

The Multinational *Arabidopsis thaliana* Steering Committee 2012 Report

Annual Report 2012 2020 Roadmap - From bench to bountiful harvests

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Table of Contents

Foreword to the Report	5
Executive Summary	6
2020 Roadmap	8
Progress and Activities of the Multinational Arabidopsis Steering Committee	16
Progress and Activities of MASC	
Scientific Highlights	
Arabidopsis Community Projects and Resources	
Broader Impacts of Arabidopsis Research	24
Impacts on Industry	
Examples of Translation Research Using Arabidopsis	
Reports of the MASC Subcommittees	30
Bioinformatics	
Metabolomics	
Natural Variation and Comparative Genomics	
ORFeomics	
Phenomics	
Proteomics	
	40
The International Arabidopsis Functional Genomics Community	
Country Highlights	
Argentina	
Australia and New Zealand	
Austria	
Czech Republic	
Finland	
India	
Ireland	
Israel	
Italy	
Japan	
The Netherlands	
Sweden	
Switzerland	
United Kingdom	
United States	
Members of the Multinational Arabidopsis Steering Committee	68
Members of the Multinational Arabidopsis Steering Committee Subcommittees	69

Foreword to the Report

This is the 2011/2012 annual report of the Multinational Arabidopsis Steering Committee (MASC). In 1990 nine scientists from the United States, Europe, Japan and Australia formed an ad hoc committee to promote large-scale studies in *Arabidopsis thaliana*. A report outlining a plan for international cooperation was prepared and the Multinational *Arabidopsis thaliana* Genome Research Project (1990- 2001) was initiated. The aim of this project was to understand at the molecular level the physiology, biochemistry, growth and development of a flowering plant. A significant goal was to determine the complete sequence of the Arabidopsis genome by the year 2000, concurrent with the development of other vital resources and collaborations. The international scientific community agreed to cooperate on several objectives including: the identification and characterization of the structure, function, and regulation of Arabidopsis genes; development of technologies for genome studies; establishment of biological resource 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 established to implement overall research coordination and was charged with annually reviewing scientific progress and identifying needs and new opportunities for the global Arabidopsis research community. MASC also acts in an advisory capacity to various national funding agencies.

The Multinational *Arabidopsis thaliana* Genome Research Project completed the sequencing of the reference Arabidopsis genome in 2000. The success of this project inspired the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project, an ambitious plan to determine the function of every Arabidopsis gene by the year 2010. Numerous laboratories internationally took part in this project and very large datasets and resources were generated leading to breakthroughs in understanding the fundamental processes underlying plant growth development and responses to the environment. The success of this project is the result of numerous factors, including the ease of manipulation of Arabidopsis, the synergistic development of a powerful set of tools, the ease of access to stocks and other key reagents, the collegiality of the Arabidopsis scientific community and the generous support from various national funded 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' has been unprecedented. Studies originally conducted in Arabidopsis are increasingly resulting in the development of new solutions to global agricultural challenges. As research continues, new large-scale funding mechanisms need to be in place to continue the promotion of discovery in this reference plant. Equally as important are the needs for strong funding in support of individual research labs doing creative work focused on a smaller scale, and for projects that link basic and applied approaches. Given the increasingly important role that Plant Science will play in the future, new support

mechanisms for Arabidopsis resources should be identified. For example following two community workshops to consider how the very large amount of data generated by Arabidopsis researchers can be managed (and funded) in a coordinated manner internationally, the creation of the International Arabidopsis Informatics Consortium (IAIC) funded by a variety of sources was proposed (IAIC, (2010) An International Bioinformatics Infrastructure to Underpin the Arabidopsis Community. *Plant Cell* (22): 2530-2536). In 2011, the IAIC became a reality (<http://www.arabidopsisinformatics.org/>) and more information on the development of this infrastructure can be found on page 21.

Building upon its well-established tradition for international co-operation in 2010 MASC began working on a road map for the next decade. This document, entitled "From Bench to Bountiful Harvests" (pg 8-15) aims to inform scientists, funding bodies and decisions makers on the future foci of Arabidopsis research. We expect the road map will help all Arabidopsis researchers to continue to provide the underlying knowledge that will be essential to combat the current global challenges we face.

This report details progress made over the last year by the international Arabidopsis community including highlights from intensive efforts in basic research and advances in translating basic to applied research. Although the timeframe of translation into applied research can be long, and the outcomes unpredictable, the very rapid increase in publication rate and patent filing in the last 15 years indicates what we might expect in the next decade. This report demonstrates the continued high level of cooperation that exists throughout the global community and the impressive returns that funding agencies gain from supporting Arabidopsis research.

The Multinational Arabidopsis Steering Committee
May 2012

Executive Summary

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

The highly active and enthusiastic Arabidopsis community around the world continues to attract new researchers. According to The Arabidopsis Information Resource (TAIR), 23,130 researchers and 9,024 labs total are registered at TAIR as of 9th April 2012. Of these, the records for 9,563 people and 3,831 labs were updated in the past 5 years.

It is interesting to note that the number of people and laboratories updated in the past five years continues to increase, suggesting that the increasing number of researchers and laboratories registered at TAIR represents an increase in active users, not just the gradual accumulation of inactive accounts. Arabidopsis continues to be an ideal training system for future generations of researchers with broadened expertise, for example, through the recent development of systems biology projects, which combine classical 'wet lab' approaches with, advanced computational methods. Resources must continue to be coordinated in order to maximize the efforts of the various labs around the world. It remains as true today as it was eleven years ago at the release of the reference genome, that only sustained collaborations and timely sharing of data, stocks, and other resources will enable the Arabidopsis community to achieve its ambitious goals.

Highlights in *Arabidopsis* research

The past year continued to be strong for *Arabidopsis* publications. 3,804 *Arabidopsis* peer-reviewed research papers were published in 2011, a near 10-fold rate increase over 1994 (when 402 peer-reviewed papers were published; Fig. 1, page 17). This report includes summaries of just a few research highlights in the past year (pages 17-20) including:

- Discovery of a common molecular player in flowering and stomatal opening
- Publication of the proteome-wide binary protein-protein interaction map of *Arabidopsis* (interactome)
- Discovery of the 'evening complex' which is used to gate the timing of stem growth
- Insight into the cell to cell transport of mobile transcription factors
- Insight into symmetrical cell division; equations from statistical mechanics
- Insight into the rate of spontaneous epigenetic changes
- Discovery of the plant oxygen sensor

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 continue to increase: in 2011 there were 1,210 utility patents referencing *Arabidopsis* compared to 23 in 1994, an over 50-fold increase (See Fig. 2, page 24. In the same timeframe, a 63- and a 7-fold increase have been recorded for European and world's published applications (i.e. patents) referencing *Arabidopsis* (See Fig.3 and Fig.4, page 25). 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 25-29):

- Development of miniSOG, a protein tagging tool for electron microscopy
- Insight into C₄ photosynthesis
- Discovery of a pectin synthesis complex that contributes to the understanding of this economically valuable polysaccharide
- Development of EASE, a tool to spatially and temporally regulate gene expression
- Enhanced poplar growth by expressing an *Arabidopsis* oxidative stress kinase
- A summary on *Arabidopsis* contributions to the discovery of vitamin biosynthetic pathways
- A chemical genomics approach in *Arabidopsis* identifies small

molecules that protect cereal crops from fungal infestation.

New initiatives announced this year

- Japan - New 3-years project, "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society", started in 2011 with support of the Strategic Japanese-US Joint Research Program (JST in Japan and NSF in US), PIs are Kazuki Saito of RIKEN, Japan, and Lloyd Sumner of Noble Foundation, US.
- UK - The Biotechnology and Biological Sciences Research Council (BBSRC) will coordinate a new European Commission-funded network that aims to coordinate plant science research across Europe and beyond. The network, (ERA-NET for Coordinating Action in Plant Sciences - ERA-CAPS) will run until 2014

MASC Subcommittees

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

- Bioinformatics - The first major International Arabidopsis Informatics Consortium (IAIC) community meeting was held in a workshop at the 2011 ICAR in Madison (Wisconsin, U.S.A.). Further progress towards developing a new "Arabidopsis Information Portal" (AIP) was made at a Design Workshop in Atlanta (Georgia, U.S.A.) in December 2011, attended by computer scientists, plant biologists, funding agencies, and other organismal database experts. A white-paper based on discussions from the Design Workshop is in preparation and should be available by the summer of 2012.
- Metabolomics - A MASCM (Multinational Arabidopsis Steering Committee Metabolomics) gator portal is under development. The webinterface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases in a way comparable to that offered by the MASCP (MASC Proteomics) gator portal (<http://gator.masc-proteomics.org/>).
- Natural Variation and Comparative Genomics - The first ~100 genomes of the *Arabidopsis* 1001 genomes project have been generated. Genome sequences for *Arabidopsis lyrata*, *Brassica rapa* and the extremophile *Thellungiella parvula* have been generated. The subcommittee has also developed specific goals towards the 2020 Roadmap 'From bench to bountiful harvests'.
- ORFeomics - Inclusion of the ORF and cDNA clones table in the annual report was encouraged. Joe Ecker will step down as chair and Motoaki Seki is the new chair of this subcommittee.
- Phenomics - Subcommittee members continue to track progress by the various phenomics efforts underway worldwide including, insertion lines, phenotyping platforms and facilities, databases, phenomics meetings, and community events including the participation in the International Plant Phenotyping

Network. The subcommittee has also developed specific goals towards the 2020 Roadmap 'From bench to bountiful harvests'.

- Proteomics - Subcommittee members continued to develop and maintain public online proteomic resources for the community. Recent examples include the gel-based proteomic resource GelMap, which provides digital versions of 2-DE and BN-PAGE with hyperlinks to identified proteins and MS/MS data. This resource has also been integrated into the MASCP Gator along with the P3DB plant phosphorylation database Thelen. The subcommittee has also developed specific goals towards the 2020 Roadmap 'From bench to bountiful harvests'.

MASC recommendations and goals for the next decade

The goals in this annual report are the goals of the Roadmap.

- Build a predictive model of an *Arabidopsis* plant from its molecular parts;
- Exploit the wealth of natural variation that exists in *Arabidopsis* to further our understanding of adaptation and evolution;
- Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa;
- Build the International Arabidopsis Informatics Consortium (IAIC), an international informatics and data infrastructure;
- Deepen International Cooperation and Coordination;

Detailed info on these goals can be found in the Roadmap section (pp 8-15).

From Bench to Bountiful Harvests.

A Roadmap for International Arabidopsis Research 2011-2021

Summary

As a number of projects and funding programmes involving Arabidopsis research came to a close in 2010, the international Arabidopsis community decided to articulate a new road map for Arabidopsis research entitled "From Bench to Bountiful Harvests" to inform scientists, funding bodies and decisions makers on the future foci of Arabidopsis research.

Drawing from a number of reports, discussions and recommendations that have emerged in recent years including the more recent 'EU 2020 Vision for Plant Science' (6) and 'An international Model for the Future of Plant Science' (7), this document details the future direction of an internationally coordinated road map for Arabidopsis research within the wider Plant Science landscape.

This roadmap aims to continue the substantial international effort on Arabidopsis research to understand the fundamental processes of plant biology with sufficient detail to engineer plant specifically to meet the future needs of society.

To achieve these goals, it will be necessary to integrate vast amounts of heterogeneous quantitative data generated both in the laboratory and in the field. The integration of these data at many levels of biological organisation, including different accessions of Arabidopsis and its close relatives, will allow researchers to build functional networks from the single molecule to the whole plant community, that will in turn provide the knowledge required to address current global challenges.

To establish an effective pipeline from the laboratory to the field and vice versa the Multinational Arabidopsis Steering Committee in consultation with the wider community have formulated a road map for the future of Arabidopsis research which is based on the following objectives:

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

This will require embracing novel technologies to collect data that capture the complexity of the biological system both in the laboratory and in the field, thus providing a link to environmental factors enabling the construction of *in silico* models with predictive value.

