC06034) supported by the Ministry of Education of CR both including selected laboratories from several institutions including Institute of Experimental Botany ASCR Prague/Olomouc (coordinator), Masaryk University and Mendel Agricultural University in Brno, Palacký University in Olomouc, Institute of Photonics ASCR, Institute of Chemical Technology and Charles University all three in Prague. Equally Research Center “GENOME” (LC06004) also supported by the Ministry of Education of CR and coordinated by the Institute of Biophysics ASCR (Brno) is focused on plant genome structure and dynamics and based on Arabidopsis as one of the major models and includes Charles University and Institute of Experimental Botany ASCR (Prague) and the Institute of Molecular Plant Biology ASCR (Ceske Budejovice).
- Upcoming years should be positively affected by the implementation of major EU investments into the Czech Republic scientific infrastructure. Research involving basic plant research using Arabidopsis as a model is carried out in two centers in Moravia, which are of major importance - “Centre of the Region Hana for Biotechnological and Agricultural Research” (http://www.cr-hana.eu/en/index.html) in Olomouc combining researchers from Palacky University, Crop Research Institute (VURV) and Institute of Experimental Botany ASCR and “Central European Institute of Technology” (http://www.ceitec.eu/) in Brno which will include a substantial unit devoted to genomics and proteomics of plant systems. It is expected that these new research facilities will attract also top scientists from abroad. In general however plant sciences in the Czech Republic will still rely mostly on the local funding possibilities with the efforts to recruit more EU financial resources.

Highlights 2010

- Mozgová, I Mokros, P Fajkus, J (2010) Dysfunction of chromatin assembly factor 1 induces shortening of telomeres and loss of 45S rDNA in *Arabidopsis thaliana*. Plant Cell (22): 2768-80
- Dvorackova, M Rossignol, P Shaw, PJ Koroleva, OA Doonan, JH Fajkus, J (2010) AtTRB1, a telomeric DNA-binding protein from Arabidopsis, is concentrated in the nucleolus and shows highly dynamic association with chromatin. Plant Journal (61): 637–649

- Fendrych, M Synek, L Pecenkova, T Toupalova, H Cole, R Drdova, E Nebesarova, J Sedinova, M Hala, M Fowler, JE Zarsky, V (2010) The Arabidopsis Exocyst Complex Is Involved in Cytokinesis and Cell Plate Maturation. The Plant Cell (22): 3053-3065
- Hala, M Soukupova, H Synek, L Zarsky, V (2010) Arabidopsis RAB geranylgeranyl transferase beta-subunit mutant is constitutively photomorphogenic, and has shoot growth and gravitropic defects. Plant Journal (62): 615-27

Tools and resources

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

Finland

http://www.arabidopsis.org/info/2010_projects/Finland.jsp
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To avoid unnecessary overlaps investing in the newest technologies and equipment, Finnish universities have been organized into biocenters. Technology services are provided by Biocenter Finland infrastructure networks. Biocenter Finland is an umbrella organisation of biocenters in six Finnish Universities (Helsinki, Kuopio, Oulu, Tampere and Turku, and the Åbo Akademi University). Biocenter Finland provides funding for nationwide technology services in the partner biocenters for the benefit of the entire scientific community. Arabidopsis research is carried out within the Biocenter framework.

Arabidopsis institutions and principal investigators:

- University of Helsinki: Tapio Palva, Jaakko Kangasjärvi, Ykä Helariutta, Mikael Brosche, Ari Pekka Mähönen
- University of Turku: Eva-Mari Aro, Eevi Rintamäki, Paula Mulo, Saijaliisa Kangasjärvi
- University of Oulu: Outi Savolainen
- University of East FInland: Sirpa Kärenlampi

Current research avenues:

- Heavy metal tolerance mechanisms (Kärenlampi; http://www.uef.fi/biotieteiden-laitos/kasvibiotekniikka). The hyperaccumulator *Thlaspi caerulescens* belongs to the same taxonomic family (Cruciferae) as *Arabidopsis thaliana*. The specific aim is 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.
- The Plant Stress group (Jaakko Kangasjärvi) investigates the role of reactive oxygen species (ROS) as signaling molecules. They use genomic, genetic, molecular and biochemical strategies with Arabidopsis to identify the central components in ROS perception and signal transduction and understand their functions. Within the ERA-PG network "Plant Receptor-like Kinases in ROS Signaling" (PROSIG) they investigate the role of plasmamembrane located receptor-like kinases (ROS) in the response to ROS. Their forward genetics screens have yielded novel insights into how ROS mediate various cellular responses to stresses and developmental cues. In addition to these mutant-based approaches they have also take advantage of natural variation within Arabidopsis. They have identified the genetic loci that confer enhanced sensitivity or tolerance to ROS in natural accessions and are analyzing their molecular functions.
- Paula Mulo (University of Turku) together with her German collaborators has shown that the photosynthetic ferredoxin-NADP(+) oxidoreductase (FNR) is an important mediator between membrane-bound light reactions and metabolic pathways in chloroplast.
- Plants need a highly responsive regulatory system to keep photosynthetic light reactions in balance with the needs and restrictions of the downstream metabolism. Eva-Mari Aro lab (University of Turku) has shown that membrane-bound protein kinases STN7 and STN8 form an important regulatory loop that optimises plant growth under naturally fluctuating light conditions.

Publication highlights:

- Semane, B Dupae, J Cuypers, A Noben, JP Tuomainen, M Tervahauta, A Kärenlampi, S Van Belleghem, F Smeets, K Vangronsveld, J (2010) Leaf proteome responses of *Arabidopsis thaliana* exposed to mild cadmium stress. Journal of Plant Physiology (167): 247-254
- Tikkanen, M Grieco, M Kangasjärvi, S and Aro, EM (2010) Thylakoid protein phosphorylation in higher plant chloroplasts optimises electron transfer under fluctuating light. Plant Physiology 152(2): 723-735.
- Vahisalu, T Puzõrjova, I Brosché, M Valk, E Lepiku, M Moldau, H Pechter, P Wang, YS Lindgren, O Salojärvi, J Loog, M Kangasjärvi, J and Kollist, H (2010) Ozone-triggered rapid stomatal response involves the production of reactive oxygen species, and is controlled by SLAC1 and OST1. Plant J. (62): 442-53
- Jaspers, P Overmyer, K Wrzaczek, M Vainonen, JP Blomster, T Salojärvi, J Reddy, RA and Kangasjärvi, J (2010) The RST and PARP-like domain containing SRO protein family: analysis of protein structure, function and conservation in land plants. BMC Genomics. (11): 170
- Carlsbecker, A Lee, J-Y Roberts, C Dettmer, J Lehesranta, S Zhou, J Lindgren, O Moreno, M Vaten, A Thitamadee, S Campilho, A Sebastian, J Bowman, JL Helariutta, Y Benfey, PN. Cell signaling by microRNA165/6 mediates gene dosage dependent root cell fate. Nature (465): 316-21

Ireland

http://www.arabidopsis.org/portals/masc/countries/Ireland.jsp
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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 no private sector institutions working with *Arabidopsis thaliana* in Ireland. Website: www.plantresearchireland.org/

Irish Arabidopsis research groups

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

- Prof Charles Spillane, Genetics and Biotechnology Lab, National University of Ireland Galway (NUIG), Ireland.
- 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.