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

By utilising emerging technologies, such as next generation sequencing and phenotyping platforms, Arabidopsis ecotypes and Arabidopsis relatives will be analysed to uncover genetic variation thus developing an efficient method to allow prediction of phenotype from genotype.

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

Promoting exchange of information and personnel between the laboratory and the field and engaging with other plant communities will provide an efficient two-ways exchange flow. This will facilitate the translation of basic biology, increase the awareness of the needs and requirements of agriculture and commerce and help us to understand how basic science can best be feed into to practical applications.

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

Developing an integrated system to coordinate, store, visualize and analyze the heterogeneous data produced by objectives A-C, will provide the infrastructure required to enable the accomplishment of the above objectives. This will require strong links with data providers and users form other scientific communities as well and collaborations with computational experts. An International Informatics Consortium will permit the integration of existent databases and develop standards to facilitate access to all public data.

E. Deepen International Cooperation and Coordination;

International cooperation and coordination will be necessary to achieve all objectives of this roadmap, to minimise duplication of efforts and maximize efficient use of resources through collaboration.

The next decade will present many challenges for plant science, including the sustainable production of food and energy. To meet these challenges the international plant research community will need to maintain the fundamental research that provides key advances in understanding whilst simultaneously guaranteeing that this augments practical advances through efficient knowledge sharing and beneficial collaborations. For example, research in commercially important species such as wheat is beginning to blossom but technology advances have yet to become available to overcome the obstacles posed by their less tractable genetics. It is therefore of fundamental importance that Arabidopsis continues to evolve to be the key plant for providing the underpinning information on basic plant biology. For this purpose the integration of Arabidopsis research with its close relatives and other plant species and model organisms will be key to the future success of plant research.

To achieve the new decadal vision "From Bench to Bountiful Harvests" researchers must continue to build on the ever-expanding sets of data, tools and resources so that plant science can develop more vigorously than ever before.

Foreword to the Roadmap

In the decade since the *Arabidopsis* genome has been sequenced (1) research on this reference plant has flourished. Publicly available shared genomic tools and resources such as structural and functional genome annotation (2,3) and collections of genome wide insertion mutations (4) have allowed researchers to make major advances in plant and general biology. The outstanding progress that has been achieved over the past decade results from the substantial investment and support from funding bodies across the globe and a collaborative international community with the Multinational *Arabidopsis* Steering Committee (MASC) at its centre.

In 2010 a number of projects and funding programmes for *Arabidopsis* research that began a decade earlier came to a close. The international *Arabidopsis* community therefore decided to come together to articulate a new vision for *Arabidopsis* research entitled 'From Bench to Bountiful Harvests' to help inform scientists, funding bodies and decisions makers as to the future direction of *Arabidopsis* research. This vision is based on the discussions and recommendations of a set of reports that have been commissioned in recent years to evaluate the past success of *Arabidopsis* and plant biology and the role plants will play in our future including, '2020 Vision for Plant Biology' (5), 'EU 2020 Vision for Plant Science' (6) and 'An International Model for the Future of Plant Science' (7).

The goal of this new decadal vision 'From Bench to Bountiful Harvests' is to understand the fundamental processes of plant biology with sufficient detail to be able to accurately predict both outputs of the system and the effect of perturbations. Only by obtaining an in-depth of knowledge of how a genome sequence is translated into a continuum of processes from the single molecule to cells, to tissues, the whole plant, populations of plant, and finally the field, will researchers be able to solve the perplexing question of how genotype maps to phenotype. This information is essential in order to engineer plants specifically to meet societies future needs.

Achieving the objectives of the roadmap will require precise quantitative data obtained at many levels that can be used to build functional networks of interactions from the single molecule to the whole plant community. In addition the parallel development of informatics and computational platforms to collect, store, visualize and interpret the diverse array of biological data will be essential. These ambitious goals will require considerable effort and coordination. It will be a significant challenge to combine heterogeneous data types into *in silico* models with predictive value. However the outputs and breakthroughs generated by this effort will drive plant science forward in the future.

As we progress into the next decade a major challenge faced by plant sciences is how to maintain curiosity-based research that generates fundamental advances whilst simultaneously ensuring that this new knowledge flows into practical programmes such as plant

breeding. To help achieve this balance it will be essential that *Arabidopsis* is not viewed as separate from the broader plant science community. Rather, *Arabidopsis* research should be an essential component in a continuum of discovery from the basic to the applied in which plant scientists collaborate with each other and scientists from other disciplines to ensure that underpinning knowledge generated at the bench can be exploited in the field.

Introduction

Humans depend on plants for almost every aspect of life, from the food we eat to the medicine we rely upon. However this interdependent relationship is being stretched to its limits as a result of an ever-increasing world population and the effects of climate instability. Understanding how plants grow, develop and interact with their environment is therefore more important now than ever. Only by continuously expanding our knowledge of plant processes can we hope to meet the pressing need for food, feed, fuel, shelter and to mitigate the negative effects of climate change.

Arabidopsis thaliana is a member of the Brassicaceae family that includes mustard, cabbage and oilseed rape. As a result of its small size, rapid generation time, small genome and ability to generate a large amount of seed by self-pollination *Arabidopsis* has emerged as the organism of choice to study plant biology. This has led to a significant investment in *Arabidopsis* research over past decades that have generated a fully annotated genome and a myriad of tools and resources, which, in turn, have led to a flourishing international community of researchers. Combined, these efforts have made *Arabidopsis* the most studied of all flowering plants and a reference for all biology; in 2010 over 3,400 peer-reviewed papers were published on *Arabidopsis* (8). By focusing on a single tractable system, the international community has made dramatic advances in our understanding of plants and basic biology including the identification of the major plant hormone receptors (9-17), the elucidation of florigen (18-19) and the identification of small RNAs (20-21). As a result of this outstanding progress, the *Arabidopsis* research community is now ideally placed to help address current and future global challenges.

Plant science is currently undergoing an era of great change that is being driven by genome scale technologies, theoretical based approaches and informatics. As we look to the future, new technologies such as next generation sequencing will inevitably lower the barriers to research into previously intractable economically important plants, as well as lesser-studied wild plant species. As a consequence of this progress, genomic approaches will be applied to a wider range of plant species, which will in turn allow the fundamental knowledge, accrued in *Arabidopsis* to be more readily translated into plants of agricultural and commercial importance. The broad availability of emerging technologies is also driving a convergence of disciplines and fields across plant biology that have been historically separate, e.g., plant breeding and ecology.

Arabidopsis research has played a central role in bringing about revolutionary changes. The wealth of information and resources available for Arabidopsis, in addition to the inherent strengths that led to its initial adoption as a reference system, will increase the importance of Arabidopsis as the nodal experimental model system for plant science for the foreseeable future. The vast toolbox that is available to Arabidopsis researchers is likely to result in this being the plant species in which novel forms of data are first accrued and exploited, and new techniques tested and perfected. Arabidopsis is also uniquely placed to contribute to our understanding of ecology and evolution. The abundant natural variation that exists amongst Arabidopsis accessions and relatives coupled with a rich knowledge base make Arabidopsis ideally suited for understanding adaptation and evolution at the mechanistic level.

Despite these and other advantages, Arabidopsis is not the best model system to study a number of plant processes, such as C₄ metabolism or nitrogen fixation. At the same time, there are examples in which Arabidopsis research has contributed to our understanding of plants in some very unexpected areas. Arabidopsis is not a halophyte yet a clever screen for salt hypersensitivity (22) provided a plethora of information on a signalling pathway that is not only central to salt tolerance and sodium homeostasis in Arabidopsis but that also exists in crops and halophytes (23-28). It will therefore be essential that Arabidopsis along with a small number of other key plant species continue to be utilised for focused studies of plant biology.

Research in Arabidopsis is central to our ability to generate fundamental knowledge that can inform a broad research base impacting on medical, plant, environmental and evolutionary sciences, and to provide plant breeders with the knowledge and resources (i.e. techniques and tools) to achieve sustainable crop production. If Arabidopsis research is to help address the current challenges facing the planet, we must therefore ensure that Arabidopsis is the first step in a pipeline that begins in the laboratory and ends in the field.

From bench to bountiful harvests – An International Coordinated Roadmap for Arabidopsis Research

In the last decades of the 20th Century, Arabidopsis and plant biology research largely focused on a reductionist approach to answering biological questions. Studies often centred on understanding a single gene/group of genes in specific pathways or processes. This approach had been extremely successful, and built a solid foundation from which Arabidopsis research community was able to move onto the era of genomics toward the end of the 1990's. Completion of the whole genome sequence of Arabidopsis in 2000 opened up a new way to study life processes in plants. New methodologies such as systems biology are revealing that genotype to phenotype relationships are much more complex than previously thought; mutations don't always generate distinct phenotypes and/or a phenotype is often dependent on environmental conditions. We therefore have to re-evaluate concepts such as a distinct genetic blueprint in which there is a simple linear relationship between a gene and its biological output. A major challenge for the future is to understand this level of complexity so that genomic sequences can be linked to physiological outcomes. This will provide the fundamental knowledge base required for the rational improvement of plants for traditional agri-

culture, for the vast array of plant-based products, and for efforts to improve our environment.

We therefore propose a new decadal vision for International Arabidopsis research "From Bench to Bountiful Harvests". The goal of this effort will be to understand the fundamental processes of plant biology in sufficient detail to accurately predict both outputs of the system and the effect of perturbations. This will require an in-depth knowledge of how the genome is translated into a continuum of processes from the single molecule, to cells and tissues, the whole plant, plant populations, and finally the field. Such a goal will present a substantial challenge for the next decade as it will require accurate and quantifiable data obtained at many levels including transcripts, methylation patterns, chromatin patterns, comparative genomics, proteomics, metabolomics, protein interactions, protein location and temporal data. This quantitative data must then be translated into functional networks at various scales, linked to mathematical models, compared across thousands of accessions, and associated with meteorological and geographical information so that we can eventually provide real time data and information as a plant grows or an epidemic unfolds. Such a vision will also demand new research tools, the development of new experimental methods and an internationally coordinated data infrastructure to collect, store, visualise and interpret this diverse array of biological and theoretical data.

The investments made in Arabidopsis over the past decades have created a wealth of data, tools and resources, which in turn have led to the creation of a flourishing and collaborative international body of researchers. As a result of this investment the Arabidopsis research community is now uniquely positioned to address the goals outlined in this document.

Objectives

To achieve the vision of 'Molecules to Fields' the international Arabidopsis community have identified five main objectives

- A. Build a predictive model of an Arabidopsis plant from its molecular parts
- B. Exploit the wealth of natural variation that exists in Arabidopsis to further our understanding of adaptation and evolution
- C. Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa
- D. Build the International Arabidopsis Informatics Consortium (IAIC), an international informatics and data infrastructure
- E. Deepen International Cooperation and Coordination

A. Build a Predictive Model of Arabidopsis from its Molecular Parts

The profusion of genome scale datasets that have emerged over the past years has allowed researchers to address how pathways function and interact globally. This type of 'systems based' approach has illustrated that a plant is not just a sum of its constituent parts but a complex set of interactions that occur on various levels and scales to generate phenotypes at the whole plant and population level.

Systems biology approaches have begun to transform our under-

standing of how genes function as part of a whole system. By exploiting and combining ‘omics’ data such as transcriptomics, transcription factor binding, proteomic and metabolomic data researchers have already begun to reconstruct networks and pathways, infer functional interactions and uncover emergent properties. However, this is just the beginning. As technology advances, larger and more diverse datasets will become available. When integrated together it will become possible to build and combine computational and theoretical models that enhance our understanding of the complex and dynamic networks that underpin plant growth and development.