Funding sources for Arabidopsis research in Ireland include Science Foundation Ireland; Department of Agriculture, Fisheries and Food; Irish Research Council for Science, Engineering and Technology; and the European Union.

Irish scientific highlights

Recent publications from Irish plant research groups working on Arabidopsis thaliana include:

- Wolff, P Weinhofer, I Seguin, J Roszak, P Beisel, C Donoghue, MTA Spillane, C Nordborg, M Rehmsmeier, M Köhler C (2011) High-Resolution Analysis of Parent-of-Origin Allelic Expression in the Arabidopsis Endosperm. PLOS Genetics (in press).
- Rae, L Lao, NT Kavanagh, TA (2011) Regulation of multiple aquaporin genes in Arabidopsis by a pair of recently duplicated DRB transcription factors. Planta. DOI: 10.1007/s00425-011-1414-z
- Donoghue, MT Keshavaiah, C Swamidatta, SH Spillane, C (2011) Evolutionary origins of Brassicaceae specific genes in *Arabidopsis thaliana*. BMC Evol Biol. (18) 11:47
- Wellmer, F Riechmann JL. (2010) Gene networks controlling the initiation of flower development. Trends Genet. (12): 519-27
- Wendt, T Doohan, F Winckelmann, D Mullins, E (2010) Gene transfer into *Solanum tuberosum* via Rhizobium spp. Transgenic Res. (20): 377-86
- Petti, C Khan, M Doohan, F (2010) Lipid transfer proteins and protease inhibitors as key factors in the priming of barley responses to Fusarium head blight disease by a biocontrol strain of *Pseudomonas fluorescens*. Funct Integr Genomics 10: 619-27
- Doyle, SM McCabe, PF (2010) Type and cellular location of reactive oxygen species determine activation or suppression of programmed cell death in Arabidopsis suspension cultures. Plant Signal Behav. (5): 467-8
- Graciet, E Mesiti, F Wellmer, F (2010) Structure and evolutionary conservation of the plant N-end rule pathway. Plant J. (61): 741-51
- Doyle, SM Diamond, M McCabe, PF (2010) Chloroplast and reactive oxygen species involvement in apoptotic-like programmed cell death in Arabidopsis suspension cultures. J Exp Bot. (61): 473-82
- Jansen, MA Martret, BL Koornneef, M (2010) Variations in constitutive and inducible UV-B tolerance; dissecting photosystem II protection in *Arabidopsis thaliana* accessions. Physiol Plant. (138): 22-34

Israel

http://www.arabidopsis.org/portals/masc/countries/Israel.jsp
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In 2010, ~80 research articles employing Arabidopsis were published from groups in Israel, doubling the output from the previous year. These included such diverse subjects as bioinformatics, metabolic engineering, photosynthesis and molecular development. The major centers of Arabidopsis research are in The Hebrew University of Jerusalem (Faculty of Agriculture), Tel Aviv University, the Agricultural Research Organization (Volcani Center), the Weizmann Institute of Science, and the Ben Gurion University of the Negev (Sde Boker Campus).

Funding for basic research in decline:
In a further effort to encourage project more immediately related to agriculture (and thus curtail basic research, primarily involving Arabidopsis), BARD (The United States - Israel Binational Agricultural Research and Development Fund) announced that no more than 25% of awards could go to “proposals whose outcomes are expected to have application in more than seven years”, or in other words for Arabidopsis-based research. This came one year after BARD cancelled their “Model System and Functional Biology in the Service of Agriculture” panel, the panel that funded the majority of Arabidopsis research. The Israel Science Foundation and European Community remain the major source of funding for basic research employing Arabidopsis.

Newly opened facilities:
The Manna Center for Plant Biosciences at Tel Aviv University is fully operational with the addition of three Percival two-tiered growth chambers and a FloraLED chamber.

Returning young scientists:
Bar-Ilan University hired Dr. Gadi Miller from the lab of Ron Mittler in Nevada, USA.

International collaborations:
Formal international agreements for collaborations and student exchanges have been formalized between the The Center for Plant Cell Biology at the University of California at Riverside (CEPCEB) and two places in Israel: the Manna Center for Plant Biosciences at Tel Aviv University and the Department of Plant Sciences at Weizmann Institute of Science.

Italy

http://www.arabidopsis.org/portals/masc/countries/Italy.jsp
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Newly awarded Arabidopsis projects:

- No new Arabidopsis-related large initiatives have been initiated this year in Italy.
- Sabrina Sabatini (Sapienza University, Rome) is the recipient of a European Research Council Starting Grant for the research: "To the root of organ growth: the control of root meristem activity in Arabidopsis" (ERC-2010-StG - n° 260368).
- C. Tonelli (University of Milan) has been awarded a National Research grant by the Italian consortium AGER (www.progettoager.it) with the aim to validate in Arabidopsis grape genes putatively involved in response to drought and salt stress. The group of F.Cervone/G. de Lorenzo (Sapienza University, Rome) has been awarded a grant from the Italian Ministry of Forestry and Agriculture.

Current Arabidopsis Projects:

- The groups of M.Cardarelli/P. Costantino and of M.M. Altamura (Sapienza University, Rome) are involved in the second year of a COST action FA0903 on "Harnessing Plant Reproduction of Crop improvement".
- The groups of S.Sabatini/P.Costantino and of M.M. Altamura (Sapienza University, Rome) are involved in the second year of the Project of National Interest (PRIN): "The cytokinin/auxin interaction in the control of Arabidopsis root architecture" funded by the Italian Ministry of University and Scientific Research (MIUR, http://www.miur.it).
- The groups of G.Serino/P.Costantino (Sapienza University, Rome) and G. Frugis (CNR, Rome), in collaboration with Q. Xie (CAS, China) and LJ. Qu (PekingUniversity) are continuing their collaborations funded whithin the frame of the Executive Programme of Scientific and Technological Cooperation between Italy and China and promoted by the Italian Ministry of Foreign Affairs.
- The group of F.Cervone/G.de Lorenzo (Sapienza University, Rome) is being supported by the ERC Advanced Grant FUEL-PATH "Exploiting the saccharification potential of pathogenic microorganisms to improve biofuel production from plants".
- P. Costantino (Sapienza University, Rome) is the Italian scientific representative in the UK coordinated ERA-Net proposal: ERA-CAPS (Concerted Actions in Plant Sciences).

Relevant Arabidopsis genomics tools and resources:

- Several useful engineered Arabidopsis lines have been created, among which ACA8 (*Arabidopsis thaliana* Ca^{2+}-ATPase isoform 8) deletion and single point mutants by the group of Bonza/de Michelis (University of Milan), and *Atpme3* KO mutants by the group of F.Cervone/G. de Lorenzo (Sapienza University, Rome). The same group has also generated plants overexpressing fusion proteins between extracellular and intracellular domains of the WAK1 and EFR and FLS2 and EFR receptors, as well as plants overexpressing the *MEI* genes. Tissue- and cell- specific promoters have been generated by the M.Galbiati/C.Tonelli group (University of Milan).

Highlights of groundbreaking Arabidopsis journal articles:

- Landoni, M De Francesco, A Galbiati, M Tonelli, C (2010) A loss-of-function mutation in the *Calmodulin2* gene affects pollen germination in *Arabidopsis thaliana*. Plant Mol Biol (74): 235-47
- Bonza, MC Luoni, L (2010) Plant and animal type 2B Ca2+-ATPases: evidence for a common auto-inhibitory mechanism. FEBS Lett (584): 4783-8
- Lionetti, V Francocci, F Ferrari, S Volpi, C Bellincampi, D Galletti, R D'Ovidio, R De Lorenzo, G Cervone, F (2010) Engineering the cell wall by reducing de-methyl-esterified homogalacturonan improves saccharification of plant tissues for bioconversion. PNAS (107): 616-21
- Brutus, A Sicilia, F Maccone, A Cervone, F De Lorenzo, G (2010) A domain swap approach reveals a role of the plant wall-associated kinase 1 (WAK1) as a receptor of oligogalacturonides. (107): 9452-7
- Moubayidin, L Perilli, S Dello IOio, R Di Mambro, R Costantino, P Sabatini, S (2010) The rate of cell differentiation controls the Arabidopsis root meristem growth phase. Curr Biol (20): 1138-43
- Gabriele, S Rizza, A Martone, J Circelli, P Costantino, P Vittorioso, P (2010) The Dof protein DAG1 mediates PIL5 activity on seed germination by negatively regulating GA biosynthetic gene *AtGA3ox1*. Plant J (61): 312-23

Outreach conferences:

C. Tonelli (University of Milan) was the organizer of the 6th conference on the Future of Science, held in Venice on September 19-21, 2010.

Japan

http://www.arabidopsis.org/portals/masc/countries/Japan.jsp
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Arabidopsis research centres:

Developing research platforms for 'omics' analysis including metabolomics, hormonomics, transcriptomics and proteomics is a major aim of Institute laboratories in Japan. Major Arabidopsis metabolomics research in Japan is carried out at the RIKEN Plant Science Center (PSC) and at the Kazusa DNA Research Institute. These two institutes serve as analytical platforms for plant metabolome analysis. Hormonomics or hormone profiling is mainly carried out at RIKEN PSC. Transcriptome and Epigenome analysis based on tiling array and high-through put sequencers are mainly carried out at RIKEN PSC and at the National Institute of Basic Biology (NIBB). Proteome analyses are carried out at the Nara Institute of Science and Technology (NAIST) and RIKEN PSC.

A. RIKEN groups include the Plant Science Center (PSC), the BioResource Center (BRC) and the Bioinformatics and Systems Engineering division (BASE).
The RIKEN PSC (http://www.psc.riken.jp/english/index.html) has established the following platforms; (1) Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi), (2) Hormonomics platform (systematic analysis of plant hormones) (Hitoshi Sakakibara, Yuji Kamiya), RIKEN Plant Hormone Research Network http://hormones.psc.riken.jp/ (3) Transcriptomics by using tiling array in collaboration with RIKEN BASE (http://omicspace.riken.jp/gps/) (Motoaki Seki, Tetsuro Toyoda, Kazuo Shinozaki), (4) Proteomics analysis (Hirofumi Nakagami, Ken Shirasu) https://database.riken.jp/sw/links/en/ria1021i (5) Phenotype analysis of *Ds*-tagged lines, and Full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (Minami Matsui, Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki) http://amber/gsc.riken.jp/act/top.php http://rarge.psc.riken.jp/ http://rarge.gsc.riken.jp/phenome/ (6) Collection and phenome analysis of Ds- or T-DNA tagged mutants for nuclear–encoded chloroplast protein genes (Fumiyoshi Myouga, Kazuo Shinozaki) The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/). RIKEN PSC established the Arabidopsis MS/MS spectral tag database, widely-targeted metabolomics technology, and Arabidopsis metabolome expression database AtMetExpress (Plant Physiol., 152, 566-578 (2010)); Arabidopsis MS/MS spectral tag (MS2T) viewer (http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html); ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (http://spectra.psc.riken.jp/); Arabidopsis metabolome expression database AtMetExpress: (http://prime.psc.riken.jp/lcms/AtMetExpress/). Widely used metabolomics (http://prime.psc.riken.jp/?action=wide_index); Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search).
PSC (Hirofumi Nakagami, Ken Shirasu) and Keiko University (Yasushi Ishihama) developed a high-throughput shotgun phosphoproteomics tool for plants and phosphorylation site databases (http://phosphoproteome.psc.database.riken.jp and http://pepbase.iab.keio.ac.jp) including MS/MS spectra.
In PSC, a new project started to identify novel small ORFs in Arabidopsis genome for the discovery new functions of small polypeptides (PI: Kosuke Hanada, supported by BRAIN). RIKEN and Tokyo University of Agriculture (Kazuo Shinozaki and Teruaki Taji) analyzed 1,047 full-length cDNA clones from an Arabidopsis-related model halophyte, *Thellungiella halophila*. The full-length cDNA clones are available from the RIKEN BRC.

B. RIKEN BRC, Experimental Plant Division (M. Kobayashi, kobayasi@rtc.riken.jp) participates to the National BioResource Project and distributes Arabidopsis resources including transposon-tagged mutants, FOX lines, Arabidopsis full-length cDNA clones and Arabidopsis T87 cells. Full-length cDNA clones and cultured cells of various model plants, including the model moss *Physcomitrella patens,* model tree *Populus nigra* and model biofuel crop *Manihot esculents*, also preserved and distributed from RIKEN BRC. More than 1,400 laboratories and groups in the world have already received materials from RIKEN BRC (http://www.brc.riken.go.jp/lab/epd/Eng/).

C. RIKEN BASE (Tetsuro Toyoda) (http://www.base.riken.jp/) (1) Japan's national integrated database project covering Arabidopsis omics information resources (https://database.riken.jp/sw/links/en/crib158s39i/), (2) PosMed (Positional Medline) for Arabidopsis genes is an intelligent search engine integrating genome information and literature (http://omicspace.riken.jp/PosMed/) (3) GenoCon: International Genome Design Contest in Arabidopsis (http://genocon.org).

D. Kazusa DNA Research Institute (Daisuke Shibata). New releases of the KaPPA-View4 viewer (http://kpv.kazusa.or.jp/kpv4/) for integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, MassBase (http://webs2.kazusa.or.jp/massbase/), 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/).

New Arabidopsis Initiatives:

- Two 5-year projects supported by the Grant-in-Aid of MEXT: 1. Environmental sensing of plants: Signal perception, processing and cellular responses (2010-2015), Akira Nagatani, Kyoto University 2. Integrated Analysis of Strategies for Plant Survival and Growth in Response to Global Environmental Changes (2010-2015), Jian Feng Ma, Okayama University, Institute of Plant Science and Resources
- ERATO Higashiyama Live-Holonics Project (2010-2015, 1.8 billion yen) Head: Tetsuya Higashiyama, Nagoya University. This project aims to examine cells and extracellular signaling molecules of living material with complete control under the microscope, by developing new imaging technologies.
- Construction of Plant Science Infrastructure for Realizing a Low-Carbon Society is in progress. (2.7 billion yen). The following research platforms are hosted at 9 Research Institutes and Universities (RIKEN, NAIST, NIBB, Tohoku Univ., Tsukuba Univ., Univ. of Tokyo, Nagoya Univ., Kyoto Univ. and Okayama Univ.): Research platforms are 1. Metabolome, 2. Hormonome, 3. Ionome, 4. Photosynthesis and Nitrogen Metabolism, 5. Genome, Epigenome and Transcriptome, 6. Proteome, 7. Imaging, 8. Transformation, 9. Assessment and Support of Plant Growth.
- At RIKEN a Biomass Engineering Program (www.riken.jp/bmep/english/index.html), involving a ten-year plan for activities for research and technological development that are designed to establish a consistent and innovative bioprocess that will lead plant biomass production to chemical materials and bioplastics (final products), has been launched.