Arabidopsis provides an ideal plant system in which to undertake a system-based approach to build a computable plant. In common with other plants, Arabidopsis has a simple body plan of repeating units, a small set of stem cells that continually develop organs throughout the whole life cycle, and unlike animals, all plant growth is postembryonic. Plant development and growth is also very robust as a result of the sessile nature of plants allowing researchers to easily impose internal/external perturbations and measure the effects from the molecular level to the whole plant. However, it is the unparalleled breadth and depth of Arabidopsis data that are available to researchers that sets Arabidopsis apart from other plants. These data, coupled with the ease of genetic manipulation and myriad of genetic resources, allow researchers to easily and consistently test hypothesis generated by modelling approaches. Thus Arabidopsis is a very amenable organism in which to generate the systems level understanding of biological organisation that will be required for the rational engineering of plants to meet the challenges we face.

Goals:

- 1 Collect and collate accurate and quantifiable data obtained at multiple levels of abstraction including a wide range of genomic transcripts, methylation patterns, chromatin modification patterns, comparative genomics, proteomics, metabolomics, DNA–protein interactions, protein–protein interactions, protein location, cell type specific, phenomic, spatial and temporal data. Collected data must also describe the variation amongst Arabidopsis accessions and relatives. The scale of this task should not be underestimated and will need to be repeated as new concepts, tools and technologies arise. (ongoing)
- 2 Continue to develop collections of mutants and mutant lines for researchers to test hypotheses generated from modelling approaches. This needs to be accompanied by support of public and accessible stock centres that enable all researchers to access this material (ongoing)
- 3 Develop new research tools and experimental methods to address the lack of global assays for a number of plant processes. For example at present proteomics is currently limited by an inability to observe and quantify the entire proteome. It is envisioned that over the next decade advances in mass spectrometry will address many of these shortcomings and that the use of approaches such as specific protein markers (peptides for SRM analysis) will enable large scale protein quantitation from complex samples to occur. (ongoing)
- 4 Fully exploit emerging technologies. For example Next Generation Sequencing is providing unparalleled opportunities for novel applications (29). Any cellular process or assay for which the output is nucleic acid based can in theory be exploited by next generation sequencing to generate a toolkit that is specific, sensitive, quantitative and flexible enough to deal with the unknown novelty of sequence

regulation that has yet to be discovered (ongoing)

- 5 Build the International Arabidopsis Informatics Consortium (IAIC), an international informatics infrastructure that is able to handle, store, visualise and interpret a diverse array of biological and theoretical data that has already been generated and data that will be created in the future. (short term)
- 6 Translate quantitative data into functional network models and maps that describe plant processes at various levels of organisation and temporal and spatial scales. (medium term)
- 7 Develop new methods for modelling across scales to build a computation/mathematical model that stretches from the molecule to the field. (mid-long Term)
- 8 Compare and integrate models to generate an *in silico* Arabidopsis plant. (long term)
- 9 Combine this *in silico* model with meteorological and geographical data to provide data and information from the field as a plant grows or an epidemic unfolds. (long term)
- 10 Provide training for plant scientists in computational science and theoretical approaches. (ongoing)
- 11 Encourage further collaboration between plant biologists and theoretical scientists. (ongoing)

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

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 analysis of natural variation because of the ease of manipulation, breadth and depth of understanding of genetic and biochemical pathways and most importantly its abundance of natural variation. Combined, these attributes have allowed the largest number of genes and nucleotide polymorphisms underlying natural variation to be uncovered in Arabidopsis compared to any other plant species (30). Despite this success, it still remains a considerable challenge to map genotype to phenotype. A great deal of the natural variation we observe results from complex, quantitative, multi-gene traits, which are greatly influenced by environmental factors. Recent advances and cost reduction in high throughput sequencing combined with progress in statistical techniques indicate that it will be possible to identify the causal genetic polymorphism underlying natural variation via genome wide association (GWA). GWA exploits variation in a collection of genotypes/individuals to identify genotype-phenotype associations. Projects to explore this emerging area are already underway and the most ambitious of these is the 1001 Genomes project (31), which aims to identify the whole-genome variation in 1001 Arabidopsis accessions. By providing access to this unexploited wealth of variation, Arabidopsis researchers can begin to link phenotypic differences with genotypic variations on a global scale.

In addition to variation in DNA sequence, large scale data sets from other ‘omic’ technologies such as proteomics, metabolomics ionomics and epigenomics are also beginning to be utilised to assess the

variation that exists at different levels of biological organisation and molecular regulation. By combining large scale 'omic' data sets obtained across populations it is possible to bring the power of systems biology to quantitative genetics. This approach can be used to construct and infer biologically meaningful regulatory networks (32-34) that can reveal emergent properties that play a role in systems robustness and adaptability, and are crucial to the survival and adaptation of species.

Natural variation and comparative genomics are also helping to provide insights into another fundamental question in biology. Why does the genome sequence of *Arabidopsis* make an *Arabidopsis* plant and not one that looks more like *Capsella*, *Brassica*, *Cleome* or cotton? Or to put it another way, how do specific genetic differences result in the diverse phenotypes of different plant species? *Arabidopsis* and its sequenced relatives are providing researchers with an unsurpassed set of tools to analyse the genetic basis of developmental, metabolic or physiological differences. This will help to deliver a genetics based view of evolution and ecology and ultimately provide an understanding of how the diversity within the plant kingdom is encoded.

By combining the power of emerging technologies with the extensive knowledge base that has 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.

Goals:

- 1 Continue to develop genomic sequencing and computational resources in order to understand and utilize the natural variation of *Arabidopsis* and related species. This will include close interactions with the Brassicaceae Map Alignment Project (BMAP) and the 1001 *Arabidopsis* Genomes project. (short/medium term)
- 2 Survey the variation in *Arabidopsis* and related species at numerous levels of biological organisation and regulation including genomic, proteomic, metabolomic, and epigenomic to infer biological networks. (medium term)
- 3 Develop tools and techniques to facilitate the identification of QTLs that have subtle effects on plant phenotypes (on going)
- 4 Utilise the information gathered in *Arabidopsis* and related species to undertake comparative genomics/ comparative evolution/ comparative ecological genomics (On going)
- 5 Develop appropriate open access informatics and data infrastructure for storage, retrieval and analysis of variation and QTL data (short/medium term)
- 6 Develop accessible statistical and computational methods for the analysis of natural variation and QTL data. (short/medium term)
- 7 Analyse ecotypes and *Arabidopsis* relatives in association with their rhizosphere, endophyte and epiphyte communities in various ecological settings. (medium/long term)
- 8 Develop high-throughput methods for measuring phenotypes in the lab and the field (on going)
- 9 Develop a multi-scale artificial field model towards natural conditions. Similarly to model a plant in the lab, growth conditions will need to be established, including temperature, light, diurnal cycle, nutrition solution and growth medium along with other parameters. Physiologically relevant conditions similar to those experiments by plants in the field are required to extrapolate laboratory results for conclusions with agronomical relevance. (mid-long term)

- 10 Extend systems monitoring from the defined conditions of the laboratory to the variable conditions of the field. (long term)

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

Plant science is currently undergoing an era of great change that is being driven by genome scale technologies, theoretical approaches and informatics. For example, the advances we have witnessed in genome sequencing will inevitably lower the barriers to research using previously intractable economically important plants, as well as lesser-studied and wild plant species. As a consequence, the fundamental knowledge that has been accrued in *Arabidopsis* can now more readily inform the development of tools and techniques, such as marker assisted breeding, for the generation of improved crops for agriculture and commerce. The broad availability of emerging technologies is also driving a convergence of disciplines and fields within plant biology that have been historically separate. This period of revolutionary change provides plant biologists with an opportunity to work together to construct a pipeline from basic to applied science that is capable of tackling global problems.

Although not of economical importance per se, *Arabidopsis* will have a major role to play in providing the first step in this pipeline. The investments that have been made in *Arabidopsis* research over past decades have generated a fully annotated genome and multitude of publicly available tools and resources, as well as a highly trained and creative international body of researchers. The *Arabidopsis* community is therefore ideally positioned to deliver underpinning knowledge in key areas such as the regulation of carbon fixation, growth, development, nutrient uptake, source-sink relationships and biotic and abiotic stresses. A detailed knowledge of these fundamental processes will provide the basis for the rational improvement of plants to meet our needs for food, fuel, shelter, plant based products and to mitigate the effects of climate change.

As we progress into the next decade and beyond, a major challenge that plant researchers will face is how to maintain curiosity-based research that generates the fundamental advances, whilst simultaneously ensuring that this new knowledge flows into plant breeding programmes. To help achieve this delicate balance it will be essential that *Arabidopsis* is not viewed as separate from the wider plant science community but rather as an essential component in a continuum of discovery from the basic to the applied.

To achieve this objective we will need to meet the following goals:

- 1 Undertake the approaches outlined section in sections A and B to help us understand important complex traits such as: yield, cell wall biogenesis, plant disease resistance, water-use efficiency, nutrient-use efficiency, photosynthesis, generation of biomass and growth. This is needed to generate a knowledge base that can help develop plants to meet our future needs. (ongoing)
- 2 Promote active dialogue, knowledge and data exchange between plant communities and various fields of expertise. This will increase awareness of the richness of plant research, bring together previously separate communities, and help identify potential bottlenecks and barriers to translation. (ongoing)
- 3 Develop a data and informatics infrastructure in which underpinning

- knowledge generated in Arabidopsis can flow easily to plant breeding. (Short/medium term)
- 4 Showcase examples of the role of Arabidopsis in rational improvement of plant species for agriculture and other plant-based industries through the annual MASC report and annual International Conference on Arabidopsis (ICAR). (ongoing)
 - 5 Promote exchanges of information and personnel between Arabidopsis groups and those working on other plant species and vice versa to increase the flow of knowledge and expertise between different communities and to help develop an understanding of how translation from basic to applied research could be improved. Combined with workshops, conference sessions and representation with the other plant communities, this would promote an efficient two-way knowledge exchange. (ongoing)
 - 6 Promote knowledge exchange with data providers/users of other model organism communities and facilitate interactions with computational/theoretical researchers. (ongoing)

D. Build an International Informatics and Data Infrastructure

Over the past decade there has been an unprecedented explosion of data, tools and resources. In virtually all areas of experimental biology, databases and repositories have evolved to become a central tool in the modern laboratory, with *in silico* experiments now regularly playing a role in the processes of scientific discovery.

In common with many other communities, Arabidopsis researchers have to deal with a range of new data types, informatics approaches and tools, whilst simultaneously trying to cope with the mountain of data that they are faced with on a daily basis. In order to provide solutions to these challenges members of the International Arabidopsis community recently came together to assess its future informatics needs. The major conclusion of the meetings was that the Arabidopsis community was at a critical junction and it was recommended that it should move beyond current structures to develop novel approaches to data management access and integration via the initiation of the International Arabidopsis Informatics Consortium (IAIC) (35). The IAIC would consist of globally distributed system of data and resources that would be managed by a single international consortium capable of leveraging expertise and funding on a global scale. Existing data and databases will be the basis for the new infrastructure. The development of such an international consortium would be essential to achieving the goals outlined in this vision document, as they are heavily reliant upon the development of an appropriate cyber-infrastructure that is able to handle, store, visualize and interpret this diverse array of biological and theoretical data.

Only by developing a coordinated infrastructure will we be able to take full advantage of the current 'data deluge' and exploit future technological advances. This will allow researchers to effectively translate data and information into scientific understanding and improve our ability to address global challenges.

Goals:

- addition to those previously generated by the Arabidopsis community (short term)
- 2 Develop an infrastructure that is flexible enough to respond to new/future approaches in data management, access and integration. (short term)
- 3 Develop appropriate data standards and establish their widespread use within the community (short term)
- 4 Generate an infrastructure that promotes data exchange and collaboration. For example, to ensure that integration of data allows users to move vertically between Arabidopsis associated data as well as horizontally to other plant species and model organisms. (short/medium term)
- 5 Ensure all data and resources generated are available via the appropriate public data repositories. (ongoing)
- 6 Ensure there is interoperability between the data and resources generated by the Arabidopsis community and those generated by other communities. (ongoing)
- 7 Establish strong links with other data providers/ users and computational experts to allow exchange of information and best practice. (ongoing)

E. Deepen International Cooperation and Coordination

The challenges that plant biologists must address are too large for any single country to tackle alone. International coordination of both research and investment will therefore be essential to the future success of plant science research.