Arabidopsis genomics tools and resources

- RIKEN resources and tools

Resources from RIKEN BRC (http://www.brc.riken.go.jp/lab/epd/Eng/)
Arabidopsis MS/MS spectral tag (MS2T) viewer (http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html)
Arabidopsis metabolome expression database AtMetExpress (http://prime.psc.riken.jp/lcms/AtMetExpress/)
Widely targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index)
ReSpect (RIKEN MSn Spectral Database for Phytochemicals, http://spectra.psc.riken.jp/)
Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search)
Omicspace of RIKEN BASE (http://omicspace.riken.jp/gps)
RIKEN Plant Hormone Research Network (http://hormones.psc.riken.jp/)
The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/).
RIKEN 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/)
Kazusa tools
The KaPPA-View4 viewer (http://kpv.kazusa.or.jp/kpv4/)
MassBase (http://webs2.kazusa.or.jp/massbase/)
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/).

Major funding sources for Arabidopsis functional genomics

- RIKEN and Kazusa projects are supported by MEXT and Chiba prefecture, respectively.
- Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT), www.jsps.go.jp/english/e-grants/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)
- JST-NSF project on the promotion of “metabolomics related to low carbon society” between Japan and USA.

Awards to Arabidopsis researchers:

Dr. Kiyotaka Okada (NIBB) received the JSPP award from Japanese Society of Plant Physiologists. Dr. Masao Tasaka (NAIST) received the BSJ Award of the Botanical Society of Japan.

Arabidopsis Conferences:

- 21st International Conference on Arabidopsis Research (ICAR 2010) (http://arabidopsis2010.psc.riken.jp/) was held on June 6-10, 2010 in Pacifico Yokohama, Yokohama, Japan. ICAR 2010 highlighted recent advances in Arabidopsis research and its translational research using crops and trees. About 1,300 plant researchers (700 from overseas) attended the meeting. It was the second biggest ICAR.
- The 2nd international NIBB-MPI joint symposium "Plant Science Communications 2010" was held 16th -18th of November 2010 at the Okazaki Conference Center.

The Netherlands

http://www.arabidopsis.org/portals/masc/countries/Netherlands.jsp
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New Arabidopsis Programmes:
The two programmes, the Centre for BioSystems Genomics 2012 (CBSG2012) and the Netherlands Proteomics Centre 2 (NPC2), both with substantial components of Arabidopsis research, have led to more publications over the past 12 months. CBSG2012 is predominantly oriented towards crop plants with a contribution for Arabidopsis research and translation of results into applications in crops. NPC2 is organized around proteomics technology and is devoted predominantly towards animal systems, with an Arabidopsis contribution aimed at the isolation of membrane receptor and transcription factor complexes and networks. One NWO-VENI innovation grant was awarded to an Arabidopsis project of a junior scientist.

Scientific Highlights for the Netherlands:

- Through a transcriptomics approach, Dolf Weijers and his team identified a novel mobile transcription factor (TMO7) that mediates root initiation in the early embryo in response to the auxin-dependent transcription factor MONOPTEROS (Schlereth, A Möller, B Liu, W Kientz, M Flipse, J Rademacher, EH Schmid, M Jürgens, G Weijers, D (2010) MONOPTEROS controls embryonic root initiation by regulating a mobile transcription factor. Nature (464): 913-916
- Using chromatin immunoprecipitation-based techniques (Kaufmann, K Muiño, JM Østerås, M Farinelli, L Krajewski, P Angenent, GC (2010) Chromatin immunoprecipitation (ChIP) of plant transcription factors followed by sequencing (ChIP-SEQ) or hybridization to whole genome arrays (ChIP-CHIP). Nature Protocols (5): 457- 72) the group of Gerco Angenent identified targets of the floral orchestral gene APETALA 1. While AP1 initially acts as a repressor, later in floral development as an activator thus integrating growth, patterning, and hormonal pathways (Kaufmann, K Kellmer, F Muiño, JM Ferrier, T Wuest, SE Kumar, V Serrano-Mislata, A Madueño, F Krajewski, P Meyerowitz, EM Angenent, GC Riechmann, JL (2010) Orchestration of Floral Initiation by APETALA1. Science (328): 85-89).

Sweden

http://www.arabidopsis.org/portals/masc/countries/Sweden.jsp
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Arabidopsis functional genomics in Sweden

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. Major sites of Arabidopsis functional genomics research are Gothenburg University; The Swedish University of Agricultural Sciences (SUAS) in Alnarp, Uppsala and Lund; Lund University; Umea Plant Science Centre (UPSC; Umea University and SUAS in Umea) and Uppsala University. In complement to Arabidopsis, 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 *Populus 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.

Major Arabidopsis Research Institutes:

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

- Gothenburg University, Department of Plant and Environmental Sciences, Plant Cell and Molecular Biology http://www.dpes.gu.se/english/Research/Plant_molecular_biology/
- The Swedish University for Agricultural Sciences (Uppsala); http://www.slu.se/en/faculties/nl/about-the-faculty/departments/department-of-plant-biology-and-and-forest-genetics/research/
- Umea Plant Science Centre (UPSC); http://www.upsc.se
- Uppsala University; http://www.ebc.uu.se/

Arabidopsis National Resource Centres:

- 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,"resources").

Major funding sources for Arabidopsis functional genomics:

- 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 of 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 (info@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
- There are a plethora of private foundations where it is possible to apply for support. Each University may also have their internal calls to support curiosity driven and strategic research.
- There are also 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 to national funding opportunities, the European Research Council (ERC) and the European Union fund several

projects using Arabidopsis. As a prominent example ERC recently awarded Dr Marcus Grebes at Umea Plant Science Centre a “Starting Grant” for a project that aims to elucidate plant cell polarity using Arabidopsis.

Research highlights

The Swedish community of Arabidopsis scientists headed or contributed to more than 60 experimental papers in the last year, a selection is shown below.

- Boutté, Y Frescatada-Rosa, M Men, S Chow, C-M Ebine, K Gustavsson, A Johansson, L Ueda, T Moore ,I Jürgens, G Grebe, M (2010) Endocytosis restricts Arabidopsis KNOLLE syntaxin to the cell division plane during late cytokinesis. EMBO Journal (29): 546-558
- Eklund, M Ståldal, V Valsecchi, I Cierlik, I Eriksson, C Hiratsu, K Ohme-Takagi, M Sundström, J Thelander, M Ezcurra, I Sundberg, E (2010) The Arabidopsis STYLISH1 protein acts as a transcriptional activator regulating auxin biosynthesis. Plant Cell (22): 349-353
- Weinhofer, I Hehenberger, E Roszak, P Hennig, L Köhler, C (2010) H3K27me3 profiling of the endosperm implies exclusion of polycomb group protein targeting by DNA methylation. PLoS Genet (6): e1001152.
- Sjögren, LL and Clarke, AK (2011) Assembly of the chloroplast ATP-dependent Clp protease in Arabidopsis is regulated by the ClpT accessory proteins. Plant Cell (23): 322-332
- Carlsbecker *et al*. (2010) Cell signalling by microRNA165/6 directs gene dose-dependent root cell fate. Nature (465): 316-321
- Zhao, Z Andersen, SU Ljung, K Dolezal, K Miotk, A Schultheiss, SJ Lohmann, JU (2010) Hormonal control of the shoot stem-cell niche. Nature (465): 1089-1092

Switzerland

http://www.arabidopsis.org/portals/masc/countries/Switzerland.jsp
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Plant biology is flourishing in Switzerland and ranges from research in ecology and evolution to regulation of physiological processes, epigenetic regulation and biotechnology using Arabidopsis, model crops and ecological habitats. Arabidopsis research in Switzerland has a strong focus on chloroplast biology (e.g., photosynthesis, chlorophyll metabolism, protein transport), light-regulated growth and development, epigenetic regulation, molecular aspects of symbiosis and pathogenesis, cell wall formation, transport processes and vitamin biosynthesis. Most of the Arabidopsis research in Switzerland discussed below will continue in the next few years.

Plant Swiss Network:
In 2009 Swiss plant researchers received a 4.8 MCHF grant from the Rector's Conference of the Swiss Universities (CRUS) to create a Swiss network in plant sciences under the leadership of Thomas Boller. In 2010 the Swiss Plant Science Web (SPSW) was established (http://www.swissplantscienceweb.ch), which include Arabidopsis researchers in the Zurich-Basel Plant Science Center (ETH Zurich, Universities of Zurich and Basel), BeNeFri Plant Sciences (Universities of Bern, Neuchâtel and Fribourg) and Arc Lémanique Plant Sciences (Universities of Geneva and Lausanne). In addition to coordinating educational and training activities in plant sciences, SPSW facilitates communication among Swiss plant researchers and with international plant research centers, and supports research infrastructures of the three regional networks. SPSW is a good entry point to learn more about plant sciences and Arabidopsis research in Switzerland.

Major funding sources:
- Arabidopsis research is mainly supported by the Swiss National Science Foundation (SNF, http://www.snf.ch), which provides competitive funding for basic research, fellowships and junior professor positions (SNF Assistant Professors).
- If Arabidopsis research also includes more applied aspects, funding can be obtained from the Innovation Promotion Agency (CTI), which supports technology development and transfer to the commercial sector.
- The Swiss systems biology initiative SystemsX.ch (http://www.systemsx.ch) also supports Arabidopsis research in two major projects, PlantGrowth (http://www.systemsx.ch/index.php?id=150) and MetaNetX (http://www.systemsx.ch/index.php?id=299), which take quantitative approaches to plant development and metabolic network reconstructions using Arabidopsis as model plant organisms.
- In addition to large European Framework Program 6 and 7 projects that use Arabidopsis as model organism and involve Swiss research teams (e.g., AGRON-OMICS, http://www.agron-omics.eu/; TiMet, http://www.timing-metabolism.eu/), Arabidopsis research is increasingly supported by competitive junior (EURO 1.5 M) and senior (EURO 2.5 M) grants provided by the European Research Council.

Research Breakthroughs:
- Swiss Arabidopsis researchers are using functional genomic tools and approaches widely to gain new mechanistic insights into plant functions, but only a few examples can be highlighted here.
- Significant progress has been made in understanding epigenetic regulatory mechanisms (e.g., Köhler and Aichinger, Epigenetics, 2010; Weinhofer *et al*., PLoS Genet, 2010; Tittel-Elmer *et al*., PLoS Genet, 2010) and the function of RETINOBLASTOMA-RELATED (RBR) protein, the homolog of the animal tumor suppressor pRB (Johnston *et al*., PLoS Genetics, 2010; Borghi *et al*., Plant Cell, 2010).
- Other progress includes elucidating the synthesis and signaling function of jasmonate (e.g., Gfeller *et al*., Science Signaling, 2010) and differentiation processes (Alassimone *et al*., Proc Natl Acad Sci USA, 2010; Ilegems *et al*., Development, 2010).
- Major highlights were the discovery that self-compatibility in Arabidopsis evolved from a mutation in the male specificity gene SCR (Tsuchimatsu *et al*., Nature 2010), that pollen tube reception and fungal invasion share conserved molecular components (Kessler *et al*., Science, 2010), and that a hyperactive quantitative trait locus allele of BRX contributes to natural variation of Arabidopsis root growth vigor (Beuchat *et al*., Proc Natl Acad Sci USA, 2010).
- Progress has also been made in dissecting the mechanisms of chloroplast protein import through the TOC receptor complex (e.g., Andres *et al*., BBA, 2010; Agne *et al*., Plant Physiol, 2010) and the mechanism of zinc transport (Song *et al*., Plant Cell, 2010).

Arabidopsis Meetings:
The 7th Tri-National Arabidopsis Meeting (TNAM, Austria-Germany-Switzerland) was held in September 2010 in Salzburg (Austria) and featured national and international speakers with participants from many European countries (http://www.tnam.org/). The program highlighted the latest developments in Arabidopsis research focusing on evolution, genetics, cell biology, physiology and stress biology. The 8th TNAM in 2012 will be hosted again by Switzerland at the University of Lausanne.

Tools and Resources:

- The AGRON-OMICS consortium in collaboration with Affymetrix developed the AGRONOMICS1 Arabidopsis genome tiling array that was tested at the Functional Genomics Center Zurich (http://www.fgcz.ch) and made available to the Arabidopsis community in 2010 (Rehrauer *et al*., Plant Physiology, 2010; http://www.agron-omics.eu/index.php/resource_center/tiling-array). The array is commercially available from Affymetrix.
- Genevestigator (https://www.genevestigator.com/gv/index.jsp) initially developed at ETH Zurich continues to be the major database for gene expression information and now contains data from nearly 6,300 Arabidopsis microarrays but also gene expression data from other plants, human, animals, yeast and *E.coli*. In addition, Genevestigator can now be used with RefGenes, a new tool for identification of reliable and condition specific reference genes for RT-qPCR data normalization (Hruz *et al*., BMC Genomics, 12:156, 2011).
- A major advance has also been made in the Arabidopsis proteome with the publication of the pep2pro database available at http://www.pep2pro.ethz.ch, which features quantitative information for nearly 14,600 Arabidopsis proteins in different organs (Baerenfaller *et al*., Integrative Biology 3:225, 2011). Moreover, the quantitative protein data in pep2pro and transcript level data in Genevestigator are linked so that Arabidopsis researchers can immediately obtain full gene expression information.

United Kingdom

http://www.arabidopsis.org/portals/masc/countries/United_Kingdom.jsp
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Arabidopsis Research in the UK

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; the UK also hosts one of the two international Arabidopsis stock centres; NASC.