The Arabidopsis community has a long tradition of international collaboration and sharing of data and resources that is exemplified in the sequencing of the Arabidopsis genome (35) and the Multinational Coordinated Arabidopsis thaliana Functional Genomics Project. In each of these initiatives MASC undertook a pivotal role of community coordination to ensure success. Originally established in 1990 to promote international cooperation and assist in the free exchange of ideas and information, MASC has continued to provide a unifying voice for the international community in subsequent decades. In the current period of financial uncertainty the role of MASC will be more important than ever if we are to achieve the ambitions of the 'Bench to Bountiful Harvests' vision outlined above, leverage national investment to support this vision, and synergize outcomes.

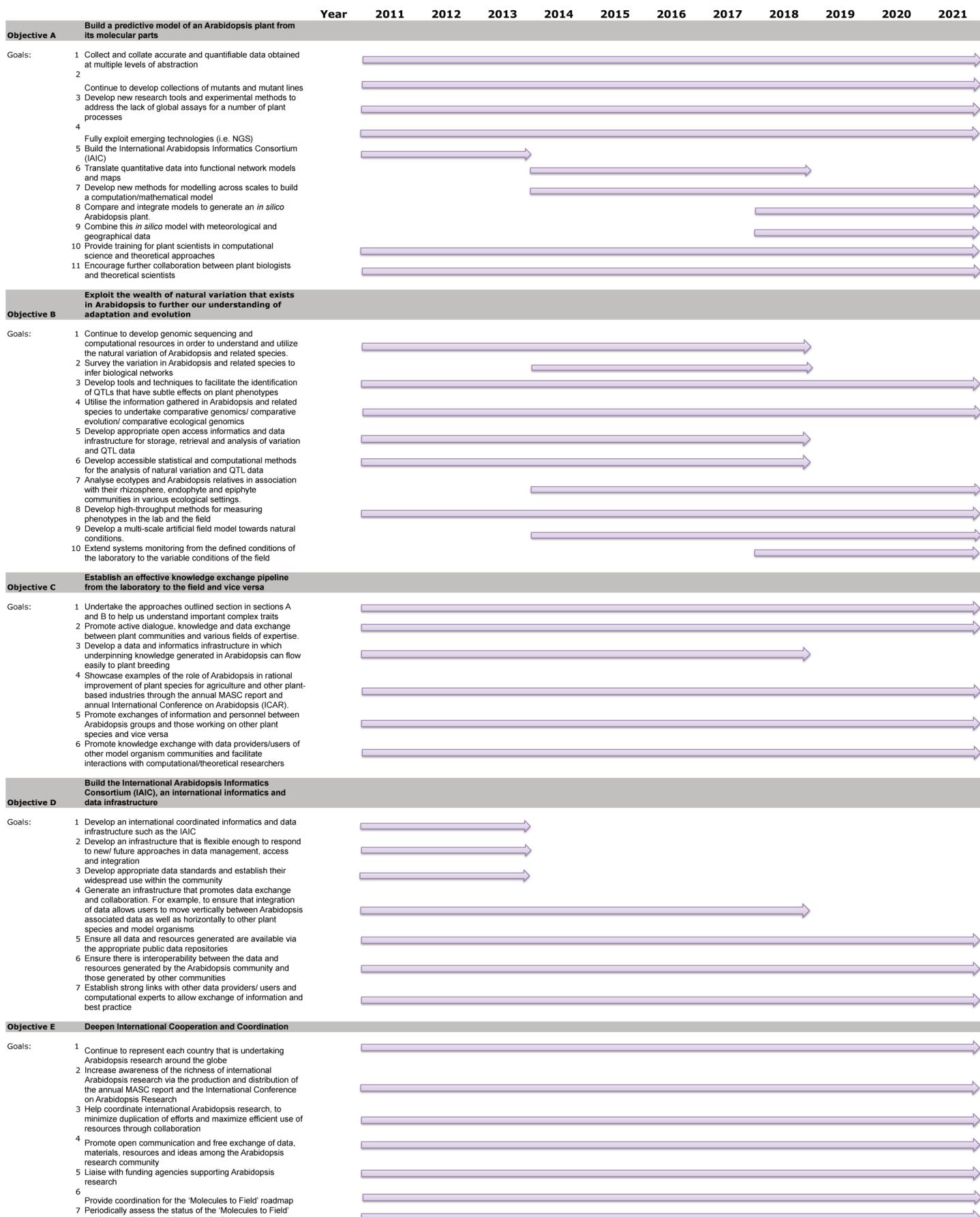
Goals:

- 1 Continue to represent each country that is undertaking Arabidopsis research around the globe. (ongoing)
- 2 Increase awareness of the richness of international Arabidopsis research via the production and distribution of the annual MASC report and the International Conference on Arabidopsis Research. (ongoing)
- 3 Help coordinate international Arabidopsis research, to minimize duplication of efforts and maximize efficient use of resources through collaboration. (ongoing)
- 4 Promote open communication and free exchange of data, materials, resources and ideas among the Arabidopsis research community. (ongoing)
- 5 Liaise with funding agencies supporting Arabidopsis research. (ongoing)

- 6 Provide coordination for the 'Bench to Bountiful Harvests' roadmap (ongoing)
- 7 Periodically assess the status of the 'Bench to Bountiful Harvests' roadmap and adjust goals as required. (ongoing)

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Progress and Activities of the Multinational Arabidopsis Steering Committee

Progress and activities of MASC in 2011/2012

In 2011, Mark Estelle (UC San Diego, U.S.A.) succeeded Kazuo Shinozaki (RIKEN, Japan) to become the MASC Chair and Wolfram Weckwerth (University of Vienna, Austria) became Co-chair. Prof Weckwerth will become the new MASC chair when Prof Estelle steps down following the annual International Conference on Arabidopsis Research (ICAR) in July 2012. 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 literature in TAIR. In 2011, 141 of 611 abstracts were linked to 386 distinct AGI, including 5 loci that were not already associated to the literature 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, 2011 and March 1, 2012, 46 different MASC pages were viewed 8,191 times, an average of about 683 views a month. The top-viewed page (7,184 views) contains information on the International Arabidopsis Informatics Consortium (IAIC) page (www.arabidopsis.org/portals/masc/IAIC). It was set up in September 2010 to inform the wider community of the bioinformatics infrastructure developments although now a separate IAIC website exists (<http://www.arabidopsisinformatics.org/>). Other frequently viewed pages include projects funded through the US NSF 2010 project (www.arabidopsis.org/portals/masc/projects.jsp), the NAASC page (www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp), the funding page (www.arabidopsis.org/portals/masc/funding.jsp) and the MASC Report page (www.arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp), which received 1,647, 747, 427 and 366 views respectively over the last year.

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, ORFeomics, Phenomics, Proteomics, Natural Variation and Comparative Genomics. A special MASC Subcommittees workshop was held at ICAR 2011 in Madison, USA, to showcase activities of the subcommittees to the wider community. A similar workshop is planned for ICAR 2012 in Vienna, India (represented by Jitendra P. Khurana and R. Srinivasan, New Delhi) has joined MASC and submitted a report.

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. Following two community workshops (Nottingham, UK, 15-16 April 2010; Washington DC, USA, 10-11 May 2010) the development of an International Arabidopsis Informatics Consortium (IAIC) was proposed. The workshop participants envisaged a distributed model with a central portal that would be funded by a variety of sources. The recommendations of the workshop participants were 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. In 2011, the IAIC became a reality (<http://www.arabidopsisinformatics.org/>) and more information on the development of this infrastructure can be found on page 21.

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>). 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

In 2011 the annual number of publications involving Arabidopsis research has increased once again. The number of peer-reviewed articles in 2011 in rice was slightly lower than that of Arabidopsis but appeared to follow the same trend. Over the past 20 years the Arabidopsis community has enjoyed the ease of manipulation of this plant and the availability of a wide range of resources that have been developed. Resources include chemically generated mutants; homozygous T-DNA insertion mutant lines; RNAi resources, artificial microRNAs; cDNA and ORF clones; large-scale microarray data; RILs and other mapping populations. Resources that are more recent additions include expanded information about the Arabidopsis proteome, metabolome and methylome, and the natural diversity found in Arabidopsis accessions. Web-based databases and browsers are also proliferating, reflecting the need to manage the vastly increasing number of datasets developed by the many 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. However, the time lapse between an original scientific discovery and its biotechnological application is often rather long and studying an organism that is easier to manipulate may be beneficial in the long term. Indeed, Arabidopsis lends itself exceptionally well to studying most aspects of basic plant biology; its well-known features include its small genome, size, high fecundity, diverse natural populations, ease of genetic manipulation and transformation, and short generation time. Studies in Arabidopsis have also greatly benefited from strong international collaborations first established over 40 years ago and strengthened during the Arabidopsis Genome project spanning the last decade across several countries and continents. With the release of the reference sequence in 2000, the 'genomic era' of Arabidopsis research truly began, allowing a rapid increase in discoveries and publications (Figure 1).

Considered alongside classic model organisms such as corn, the Arabidopsis publication record remains impressive, reflecting its ease of use as a genetic system, advanced resources and datasets, and the collegiality of the worldwide community, each of which contributed to its development as the reference plant. Between 1994 and 2011, the number of peer-reviewed Arabidopsis publications increased nearly 10-fold, while rice and corn publications increased about 5-fold and 2.6-fold, respectively (Figure 1). Over 3,800 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.

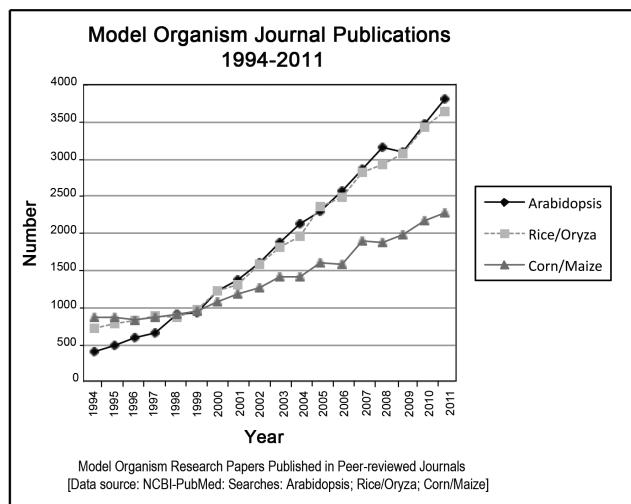


Figure 1: Model Organism Journal Publications (1994-2011)

FLOWERING LOCUS T regulates stomatal opening

By: Irene Lavagi, MASC Coordinator

During the day plants open and close the pores formed by guard cells, stomata, to control the gaseous exchange required for photosynthesis. The opening of stomata occurs in response to light intensity, CO₂ concentrations and abscisic acid. Understanding the mechanism that regulates the opening and closing of stomata is of crucial importance, as controlling the aperture of stomata allows plants to optimize photosynthesis while minimizing water loss through transpiration. The plant blue light receptor kinases phototropins (phot 1 and phot 2) that are known to trigger stomatal opening by activating the plasma membrane proton pump H⁺-ATPase in guard cells. Following this proton efflux the increasingly negative electrical potential of guard cells leads to the opening of potassium voltage gated channels, which in turn causes water to accumulate in guard cells increasing their volume and turgor pressure. The two guard cells elongate by bowing apart from one another, thereby opening the pore. However, until recently the signalling mechanism between phototropins and the H⁺-ATPase had remained unknown.