UK Funding News

- The Biotechnology and Biological Science Research Council (BBSRC) is the major funder of Arabidopsis research in the UK. The BBSRC strategy (2010-2015) highlights three priority areas for particular focus, food security; bioenergy and industrial biotechnology; and basic bioscience underpinning, making two of these three core research areas relevant to plant science and Arabidopsis research. Plant science is therefore at the core of BBSRC remit.
- The government Foresight Report "The Future of Food and Farming", which highlighted the multifaceted drivers behind food security and the need for holistic approaches in meeting the challenges of feeding the growing world population was published in early 2011. In 2010 BBSRC published its strategic plan, a coordinated multidisciplinary plan for research to help the world avoid a potential food security crisis. This new strategy provides a greater breath of scope, greater coordination and aims to increase the effectiveness of translation of research findings in practical applications and policy advice. BBSRC aims to lead world-class 21st century bioscience, promote innovation and help realise benefits for society within and beyond the UK. Arabidopsis researchers can apply for support from BBSRC through responsive mode funding.
- In January 2011, in partnership with the Bill and Melinda Gates Foundation, the UK Department for International Development and the Indian Department of Biotechnology, BBSRC launched a £20M/$32 major international research initiative to improve food security for the developing countries. This initiative aims to fund research groups in the UK, India and developing countries to improve the sustainability of vital food crops in sub-Saharan Africa and South Asia.
- BBSRC announced the investment of £26M into the Norwich Research Park, which hosts the prestigious plant science research institute the John Innes Centre and the Genome Analysis Centre (TGAC), which aims to conduct whole genome sequencing and other applications of sequencing, develop new high throughput sequencing technologies and develop a centre of excellence for bioinformatics associated with genome sequencing. The investment will underpin the transformation of the Norwich Research Park from 'World-Class Research Centre' to a 'National Research Campus' embracing a world-class commercial science park to deliver innovation from bioscience.
- In March 2011, in partnership with the US National Science Foundation, BBSRC awarded funding totaling £6.11M/$10.3M to four transatlantic research teams to improve photosynthesis with a view of increasing the yield of important crops for food production or sustainable bioenergy. The projects include:

1. CAPP (Combining algal and plant photosynthesis) - University of Cambridge, John Innes Centre, Oxford Brookes University, Carnegie Institute of Washington. Total funding: £1.25M
2. EPP (Exploiting prokaryotic proteins to improve plant photosynthetic efficiency) - University of Illinois at Urbana-Champaign, Rothamsted Research, Cornell University, University of California, Berkeley. Total funding: £1.36M
3. MAGIC (Multi-level Approaches for Generating Increased CO2) - University of Glasgow, University of Cambridge, University of Warwick, Penn State University, University of California, Berkeley. Total funding: £1.6M
4. Plug and Play Photosynthesis for RuBisCO independent fuels - University of Glasgow, Arizona State University, University of Southampton, Imperial College London, Penn State University, Michigan State University, Emory University School of Medicine. Total funding: £1.9M

UK Arabidopsis Research Network

- GARNet represents UK Arabidopsis researchers via a committee of 12 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 2010 Malcolm Bennett, Jim Murray and Smita Kurup were elected to the committee for a three year term to join the current committee of Jim Beynon, Juliet Coates, Alessandra Devoto, Stefan Kepinski, Ian Moore, Robert Sablowski and Nicholas Smirnoff. GARNet is currently chaired by Alex Webb (since 1st January 2010).
- In December 2010 GARNet launched its updated website. www.garnetcommunity.org.uk/ Refreshing the GARNet website was one of the aims of the current grant so that it reflected the remit of GARNet, which has evolved in recent years. The website has been updated so that it can be can be easily navigated

and the design is consistent throughout the pages. The old lists of useful tools and links have been reorganised into an easily searchable directory (www.garnetcommunity.org.uk/resources). The redesign of the website was also accompanied by a new logo and a more modern design of the GARNish Newsletter. (www.garnetcommunity.org.uk/newsletters).

- 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, provide a point of contact for researchers and funding agencies, promote interactions between fundamental and applied plant science and to increase opportunities for UK plant science at the international level.
- BBSRC also provides funds to support the MASC coordinator, Dr Irene Lavagi for three years (2009-2012) at the University of Warwick.

UK Plant Science Website

UK Plant Science - 'PlantSci' (www.plantsci.org.uk) was officially launched on the 10th December 2010 and aims to support Plant Scientists in their day to day research by providing the latest funding opportunities, news and information all under one leaf.

The 'PlantSci' website was initiated by GARNet to promote the communication of Plant and Crop Science research between communities or to others interested/working in the Plant Science arena. PlantSci functions as a portal to showcase the wealth of UK Plant and Crop Science R&D undertaken in the UK and act as an information hub to facilitate communication and knowledge exchange across the whole community.

PlantSci unearths all the relevant Plant Science related information, including: a wealth of information relating to funding, current opportunities, recently awarded grants and information on funding bodies that support UK Plant Science research; a searchable directory of UK plant scientists to offer detailed information on the types and kinds of research in the UK; a calendar of all the must attend conferences and meetings in Plant and Crop Science (www.plantsci.org.uk/events/upcoming-events); an entry point to the various UK Plant and Crop bodies via the 'Communities' page (www.plantsci.org.uk/communities).

To maximize the usefulness and impact to the user, community ownership of the PlantSci portal is needed and this is achieved by asking users to sign in and provide details of their research in the Find a Scientist directory to showcase their research or work in the field of plant science, to advertise meetings and to share plant related news. PlantSci embraces modern technology to achieve its goals and has even a Twitter page (twitter.com/plantscience)!

UK Plant Science Federation

In late 2010 and early 2011 representatives of a number of stakeholders, including plant research communities (MONOGRAM, UK-Brassica Research Community/OREGIN, UK-Solanaceae and GARNet), learned societies and industrial groupings met to explore the possibilities of forming 'one voice for UK Plant and Crop Science' to help build a stronger UK plant research base.

Establishing a Federation of organizations/grouping involved in UK Plant Science research and education would provided considerable added value for the whole community by pooling knowledge and expertise, identifing new opportunities and assessing where added value could be achieved by working together. In an era of reduced funding it is becoming increasingly importance to have a strong and clear voice amongst 'opinion-formers', within political and funding circles and the Federation could be one possible mechanism for achieving this.

On the 31st January representative of a variety of stakeholders from industry, research, education and learned societies agreed that a UK Plant Science Federation should be formed as a special interest of the Society of Biology and would aim to:

1. Increase the understanding and perceived importance of Plant and Crop Science amongst government, funders, industry and society in general
2. Formulate a coordinated strategy and vision for Plant and Crop Science in the UK that can be utilised to inform policy
3. Help to improve the general funding environment for UK Plant and Crop Science Research and Education
4. Create a forum for debate that is independent and inclusive
5. Provide a focus and contact point for UK Plant and Crop Science
6. To educate and inspire the next generation of Plant and Crop Scientists

A UK Plant Science Meeting to showcase the wealth of UK Plant Science is planned for spring 2012 and the Federation will be launched later in 2011

UK Meetings

Upcoming Meetings

- 2011 GARNet Meeting will be held in Cambridge, 6-7th September and is entitled 'Dynamic biology - New Levels and New Dimensions of Regulation'
- UK Plant Science Meeting, planned for spring 2012 to showcase the wealth of UK Plant Science. Tentative Venue: John Innes Centre, Norwich.