Kinoshita and colleagues have recently shown that the flowering protein Flowering Locus T (FT) is responsible for the activation of the essential plasma membrane proton pump H⁺-ATPase in *Arabidopsis thaliana* (Kinoshita et al., 2011). FT is well established as a major player of floral induction in response to appropriate day length. This recent report shows that FT is also required for the regulation of stomatal aperture in a cell autonomous manner; guard cells are not connected to neighbouring cells by plasmodesmata. *phot1 phot2* double mutant plants have been previously reported to display closed stomata in the presence of blue light, downward curled leaves and reduced H⁺-ATPase activity. A genetic suppressor screen for mutations that suppressed the *phot1 phot2* phenotype led Kinoshita and colleagues to the identification of the *scs* (suppressor of closed stomata phenotype in *phot1* and *phot2*) -1-1 mutant. Map-based cloning of the *scs1-1* suppressor locus showed that this was a null allele of the transcriptional repressor ELF3. Loss of function of *ELF3* resulted in a 50-fold increase in expression of *FT*, restored stomatal opening, leaf flattening and H⁺-ATPase activity in guard cell protoplasts. Over-expression of *FT* in *phot1 phot2* double mutant plants was also able to rescue the mutant phenotype. Loss of function of *FT* (*ft-1*) mutant plants failed to activate the guard cell

H⁺-ATPase resulting in failure to open their stomata in the presence of blue light. This evidence indicates that FT is directly or indirectly responsible for the activation of guard cell H⁺-ATPase.

Although the protein kinase that activates the H⁺-ATPase in other tissues remains to be identified, the blue-light receptor protein kinase phototropin encoded by the redundant genes PHOT1 and PHOT2 have now been identified as the H⁺-ATPase activators in guard cells.

The work presented by Kinoshita and coworkers provides evidence for the connection between the key regulatory protein for plant flowering FT and the plasma membrane proton pump H⁺-ATPase. This opens up new developmental questions including how FT can fulfill such apparently unrelated roles and whether it is a common mechanism in development to use basic biophysical systems (e.g. H⁺-ATPases) as second messengers for signal transduction.

Toshinori Kinoshita, Natsuko Ono, Yuki Hayashi, Sayuri Morimoto, Suguru Nakamura, Midori Soda, Yuma Kato, Masato Ohnishi, Takeshi Nakano, Shin-ichiro Inoue, and Ken-ichiro Shimazaki (2011) FLOWERING LOCUS T Regulates Stomatal Opening. *Curr Biol* (21): 1232-1238

The protein interactome

By: Irene Lavagi, MASC Coordinator

Studies of protein-protein interaction networks will provide important new insights into how plants have become adapted to their environments and ecosystems. A giant leap forward in this sphere was reported in 2011 when an international team published the proteome-wide binary protein-protein interaction map for the interactome network of Arabidopsis, (Arabidopsis Interactome Mapping Consortium, 2011). This contains approximately 6,200 highly reliable interactions between approximately 2,700 proteins and doubled the interaction data available for scientists to use. The findings reveal a global organization of biological processes in conjunction with many novel hypothetical links between proteins and pathways. This map and future maps will be central to facilitating future lines of enquiry and promote systems based approaches, which will enable plant researchers to better understand plant biology and in turn make improvements in crops.

For example the usefulness of this approach was illustrated in a study of the interactions between pathogen effector proteins from the bacteria *Pseudomonas syringae*, the oomycete *Hyaloperonospora arabidopsidis* and the Arabidopsis proteome (Mukhtar et al., 2011). By utilizing two pathogens which span the eukaryote-eubacteria divergence the researchers were able to illustrate that the 'effector' proteins that subvert Arabidopsis cell during the infection process target the same set of highly interconnected host proteins. Therefore irrespective of the pathogen kingdom, virulence proteins separated by ~2 billion years of evolution interact with a limited set of highly connected hubs.

Arabidopsis Interactome Mapping Consortium (2011) Evidence for Network Evolution in an Arabidopsis Interactome Map. *Science* (333): 601-607

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The timing of stem growth; a tale of ELFs and LUX

By: Irene Lavagi, MASC Coordinator

Keen observers, including Charles Darwin over one hundred years ago, observed that some plants (including crops like corn and sorghum) grow more during the night than during the day. Whilst being generally perceived as organisms growing at a slow and steady pace, plants grow rhythmically. The growth of hypocotyls in numerous plant species is gated; restricted to specific times of the day. In Arabidopsis, hypocotyl growth peaks at the end of the night and slows dramatically during the early morning. The close relationship between the time of the day and plant growth implies the involvement of the circadian clock in the regulation of plant growth. However, the mechanism that links the circadian clock with plant growth was unknown until very recently.

In a recent *Nature* publication, Nusinow and colleagues provided compelling evidence for the mechanism used by the plant circadian clock to regulate hypocotyl growth in *Arabidopsis thaliana* (Nusinow et al., 2011). In this study yeast-two and three hybrid experiments led to the identification of a novel trimeric protein complex, "the evening complex" (EC), consisting of EARLY FLOWERING3 (ELF3), ELF4, and the transcription factor LUX ARRHYTHMO (LUX). Formation of the complex *in vivo* was confirmed by co-immunoprecipitation experiments showing that ELF3 is necessary for the formation of the complex, bridging ELF4 and LUX complex formation. EC was also found to be regulated by the clock with its expression peaking at dusk. Formation of the complex was also reported to be sensitive to photoperiod peaking earlier in short days than in longer days.

elf3, *elf4* and *lux* single mutants share multiple phenotypes including an arrhythmic clock and abnormal hypocotyl growth during diurnal cycles. To investigate the actual molecular role of the EC the authors focused on its effect on hypocotyl growth. Chromatin immunoprecipitation (ChIP) experiments showed that the EC binds to the promoters of *PHYTOCHROME INTERACTING FACTOR4* (*PIF4*) and *PIF5* consequently repressing their transcription early in the evening. It has previously been shown that *PIF4* and *PIF5* are necessary for hypocotyl growth, therefore their transcriptional repression by the EC serves to gate hypocotyl elongation growth to dawn.

An important role of circadian clocks is to ensure that physiological and metabolic responses occur at the optimal time of the day. The clock provides adaptive advantages to plants allowing them to anticipate daily and seasonal environmental changes. Although it remains to be elucidated, it is possible that stem elongation is gated to dawn, as this is the time when nutrients are most available for growth. In addition to providing a fundamental advance towards our understanding of plant growth and its cyclic regulation by the clock at the molecular level, this study provides a potential research area to manipulate and control plant yield and biomass dep-

osition.

Dmitri A. Nusinow, Anne Helfer, Elizabeth E. Hamilton, Jasmine J. King, Takato Imaizumi, Thomas F. Schultz, Eva M. Farré & Steve A. Kay (2011) The ELF4–ELF3–LUX complex links the circadian clock to diurnal control of hypocotyl growth. *Nature* (475): 398-402

Chaperonins tie up the loose ends: Chaperonins facilitate KNOTTED1 transport

By: Irene Lavagi, MASC Coordinator

Cell to cell communication is crucial in the specificity of cell fate and the coordination of development. Plant cells are able to communicate by selective trafficking of transcription factors and additional signals through channels, termed plasmodesmata (PD) that traverse the cell wall and connect bordering cells. A host of mobile signalling factors are now known to selectively traffic through PD. The first plant protein to be identified to move in this way, was the homeodomain transcription factor, KNOTTED1 (KN1). Despite the central role of this pathway in transmitting molecular information between cell, the factors that contribute to selective trafficking remain largely elusive. A recent *Science* paper identifies chaperonins as essential for cell-to-cell trafficking of transcription factors (Xu *et al.*, 2011). Furthermore, the research also provides evidence that chaperonin-dependent protein trafficking is required for plant stem cell function. Xu and colleagues used an elegant genetic screen utilising the *g1* mutant, which lacks the cell-autonomous MYB transcription factor GLABROUS1 that drives trichome development in *Arabidopsis* as a tool.

Fusion of the C-terminal trafficking domain of KN1 (KN1c) to GFP::GL1 and expression of this construct (GFP::GL1::KN1c) in *g1* mesophyll cells, restored trichome development with GFP being visualized in epidermal cells. In this work, mutagenesis of the rescued line generated several trichome-lacking plants with a strongly reduced GFP signal in the epidermis. As overall expression was unaltered, it implied that transport of GL1::KN1c to the epidermal cells was compromised. The authors identified a mutation in the gene which encodes a chaperonin subunit, CCT8, as the apparent cause and show that CCT8 can interact physically and genetically with KN1 and SHOOT MERISTEMLESS (STM). This enabled the authors to identify CCT8, as a necessary component for the movement of KN1. They also demonstrate that CCT8 can interact physically and genetically with KN1, SHOOTMERISTEMLESS and TRANSPARENT TESTA GLABRA1 (TTG1), which is involved in trichome spacing. It is certainly worthy of a mention that CCT8 was not required for the trafficking of SHORTROOT, indicating that distinct pathways exist for protein trafficking between cells. Nine genes encode the eight different chaperonin subunits (CCT1-8), in *Arabidopsis*, with CCT8 being widely expressed and hence in agreement with its role in assisting the folding of a variety of proteins. The reduction of CCT1 and CCT5 by RNA interference caused similar defects to *cct8*, trichome rescue was lost, indicating that the whole chaperone complex is involved in cell-to-cell trafficking.

These findings provide evidence that the chaperonins are necessary for the cell-to-cell trafficking of a group of mobile transcription and in turn increase understanding of protein movement in plants.

Xu XM, Wang J, Xuan Z, Goldshmidt A, Borrill PG, Hariharan N, Kim JY, Jackson D. (2011) Chaperonins facilitate KNOTTED1 cell-to-cell

trafficking and stem cell function. *Science* (333): 1141-4

Plant symmetric cell division uncovered

By: Irene Lavagi, MASC Coordinator

More than 100 years ago, Errera put forward the theory that plant cells act like soap bubbles in the sense that upon division new walls are generated with minimal area and the daughter cells have the same volume. However these rules fail to describe the numerous patterns of plant cell division observed in nature. In their recent *PNAS* article Besson and Dumais (Besson and Dumais, 2011) showed that the probability of a division involves competition between alternative configurations whose geometries represent local area minima. This gives rise to inherent randomness and can be used to explain the plethora of natural patterning. The authors illustrate that the likelihood that a cell wall will be formed in agreement with Errera's rule is high in cells where the difference between the area of the globally minimal cell wall and the other candidate walls is large. Whereas the probability of agreement with Errera's rule is decreased when cells have several cell walls with an area close to the global minimum.

To quantify plant cell divisions Besson and Dumais proposed a mechanistic model for the selection of the division plane in plant cells based on microtubular dynamics. In the model strands and more specifically the associated microtubules minimize the energy required by taking the shortest route such that shorter microtubules are preferred, longer microtubules are prohibited and eventually microtubules that span the shortest axis are favored. The distribution of strands is calculated by maximizing the systems entropy, which as expected shows that as the length of a strand increases the number of strands falls exponentially and the probability of forming a strand decreases exponentially with plane size.

The work of Besson and Dumais addresses the question of cell division through statistical mechanics. By comparing cell division across land plants and algal ancestors the authors have uncovered a new rule for plant cell divisions that appears to be the default mechanism in the absence of internal and external cues. Although this rule can not predict all cell divisions these findings are a considerable development of the 19th century geometric rules.

Besson S, Dumais J. (2011). Universal rule for the symmetric division of plant cells. *PNAS* 108: 6294-9

Is it all down to a DNA sequence? Transgenerational epigenetic instability is a source of novel methylation variants.

By: Irene Lavagi, MASC Coordinator

In addition to the DNA sequence of a genome, epigenetic information can also influence gene expression, affect an organism's phenotype and be inherited by the next generation via meiosis. There are a variety of known epigenetic modifications including DNA methylation and histone deacetylation, which can suppress gene expression without altering the DNA sequence of the affected gene. Cytosine DNA methylation is a well studied epigenetic modification that is known to store epigenetic information allowing it to be stably inherited. However, the rates of spontaneous gain or loss of DNA methylation were unknown until now.

In a recent *Science* publication Schmitz and colleagues examined the changes in the DNA methylation of *Arabidopsis thaliana* over 30 generations of single-seed descendants of

(Schmitz *et al.*, 2011). The authors found that these spontaneous changes in methylation events occur more quickly than changes at the DNA sequence level and therefore have a higher level of flexibility in influencing biological traits. This interesting article shows that cytosine DNA methylation, thought to be primarily employed for gene silencing, is used in *Arabidopsis* for generating new allelic states or epialleles, which are identical genes that differ in the extent of methylation. Thereby producing phenotypic diversity in new generations without altering the genetic information.

Bisulphite sequencing provided the methylome of three ancestral lines and five descendant lines at the single base pair resolution. Almost all (91%) methylated sites were maintained across all lines. On average approximately 66,000 methylated CpG sites were identified in each line. Although this number was similar in the different lines the conservation of polymorphisms among and between ancestral and descendant populations was different. The authors estimate a lower limit of the epimutation rate to be 4.46×10^{-4} methylation polymorphisms per CpG site per generation.

The clustering of meCs (methylated cytosine) revealed that differentially methylated regions (DMRs) in the genome were mainly associated with genic regions whereas the majority of nonCG-DMRs were enriched outside of gene bodies. The transcriptional activity of eight previously documented DMRs was measured. In four of these the gain or loss of methylation was associated with a large decrease or increase in mRNA abundance indicating decreases and/or increases in gene expression. 24nt-small interfering RNAs (siRNAs) were present at each silenced epiallele, suggesting that changes are result of the RNA-directed DNA methylation (RdDM) pathway. More specifically, the methylation status of one C-DMR resulted in alternative promoter usage of *ACTIN RELATED PROTEIN 9* (At5g43500). The absence of methylation in the 5'UTR of the At5g43500.1 caused an increase in mRNA expression, with the expression of a second isoform At5g43500.2 with a transcriptional start site located further downstream was unaffected.

In general the epialleles identified in this study are meiotically stable and heritable through many generations. It is of great importance that the process of transgenerational instability and the mechanisms that trigger and/or release these epiallelic states is understood. Given the high epimutation rate uncovered in this publication it is highly likely that epigenetic changes provide a pool of variability in crop plants which could be exploited for human use eg in food, fuel and fiber production?

Schmitz RJ, Schultz MD, Lewsey MG, O'Malley RC, Urich MA, Lübiger O, Schork NJ, Ecker JR. (2011). Transgenerational epigenetic instability is a source of novel methylation variants. *Science* 334: 369-73

How do plants sense oxygen?

By: Irene Lavagi, MASC Coordinator, Giovanna Serino (Country rep for Italy), Francesco Licausi and Pierdomenico Perata (Sant'Anna, Pisa, Italy)

The mechanism used by plants to sense oxygen has long remained a mystery. This year, two *Nature* research articles have reported that *Arabidopsis* possesses a system that is able to detect low oxygen levels (1,2).

Although it may seem surprising, land plants may en-

counter oxygen-deprived conditions. This can occur when plants are submerged, as a consequence of growth in very wet soils, or after heavy rains or flooding. Both animals and plants require oxygen for mitochondrial respiration however plants lack an efficient oxygen delivery system such as the one found in animals and as a consequence reduced growth and development are often accompanied by low oxygen availability. To cope with limited oxygen availability plants have evolved mechanisms that trigger a series of responses aimed at adapting their metabolism to limited oxygen supply, thus allowing the plant to endure these conditions.

Both studies report the identification of a specific set of transcription factors, belonging to the group VII of the ethylene response factor (ERF), as responsible for initiating and orchestrating the molecular response to low oxygen levels. This sensing pathway relies on the stability and localization of these ERFs. The authors show that, in presence of oxygen the ERFs are degraded by the ubiquitin-proteasome pathway, the main cellular machinery for the degradation of specific substrates. Conversely, when oxygen levels decrease, their degradation is inhibited, allowing them to induce the transcription of hypoxia-responsive genes, which are required for the acclimation to low-oxygen conditions.

By studying different members of the same subgroup VII of ERFs, Gibbs *et al.* and Licausi *et al.* have shown that the ERFs stability is dependent on an N-terminal region that functions in an oxygen-dependent manner. This region contains a cysteine that is a hallmark of the group VII-ERFs, which when oxidized converts the VII-ERFs to substrates for the N-end rule ubiquitin pathway. Gibbs and co-workers have observed that the stability of all group VII ERFs was enhanced following mutation of the cysteine to alanine *in vitro*. They could also show oxygen-dependent destabilization *in vivo* for the hypoxia inducible ERF HRE2. Licausi and co-workers identified an ERF protein, RAP2.12, that is proposed to act as the plant's oxygen sensor. Differently from hypoxia-induced ERFs, RAP2.12 is constitutively expressed and associates with the plasma membrane. Association to the plasma membrane appears to protect RAP2.12 from cysteine oxidation, which would lead to its degradation. When oxygen level drops, as a consequence of submergence, RAP2.12 can safely re-localizes in the nucleus, where it rapidly activates transcription of hypoxia-responsive genes.

Therefore, when oxygen is abundant, cysteine oxidation leads to degradation of the ERFs. When the oxygen concentration is low—as during flooding—the absence of cysteine oxidation leads to ERFs stabilization, which accumulate in the nucleus and activate gene expression for hypoxia.

This study opens new perspectives for agriculture, as it provides a foundation for the selection of new crops that could be more tolerant to flooding.

1. D. J. Gibbs, S. C. Lee, N. M. Isa, S. Gramuglia, T. Fukao, G. W. Bassel, C. S. Correia, F. Corbineau, F. L. Theodoulou, J. Bailey-Serres, M. J. Holdsworth, Homeostatic response to hypoxia is regulated by the N-end rule pathway in plants. *Nature* 479, 415-418 (2011):

2. F. Licausi, M. Kosmacz, D. A. Weits, B. Giuntoli, F. M. Giorgi, L. A. C. J. Voesenek, P. Perata, J. T. van Dongen, Oxygen sensing in plants is mediated by an N-end rule pathway for protein destabilization. *Nature* 479, 419-422 (2011).

Arabidopsis Community Projects and Resources

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

By: Eva Huala, TAIR Director

We are well into the final two years of the TAIR project, in which we are funded at 50% and 25% of our previous operating budget. While the funding cuts require some changes to TAIR operations we will continue to do our best to provide the research community with good access to Arabidopsis data.

TAIR database and website: No further enhancements to the TAIR software are planned at this time. Existing web pages and analysis tools will be maintained to the extent possible, with lower priority given to maintaining tools and pages with low usage.

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

Genome releases: We will continue to collect gene structure updates but no new genome release is planned at this time. A file of updated gene structures will be made available on the TAIR ftp site. These updates will not be incorporated into the TAIR database or tools which will continue to use the TAIR10 dataset.

Gene function updates: Some literature curation will continue in the final two years, funded by the Gene Ontology project and the TAIR sponsorship program, allowing TAIR curators to continue capturing new gene information from the literature. This effort will focus on a small subset of all articles, chosen for their characterization of previously unstudied genes. We strongly encourage the community to contact us at curator@arabidopsis.org and provide us with their new results on gene function for well studied or newly characterized Arabidopsis genes, as well as information on gene symbols and names, expression patterns, mutant phenotypes and protein-protein interactions.

TAIR helpdesk: We will continue to answer questions from researchers and help them find and understand data in TAIR, and will carry out bug fixes to the extent possible although delayed response times should be expected.

TAIR usage: As of April 9 2012 there were 23,130 registered TAIR users and 9,024 labs registered at TAIR. Of these, the records for 9,563 people and 3,831 labs were updated in the past 5 years.

Planning for post-TAIR data access: We are currently investigating the feasibility of moving the TAIR software to iPlant where it can continue to run for a period of 1-3 years after the TAIR grant ends on August 31, 2013. This will provide the plant research community with continued access to Arabidopsis data during the transition period as the new Arabidopsis Inforamtion portal is developed and launched.

The International Arabidopsis Informatics Consortium progress update

(IAIC, www.arabidopsisinformatics.org/)

By: Blake Meyers (University of Delaware), Erich Grotewold (Ohio State University), and Joanna Friesner (North American Arabidopsis Steering Committee)

The IAIC was initiated in 2010 by members of the Arabidopsis community in response to the rapid growth in the size and complexity of Arabidopsis data combined with an expected reduction in funding for TAIR, the current primary Arabidopsis information database. The outcomes and recommendations of two earlier international workshops that culminated in IAIC formation are described in a 2010 Plant Cell publication (www.ncbi.nlm.nih.gov/pubmed/20807877). A major IAIC goal is to facilitate development of a novel, integrated, distributive, international framework with which to address the informatics needs of the Arabidopsis community now and in the future, while providing a smooth transition from the current TAIR-based central database structure to this stable, sustainable, long-term structure. In June 2011, Interim IAIC Director Blake Meyers received a four-year Research Coordination Network award from the US National Science Foundation to support community development of the IAIC (NSF Award Abstract #1062348). Meyers, the grant's PI, with five US Co-PIs and three international scientists, comprise the IAIC Steering Committee (SC). The IAIC website is describes the effort further (<http://www.arabidopsisinformatics.org/>).

The IAIC Scientific Advisory Board (SAB) was appointed in February 2012 following a three-month process involving solicitation of community nominations and recommendations from the Multinational Arabidopsis Steering Committee (MASC). SAB members include: Gloria Coruzzi (New York University, USA), Kazuki Saito (RIKEN, Japan), Magnus Nordborg (GMI, Austria), Mark Estelle (UC San Diego, USA), Mark Forster (Syngenta, UK), Paul Kersey (EBI, UK), and Xuemei Chen (UC Riverside, USA). SAB terms will be decided at ICAR 2012 with the expectation that additional community members will be requested to replace board members and serve three-year terms beginning as early as mid-2013.

The SC organized an interactive, professionally facilitated 2.5 day Design Workshop (DW) in December 2011 in Atlanta, Georgia (USA). The DW's primary goal was to convene a diverse mix of international Arabidopsis community members and cyberinfrastructure and computing experts to develop the technical requirements for the future Arabidopsis Information Portal (AIP). In short, the mission was to consider how to build the AIP, how to fund it, how to involve the broader community, and how to develop an effective action plan to implement workshop recommendations. Specifically, the 44 participants were asked to: (1) articulate the need for the AIP and how it will address the needs of the Arabidopsis community; (2) identify and prioritize the technical challenges in building the AIP and the data that must be integrated; (3) learn what the community can leverage from existing, planned and other funded resources; (4) start to identify teams and collaborators who could work together to build parts of the AIP, including core and non-core components; (5) prepare ideas and identify funding opportunities that could lead to grant proposals in the near term; and (6) start to develop the standards to allow boutique databases to "plug in" to the AIP architecture. Several representatives attended the DW from funding agencies including the NSF (USA), DFG (Germany) and BBSRC (UK).

Most DW participants had met virtually in the months pre-

ceding the workshop via three Working Groups (WGs) including Engineering/Architecture/Infrastructure, Standards/Ontologies, and Modules/Use Cases. Each WG focused on distinct, and also some overlapping, aspects of current and future community needs, technology and approaches, and how these related to AIP development. The workshop itself was interactive and involved iterative rounds of small and large group discussions with groups rotating members to maximize diverse interactions and outputs. Discussion topics included designing the ideal AIP, developing its technical requirements, and outlining major challenges to the process (e.g., technical, economic, social) and potential solutions. On the final day, participants self-organized into four groups and were tasked with the challenge to develop an outline of the ‘Ideal AIP’ based on workshop presentations and two days of discussions. Each group drafted a brief ‘requirements document’ and presented their shared vision to the larger group for discussion and feedback.

Specific workshop outcomes include: (1) identification of a number of community members that expressed interest in participating in the future development of the AIP (e.g., by contributing to grant proposals, writing articles to disseminate information to the community, or serving on the IAIC Scientific Advisory Board), (2) a first draft of the AIP Technical Requirements document which will be useful to any group(s) wishing to develop an AIP funding proposal, and (3) a first draft of a white paper aimed at the research community and funding agencies that is expected to be published in a journal this year.