Past Meetings

- Centre for Plant Integrative Biology (CPIB) study group, 4-7th January 2011, Nottingham. Mathematicians worked along with

bioligsts for three days to mathematically model plant biology process.

- 6th and 7th September 2010, GARNet Meeting entitled 'Cell and Systems' was held at Durham University.

Notable Research Breakthroughs in the UK

- Baxter L, Tripathy S, Ishaque N, Boot N, Cabral A, Kemen E, Thines M, Ah-Fong A, Anderson R, Badejoko W, Bittner-Eddy P, Boore JL, Chibucos MC, Coates M, Dehal P, Delehaunty K, Dong S, Downton P, Dumas B, Fabro G, Fronick C, Fuerstenberg SI, Fulton L, Gaulin E, Govers F, Hughes L, Humphray S, Jiang RHY, Judelson H, Kamoun S, Kyung K, Meijer H, Minx P, Morris P, Nelson J, Phuntumart V, Qutob D, Rehmany A, Rougon-Cardoso A, Ryden P, Torto-Alalibo T, Studholme D, Wang Y, Win J, Wood J, Clifton SW, Rogers J, Van den Ackerveken G, Jones JDG, McDowell JM, Beynon J, Tyler BM (2011) Signatures of Adaptation to Obligate Biotrophy in the Hyaloperonospora arabidopsidis Genome. Science (330): 1549 - 1551
- Rizzini, L Favory, JJ Cloix, C Faggionato, D O'Hara, A Kaiserli, E Baumeister, R Schaefer, E Nagy, F Jenkins, GI Ulm R (2011) Perception of UV-B by the Arabidopsis UVR8 Protein (332): 103-106
- Fan, J Crooks, C Creissen, G Hill, L Fairhurst, S Doerner, P Lamb, C (2011) Psudomonas sax genes overcome aliphatic isothiocyanate-mediated non-host resistance in Arabidopsis. Science (331): 1185-8
- Harvey, JJ Lewsey, MG Patel, K Westwook, J Heimstaedt, S Carr, JP Baulcombe, DC (2011) An antiviral defense role of AG2 in plants. PLoS 6(1):e14639
- Graf, A Schlereth, A Stitt, M Smith, AM (2010) Circadian control of carbohydrate availability for growth in Arabidopsis plants at night. PNAS (107): 9458-9463

United States

http://www.arabidopsis.org/portals/masc/countries/United_States.jsp
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North American Arabidopsis Steering Committee (NAASC)

NAASC (www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp) is composed primarily of U.S. researchers and represents Arabidopsis researchers in the U.S., Canada and Mexico. NAASC 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, such as for the 2011 meeting at the University of Wisconsin-Madison. Importantly, NAASC raises ICAR participation funds to support young scientists as well as U.S. members of under-represented groups in advanced levels of science. NAASC members also perform valuable service through membership on advisory committees and boards and as Investigators on federal grants that benefit the community.

1. Elections replace two NAASC members that rotate off the committee each year. The two newest members of NAASC, elected in spring 2011, are Jose Alonso (North Carolina State University, USA) and Nicholas Provart (University of Toronto, Canada). George Haughn and Scott Poethig conclude their four year term at the 2011 ICAR. Continuing members include Mark Estelle (UC San Diego), Jane Glazebrook (University of Minnesota), Xinnian Dong (Duke University), Blake Meyers (University of Delaware), Wolf Frommer (Carnegie Institution for Science) and Dominique Bergmann (Stanford University). The new NAASC president and representative to MASC for 2011-2012 is Mark Estelle. Jane Glazebrook will continue as NAASC Treasurer.
2. Joanna Friesner, NAASC Coordinator, supports all NAASC efforts including, among other duties, acting as lead conference organizer for North American ICARs and assisting in development of NAASC-led community initiatives such as the new IAIC (see below).
3. 2010 ICAR (Japan): Mark Estelle applied and received NSF funding to support U.S. participants including full funding for five under-represented minorities and travel awards for four early career scientists and seven invited speakers. NAASC supported travel awards for seven additional early-career scientists.
4. 2011 ICAR (U.S.): Xinnian Dong submitted a proposal to NSF requesting support for eight under-represented minorities, ten early career scientists, and several invited speakers. Blake Meyers submitted proposals to the U.S. Departments of Agriculture and Energy requesting support for additional early career scientists and several invited speakers. NSF and USDA proposals were awarded at the time of printing; DOE award decision is pending.
5. Committee service: Mark Estelle and Jane Glazebrook are co-chairs of the ICAR 2011 conference organizing committee. Scott Poethig and Blake Meyers serve on the ABRC advisory committee. All remaining NAASC members are members of the ICAR 2011 organizing committee.

The International Conference on Arabidopsis Research (ICAR) Returns to the University of Wisconsin-Madison

Madison is a site of historical significance to the Arabidopsis community. This will be the 9th time the ICAR has been held on the Madison campus out of 22 meetings spanning 47 years. The first meeting was held in Germany in 1965 and was attended by about 25 people. In comparison, ICAR 2011 is expected to have about 850 attendees. Meetings were held sporadically until 1995 when the first Madison-based ICAR occurred. At that time the community decided to hold annual meetings due to rapid advances in Arabidopsis research beginning with international cooperation to sequence the Arabidopsis genome. Meetings were then held two out of three years in Madison with each third year at an international site. It was due in large part to the significant efforts of NAASC and the generous support of U.S. funding agencies, (in particular, the National Science Foundation), that an annual ICAR has been achieved. In 2007 the Multinational Arabidopsis Steering Committee (MASC), representing the international community, decided on a new schedule that would diversify meeting effort, location and cost and facilitate participation by scientists in other regions.

The ICAR now rotates on a 3 year cycle between North America, Europe, and Asia/Pacific Rim. The 22nd ICAR, June 22-25, 2011, will once again be held at the University of Wisconsin, Madison. Conference co-chairs are Mark Estelle and Jane Glazebrook, the lead organizer is Joanna Friesner, NAASC Coordinator, and the remaining NAASC members comprise the rest of the organizing committee.

ICAR 2012 is scheduled for Vienna, Austria, and ICAR 2013 will be in Australia.

Establishing an International Arabidopsis Informatics Consortium (IAIC) in Response to Reductions in TAIR Funding

1. NAASC and MASC hosted two workshops in 2010 (UK and US locations) to consider the future bioinformatics needs of the Arabidopsis community as well as other science communities that depend vitally on Arabidopsis resources. The workshops also discussed potential solutions to funding bioinformatics storage and management. The impetus for the workshops was an immediate threat to funding of TAIR, the central Arabidopsis information point which has been a vital resource

to the Arabidopsis community through its maintenance of the Arabidopsis genome sequence, service as a portal for stock orders from ABRC from the US (and other countries), and other valuable organizing and services and resources. The workshops addressed topics including: the data types generated and used by the Arabidopsis community, the future needs of the community, and the technological, financial, and organizational sustainability of a major Arabidopsis bioinformatics resource.