Additional community IAIC activities in 2012 include presentations at ASPB (Austin, TX, USA) and ICAR 2012, including a platform talk by Blake Meyers in the ‘MASC Roadmap’ concurrent session. Members of the SC and others in the community plan to hold a workshop (pending workshop acceptance), and the SAB will convene its first meeting during ICAR. SC members anticipate that grant proposal(s) to develop the AIP will be submitted by members of the Arabidopsis community over the next year and that formal governance and oversight of the IAIC will transition from the SC to the SAB. It is also expected that the SC will continue to play an advisory and participatory role in the IAIC and the Committee will expand to include additional interested community members.

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 serve the Arabidopsis community by collecting, maintaining, propagating and distributing various resources of *Arabidopsis thaliana* and related species for research and education. The Center maintains a high number of orders, with almost 90,000 samples sent in 2011 for all resources combined. The collection approaches one million accessions. Seed stock holdings include insertion lines covering 28,937 genes, out of which 24,898 are protein-coding; the 11,000+ TILLING lines; 1,464 distinct natural accessions, some of which are genetically fingerprinted and some sequenced by the 1001 Genomes Project; 30 recombinant inbred populations; a set of near-isogenic lines; RNAi lines; transgenic lines; 50+ accessions of the genus *Brassica*; and approximately 70 accessions of other closely related species. DNA resources at ABRC include full-length ORF and cDNA clones for almost 17,000 genes, BACs covering the entire genome, BACs of nine related species, the AGRIKOLA GST entry clones, various sets of expression clones and 12,466 amiRNA

clones.

ABRC continues to diversify the collection of new resources. In addition to the T87 cell suspension culture derived from the Columbia accession, cell suspension cultures PSB-L (MM1) and PSB-D (MM2d) were recently acquired from Geert De Jaeger at VIB, Gent (Belgium). These two cultures originate from *Landsberg erecta* stem explants, were originally developed by Jim Murray and are suitable for cell cycle studies. PSB-L and PSB-D are expected to be available soon after initial quality control performed by ABRC. The donation of a new protein chip, containing 10,000 *Arabidopsis* proteins, generated by S.P. Dinesh-Kumar is expected soon.

Education resources are the most recent addition to our collection and include seeds, DNA and instructional materials. Education kits for K-12 and undergraduate levels are being developed by the combined effort of ABRC and the community. Some of these have been further developed at ABRC, as part of our “Greening the Classroom” program. In September 2011 we obtained funding from the American Society of Plant Biologists (ASPB) to further develop our education program into a central hub for *Arabidopsis* teaching resources, including the knowledgebase TRAINED (Translating Research on *Arabidopsis* Into a Network of EDucational resources). Contribution of education materials is welcome and details can be found at <http://abrc.osu.edu/donate-stocks> and <http://abrcoutreach.osu.edu>.

Confirmed SALK, SAIL, GABI-Kat, and WiscDsLox lines in this period were mostly obtained from researchers in the community, with 521 coming just from Rob Last’s laboratory. 46,052 confirmed lines, received from Joe Ecker’s laboratory at SALK Institute, represent 25,534 loci. 39,454 lines have been made available and are ready for distribution. The SALK Institute generated a new collection of SALK_200K lines, containing a number of newly identified insertions. Their release is contingent on propagation at ABRC and GenBank submission of related data. Also of note is the acquisition of the RegMap collection of 1,302 natural accessions, genotyped using a 250K SNP chip and donated by Joy Bergelson. Through the European *Arabidopsis* Stock Center (NASC), we also received a large number of JIC and AGRIKOLA lines, as well as GABI-Kat lines from Bernd Weisshaar, which are distributed as sets of 5-18 lines. The recently donated cenh3-1 GFP-tailswap haploid inducer line from Simon Chan is expected to be highly requested for generation of multiple order mutants and doubled haploids. This line has already been used as a parent to produce a recombinant doubled haploid population of 226 lines, donated by Julin Maloof in March 2012.

Receipt and distribution of Entry and Expression full length/ORFeome clones remain a priority. During the past year, we received 606 Gateway ORF and cDNA entry clones from the 2010 Associomics project (Sylvie Lalonde and Wolf Frommer) and 653 ORF expression clones representing transcription factors in the AD vector for Y1H assays from Allie Gaudinier and Siobhan Brady. Importantly, ABRC has just amended its Distribution Agreement with “Life Technologies” (previously “Invitrogen”), that will allow the distribution of Gateway vectors, many of which will be made available in the near future.

A grant entitled “Making the ABRC Business Model Possible”, awarded by NSF in March 2012, adds \$0.5M of additional support to automate many processes in our operation. This will eventually enable us to serve the community with higher efficiency, maintaining the high quality of services we have provided in the past.

The Nottingham Arabidopsis Stock Centre

(NASC, <http://arabidopsis.org.uk>)

By: Sean May, NASC Director

This year NASC enters the twitter age: <http://twitter.com/#!/NASCArabidopsis> (please see the follow button on our website) and is also available to be friended on Facebook. The former gives updates on new stock availability and this year has included: Updates on seed stocks including new large GABI-Kat batches and CH-42 silencing and silencing suppression lines from Ian Furner; Clone announcements for 1,415 new Gateway ORF clones donated by Luis Oñate-Sánchez from Madrid, and 84 Plant Nuclear Marker Collection clones from JIC/Dundee (gateway constructs of Arabidopsis nuclear and nucleolar localised protein); we have also released a novel stock type for us in the body of a collection of Arabidopsis ORF clones distributed as yeast stocks in yeast / Gateway compatible plasmids. We plan to release regular announcements on Twitter and also encourage any feedback/comments this way – please do re-tweet at will and feel free to add to our Facebook timeline. Updates on ecotype collections have also been announced this year and by the time you read this article we should have released our new GoogleMaps and GoogleEarth Browsers for Ecotypes – an experimental subset of over 1000 ecotypes has already been accessible from <http://arabidopsis.info/EcoForm> for several months. Comments or suggestions on any of these developments are welcome. In local news, we have applied for a new 5 year period of the seed centre from the UK funding body (BBSRC) and are currently awaiting news (referees comments were very positive) – by Vienna we will know the outcome. Current ordering statistics are extremely high for both seeds and array work, which is clearly useful for the grant renewal proposal. In chip news, we are seeing a greater increase in the number of AraGene-1-1-ST (informally the ‘ATH2’ chip) use relative to the increase in ATH1 orders this year, which is gratifying. The new chip includes many more probes per gene along multiple exons in each gene as well as many previously inaccessible genes (based on TAIR10) – it is also a lot cheaper than the ATH1 chip despite being an improved format with more potential http://arabidopsis.info/StockInfo?NASC_id=N797864. We will present a comparison poster of baseline hybs on both chips (Ath1 vs AraGene) at the Vienna meeting and plan to make a large number of ‘ATH2’ chip hybs publically available before then. We also plan to announce new mechanisms for open cloud access to our existing ATH1 GeneChip repository at the summer conference – see you there!

RIKEN BioResource Center

(RIKEN BRC, www.brc.riken.jp/lab/epd/Eng/)

By: Masatomo Kobayashi, RIKEN BRC Coordinator

The RIKEN BioResource Center (RIKEN BRC) celebrated its 10th anniversary last July. Resources of experimental animal (mouse), plant, microbes, mammalian cells and DNA (including human origin) are preserved at RIKEN BRC. The Experimental Plant Division (plant@brc.riken.jp) collects, preserves and distributes seed stocks of Arabidopsis that include transposon-tagged lines (RATM line; insertion site information available; 15,000+ including 2,720 homozygous lines), activation-tagged (T-DNA) lines (for phenotype screening; 36,000+), FOX lines (Arabidopsis plants that over-express Arabidopsis full-length cDNA; for phenotype screening; 9,000+), natural accessions (SASSC stock) and individual mutants

and transgenic lines generated in Japan. In addition, the Division distributes DNA resources such as full-length cDNA clones of Arabidopsis (RAFL clone; 250,000+), *Physcomitrella patens* (140,000+), poplar (20,000+), cassava (19,000+), tobacco (3,000+) and *Thellungiella halophila* (19,000+). We preserve and distribute plant cultured cell lines including Tobacco BY-2 cells and Arabidopsis T87 cells. The total number of plant material in the Division is 646,000+, and 1,536 laboratories around the world have received our materials.

In 2011, RIKEN BRC began the distribution of new FOX lines (Arabidopsis plants that over-express rice full-length cDNA) for screening purposes. Full-length cDNA clones of *Brassica rapa* (9,903 clones) and a parasitic plant, *Striga hermonthica*, (35,198 clones) were also added to our catalogue over the past 12 months. Moreover, ORF clones of Arabidopsis transcription factors (400 clones) have also become available.

We are characterizing the genotype and phenotype of natural accessions in our stock. The results will be made public through our web site soon.

RIKEN BRC has joined the Asian Network of Research Resource Centers (ANRRC) and organized the 2nd ANRRC meeting in Tsukuba, Japan in 2010. Last year, the 3rd ANRRC meeting was held in Beijing, and the forth meeting will be held on the Jeju Island in October 17-19, 2012.

RIKEN BRC started preserving back-up resources at the Harima Institute of RIKEN, which is located in western Japan. Aliquots of Arabidopsis seeds and cultured cells will be preserved in a liquid nitrogen tank placed at Harima in near future.

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 2011, the number of peer-reviewed Arabidopsis publications increased nearly 10-fold, while rice and corn publications increased roughly 5-fold and 2.6-

fold, respectively (Fig. 1, page 17). In that same timeframe, while the number of U.S. patents referencing rice and corn increased 3.3 and 2.8 fold respectively, the number of patents citing Arabidopsis increased over 50-fold (Figure 2, below).