Major Outcomes of the Workshops:

- Publication: IAIC Contributors. An international bioinformatics infrastructure to underpin the Arabidopsis community. Plant Cell 2010 22(8):2530-6 (http://www.ncbi.nlm.nih.gov/pubmed/20807877).
- Proposal to develop a new International Arabidopsis Informatics Consortium (IAIC).
- A presentation of the workshops, the report, and the findings was given during the 2010 ICAR in Yokohoma, Japan. Community feedback and discussion were solicited.
- Establishment of a preliminary IAIC website (http://arabidopsis.org/portals/masc/IAIC.jsp).
- Initial IAIC public workshop held at the Plant and Animal Genome (PAG) meeting in January, 2011.

2. NAASC member Blake Meyers (University of Delaware) took the lead on implementing the recommendation to establish an International Arabidopsis Informatics Consortium (IAIC). With assistance from Co-PI Erich Grotewold (ABRC and Ohio State University) and Joanna Friesner (NAASC Coordinator), Meyers submitted a funding proposal to the National Science Foundation's Research Coordination Network (RCN) funding opportunity. Additional Co-PIs include Doreen Ware (CSHL), Jim Carrington (Oregon State University) and Volker Brendel (Iowa State University) while additional senior personnel include Nick Provart (University of Toronto), Jim Beynon (Warwick University), Ruth Bastow (GARNet), Sonya Lowry (iPlant), and Dan Stanzione (University of Texas-Austin.) Support is intended to foster new collaborations, including across international boundaries, and encourage collaborative technologies and development of community data and meta-data standards, among other goals. The proposed IAIC would be built around a distributed model to enable flexible funding approaches to be used on an international scale. The IAIC is proposed to consist of several components:
   - The Arabidopsis Informatics Portal (AIP) that links geographically distributed resources and combines their outputs into a user-friendly interface. The AIP would be the operational center of the IAIC and personnel associated with the AIP would provide training for researchers wishing to access data and for data and resource providers wishing to interact with the IAIC.
   - Gold standard genome annotation
   - Genome/sequence curation
   - Stock and resources database(s) to enable rapid access to resources
   - Additional specific modules could be added to the above components based on funding and data availability in respective countries; e.g. comparative genomics which could involve Arabidopsis, Brassicacea, crop genomes, other species, etc.
3. Current IAIC Proposal Status: IAIC RCN funding is pending an NSF review of a revised management plan. In response to reviews that the initial steering committee lacked expertise in cyberinfrastructure and interoperability, Meyers facilitated inclusion of two members of the NSF-funded iPlant Collaborative to join the group of investigators. Dan Stanzione, a participant in both planning workshops, provides expertise in cyberinfrastructure and high-performance computing. Sonya Lowry has expertise in data management and organizational structures and how software organization impacts its architecture. They also will serve as valuable liaisons to other cyberinfrastructure researchers in the US and abroad and help to draw in the expertise provided by developers working in industry, commerce and government.
4. Next steps: Nominations to the IAIC Scientific Advisory Board (SAB) and elections are expected to begin this summer, following community discussion at the 2011 ICAR.

Conclusion of the AT2010 Project- What's next for Arabidopsis funding in the U.S.?

For the last decade, large projects in Arabidopsis genomics have been funded primarily through the NSF 2010 program. These projects were funded and managed through the core programs. The last applications for the 2010 program were funded this year. Parag Chitnis indicated that although NSF no longer has a dedicated program for receiving proposals in Arabidopsis genomics, NSF will continue to support large-scale research projects on Arabidopsis. Such grant applications should be submitted directly to appropriate NSF programs, by the deadlines for the program.

Jane Silverthorne gave a presentation at the first public meeting of the newly established IAIC (see description in the previous section) at PAG 2011 this past January. She outlined a number of relevant NSF programs that will accept proposals using Arabidopsis. U.S. researchers can read about NSF programs and their (current) deadlines by accessing the PowerPoint presentation located at the IAIC website: http://arabidopsis.org/portals/masc/IAIC.jsp

Notable Awards and Honors for U.S. Researchers Using Arabidopsis

- Presidential Outstanding Career Award 2010: Dominique Bergmann
- Election to the American Association for the Advancement of Science (AAAS) 2010- Eduardo Blumwald, Roger Hangarter, Paul Hasegawa, Roger Innes, Hong Ma, Rob McClung, Katherine Osteryoung, Heven Sze, Michael Thomashow.
- The Genetics Society of America (GSA) George W. Beadle Award for outstanding contributions to the community of genetics research- 2011: Joe Ecker.
- Awarded by the American Society of Plant Biologists (ASPB): 2010 Stephen Hales Prize: Sakis Theologis; 2010 Charles Albert Shull Award: Dominique Bergmann; 2010 Early Career Award: R. Keith Slotkin; 2010 Lawrence Bogorad Award for Excellence in Plant Biology: Nam Hai-Chua; Fellow of ASPB- 2010: Julia Bailey-Serres, Alice Cheung, Gloria Coruzzi, A.S.N. Reddy, Stan Roux, Gary Stacey, and Elliot Meyerowitz. Award Descriptions: http://my.aspb.org/?AF_Awards.

Several Notable Research Breakthroughs Involving U.S. Researchers

Several research advances deserve special mention. Genome wide association (GWA) has become popular approach in human genetics because it takes advantage of the genetic and phenotypic variation present in existing populations. To test the value of GWA for determining the genetic basis of natural phenotypic variation in Arabidopsis, Nordborg and colleagues (1) examined 107 phenotypes in a collection of 196 ecotypes genotyped for 250,000 SNPs. Although population substructure complicated the analysis, it was nevertheless possible to identify reasonable candidate genes for many of these traits. This study suggests that GWA will be of considerable value in ecological and evolutionary genetic studies of Arabidopsis.

Methods for producing doubled haploid lines (i.e., instant inbred lines) have important practical applications. In maize, it has long been possible to produce these lines using stocks that generate maternal or paternal haploid seedlings. This method has now been extended to Arabidopsis with the discovery that a mutant form of the centromere-specific protein, CENH3, induces chromosome elimination (2). These investigators produced uniparental haploid plants by crossing transgenic cenh3 mutants expressing this aberrant form of CENH3 with wild type plants; spontaneous diploidization produced doubled haploids. Now that the molecular basis of chromosome elimination is understood, it should be possible to extend this method to other species.

Finally, we would like to draw attention to a new, broadly applicable method for studying gene expression and chromatin structure in specific cells and tissues (3). In this approach (called INTACT), nuclei are tagged with biotin by co-expressing a nuclear envelope-associated protein containing a biotin ligase recognition domain, along with E. coli biotin ligase. Nuclei from specific cells or tissues are labeled by expressing the nuclear envelope protein from a cell-type-specific promoter (in combination with a ubiquitously expressed biotin ligase), and are then isolated using strepvidin-coated beads. RNA and chromatin purified from these isolated nuclei is highly specific, and can be used for a wide range of studies.

1. Atwell, S Huang, YS Vilhjalmsson, BJ Willems, G Horton, M Li, Y Meng, D Platt, A Tarone, AM Hu, TT *et al*. (2010) Genome-wide association study of 107 phenotypes in *Arabidopsis thaliana* inbred lines. Nature (465): 627-631.
2. Ravi, M and Chan, SW (2010) Haploid plants produced by centromere-mediated genome elimination. Nature (464): 615-618.
3. Deal, RB and Henikoff, S (2010) A simple method for gene expression and chromatin profiling of individual cell types within a tissue. Dev Cell (18): 1030-1040.

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The 2011 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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