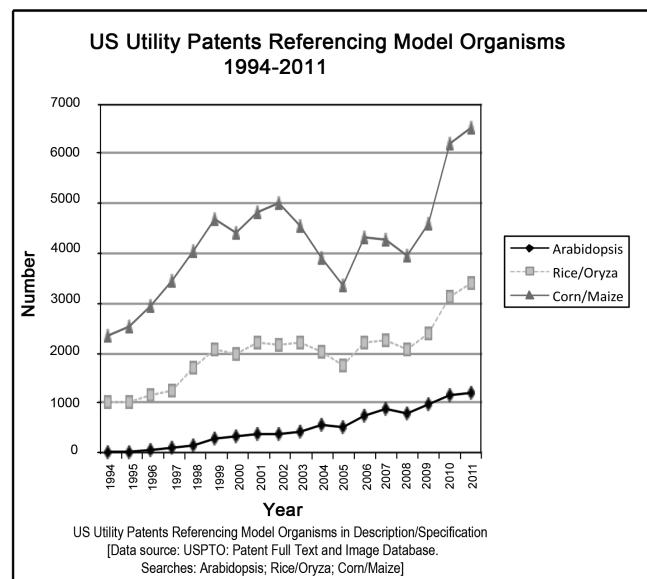


Figure 2: US Utility Patents Referencing Model Organisms 1994-2011

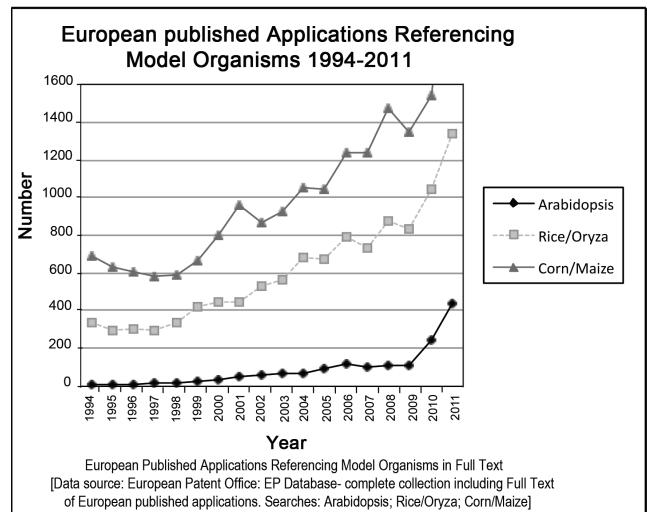


Figure 3: European Published Applications Referencing Model Organisms 1994-2011

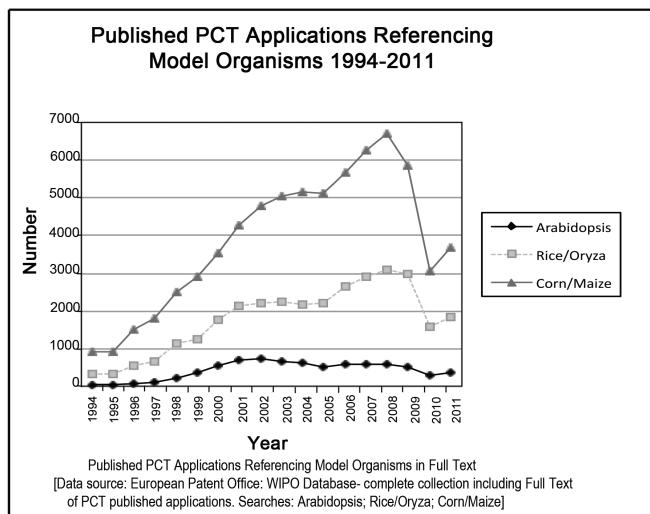


Figure 4: Published PCT Applications Referencing Model Organisms 1994-2011

The number of European and world's published applications also increased in the period between 1994 and 2011. Interestingly, a 63-fold increase was registered for European published applications referencing Arabidopsis, whereas a 4 and a 3.6 fold increase occurred for rice and corn respectively. From a world's perspective (or PCT perspective), published applications referencing Arabidopsis increased by 7-fold, whereas rice and corn registered a 5.5- and 4 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 2011, 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 June 2011, there were 144 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.

MiniSOG lights the way

By: Irene Lavagi, MASC Coordinator

Electron microscopy (EM) once revolutionised cell biology by exposing subcellular anatomy at a previously unseen level, well below that of the light microscope. Over the past 20 years light microscopy has been rejuvenated with the advent of spontaneously fluorescent proteins, which allow the tagging of proteins of interest. Until last year EM had lacked similar tags, however the small fluorescent flavoprotein called "miniSOG" engineered from Arabidopsis phototropin 2 effectively bypasses this problem (Shu *et al.*, 2011).

The LOV (light, oxygen and voltage) domain of phototropin binds flavin mononucleotide (FMN) and in so doing the excited energy state of flavin mononucleotide is consumed by phototropin leading to the formation of covalent bond with cysteine. To channel this energy into the generation of singlet oxygen (${}^1\text{O}_2$), saturation mutagenesis on the crucial cysteine residue (426) in LOV (light-oxygen-voltage) domain 2 was performed. Mutants that were identified, were fused to infrared fluorescent protein, IFP1.4, which is readily bleached by ${}^1\text{O}_2$ and screened for optimal ${}^1\text{O}_2$ production. Selected mutants then underwent further saturation mutagenesis of the residues around the chromophore binding site, in order to increase brightness. This combined with a further round of DNA shuffling and random mutagenesis generated the new protein, miniSOG. When miniSOG is illuminated blue light singlet oxygen is generated, which locally catalyzes the polymerization of diaminobenzidine into an osmophilic reaction product that is stainable by osmium and consequently observable by EM.

The authors clearly demonstrated that miniSOG fusion proteins correctly localize a plethora of well-documented proteins in tissue culture cells. However the more significant discovery, is that miniSOG functions in the tissues of multicellular organisms including *C. elegans* and intact brain of mice. For example in *C. elegans* the fusion of miniSOG to the cytochrome c targeting sequence demonstrated a correlation of fluorescence and labelling by EM with both techniques labelling the mitochondria.

Without question MiniSOG allows both high quality ultrastructural preservation and 3-D protein localization by electron tomography as well serial section block face scanning EM. MiniSOG is a small versatile label that allows the visualisation of proteins by both light microscopy and EM. Its capabilities have been proven in EM with landmarks such as the localisation of synaptic cell adhesion molecules in neuronal cells and mouse brain, which had been controversial. Will miniSOG (which started life as a plant blue light receptor) do for EM what GFP did for fluorescence microscopy?

Xiaokun Shu, Varda Lev-Ram, Thomas J. Deerinck, Yingchuan Qi, Ericka B. Ramko, Michael W. Davidson, Yishi Jin, Mark H. Ellisman, Roger Y. Tsien (2011) A Genetically Encoded Tag for Correlated Light and Electron Microscopy of Intact Cells, Tissues, and Organisms. *PLoS Biology* (9): e1001041

Towards the making of C₄ plants

By: Irene Lavagi, MASC Coordinator

The understanding of C₄ photosynthesis is of major importance not least because many of the world's most productive plants use C₄ photosynthesis. This coupled with the fact that C₄ plants are more water and nitrogen efficient inevitably raises the possibility that their benefits could be integrated into C₃ crops to increase yield. To make this translation possible a deeper understanding of the genetics of the C₄ pathway is necessary. The C₄ pathway allows CO₂ to be concentrated around RuBisCO. RuBisCO does not completely differentiate between CO₂ and O₂ and therefore an increased supply of CO₂ to RuBisCO causes a reduction in oxygenation and limits the inefficient reactions of photorespiration. C₄ plants typically possess complex modifications to photosynthesis with a key feature being the compartmentalisation of reactions between the mesophyll and bundle sheath cells.

The recent article from the group of Julian Hibberd (Kajala et al., 2012) provides evidence for the localisation of multiple genes important in C₄ photosynthesis to specific metabolic compartments through their 5' or 3' UTRs.

To put this into context with regards to some key C₄ photosynthesis proteins carbonic anhydrase 4 (CA4), pyruvate orthophosphate dikinase (PPDK) accumulate in mesophyll cells whereas phosphoribulokinase (PRK) and RuBisCO are located in the bundle sheath. To investigate this compartmentalisation of proteins researchers studied C₄ gene regulation in *Cleome gynandra*, which is the most closely related C₄ plant to *Arabidopsis*, which is a C₃ plant. Initial evidence indicating that *CgPPDK* (PPDK from *C. gynandra*) is likely to be important for photosynthesis was gained through GUS promoter fusions, which showed a 20 fold increase in accumulation of GUS driven by the *CgPPDK* promoter versus the *Arabidopsis* PPDK promoter. In addition a translational fusion between the coding sequence of *CgPPDK* and GFP showed localisation to the chloroplasts in *Arabidopsis*. Both of these lines of evidence are supportive of a role of *CgPPDK* in the C₄ pathway of *C. gynandra*. A series of truncations of *CgPPDK* clearly demonstrated the coding region was not necessary for accumulation in mesophyll cells. Instead the 5' UTR or 3' UTR alone were sufficient. The presence of both UTRs slightly increased the proportion of GUS in mesophyll cells. There are regions of sequence conservation in the UTRs of *A. thaliana* and *C. gynandra*. This conservation is sufficient to enable *A. thaliana* PPDK to accumulate in the mesophyll cells of *C. gynandra*. This led to the conclusion that the C₃ *A. thaliana* gene has mesophyll targeting cis-elements that retain specificity in a related C₄ leaf. Similarly it was found that the UTRs from C₄ genes from both *C. gynandra* and *A. thaliana* are sufficient for its accumulation in mesophyll cells. The ability of the UTRs from PPDK and CA4 of the C₃ *A. thaliana* to direct accumulation in mesophyll cells of C₄, *C. gynandra*, demonstrates that alteration to cis-elements is not necessary to confer mesophyll specific functions in the C₄ pathway. These findings suggest that functional latency in the UTRs of genes from C₃ species has been adopted by the C₄ pathway. This recruitment of existing cis-elements in C₃ genes may well have fa-

cilitated the evolution of C₄ photosynthesis.

This study highlights the importance of trans-factors in the generation of a functional C₄ leaf, in turn this provides details on the evolution and molecular background on C₄ photosynthesis.

Kaisa Kajala, Naomi J. Brown, Ben P. Williams, Philippa Borrill, Lucy E. Taylor, Julian M. Hibberd (2012) Multiple *Arabidopsis* genes primed for recruitment into C4 photosynthesis. *Plant J.* (69): 47-56.

The making of pectin; a shared effort

By: Irene Lavagi, MASC Coordinator

Regarded for a long time as a static structure, the cell wall and the polysaccharides that compose it have received an exponentially increasing interest in recent years. The cell wall has revealed itself to be a highly plastic structure responsive to a variety of inputs. To provide structural support, sustain growth and expand as a cell's size increases, the cell wall modulates signals that allow it to adapt accordingly. Changes in the methylation status of the pectin polysaccharide for example, allow cells to change shape.

The interest in understanding how cell wall polysaccharides are made and modified is not limited to pure basic research curiosity. The predicted future increase in the world population coupled with the increasing need for affordable and sustainable sources of fuel have led to increased investments in plant cell wall research. Pectins are a major component of the cell wall and are structurally very complex, requiring the action of almost 70 transferases to be synthesized. In addition to the structural and signaling roles that they play in plants, the stabilizing and gelling properties of pectin are of great interest to the food industry. Pectin is also known to have health benefits as it can lower cholesterol, serum glucose levels, inhibit cancer growth and metastasis and has prebiotic functions in the gut. The societal and economic interests in elucidating the making of this polysaccharide are therefore enormous. Understanding how pectin is made at the molecular level will provide the knowledge required for optimizing its production. A recent *PNAS* publication has uncovered a key step of pectin synthesis in the Golgi apparatus (Atmodjo et al., 2011).

With the exception of cellulose that is synthesized on site, the other cell wall polysaccharides including pectin are synthesized in the Golgi apparatus and then transported to the plasma membrane. The most abundant pectic polysaccharide is homogalacturonan (HG), accounting for 55-70% of pectin. HG is a linear polymer of alpha-1,4-linked galactopyranosyluronic acid (GalA). The enzyme galacturonosyltransferase (GalAT) catalyzes the transfer of GalA from uridine-diphosphate-GalA (UDP-GalA) onto HG acceptors to synthesize HG.

The glycosyltransferase HG:GalacturonosylTransferase 1 (GAUT1), a GalAT, localizes to the Golgi, has HG:GalAT activity and is related to another member in the GAUT family, GAUT7. Despite sharing 36% amino acid sequence identity with GAUT1, GAUT7 did not display HG:GalAT activity in mammalian tissue cultured cells (Human Embryonic Kidney 293 cells, HEK293 cells) suggesting that GAUT7 may function in a complex with GAUT1. A recent publication demonstrated that GAUT1 and GAUT7 form a complex where GAUT1 is retained in the Golgi complex via its interaction with GAUT7 (Atmodjo et al., 2011). In *Arabidopsis*, coimmunoprecipitation experiments followed by anti-GAUT1 or anti-GAUT7 immunoblotting showed that GAUT1 and GAUT7 form a complex. The findings were corroborated by a split-YFP expression experiment in

Nicotiana benthamiana where the N-terminal or C-terminal of YFP were fused to GAUT1 and GAUT7 and only the coexpression of GAUT1 and GAUT7 complemented YFP fluorescence. Microarray expression data and promoter::GUS fusions of GAUT1 and GAUT7 indicated expression patterns that are consistent with their function in a protein complex involved in cell wall synthesis. The immunoprecipitated GAUT1:GAUT7 complex was also shown to have an HG:GalAT activity as it selectively transferred HG substrates. Proteomic studies by liquid chromatography-tandem mass spectrometry revealed that 12 additional proteins may transiently associate with the GAUT1:GAUT7 core HG:GalAT complex. The size difference between the predicted (77.4-kDa) and gel-resolved (60 kDa) Arabidopsis GAUT1 led the authors to postulate that GAUT1 undergoes posttranslational proteolytic processing *in planta*. Detection of GAUT1 by antibodies raised against three different portions of its amino acid sequence revealed that the N-terminus of GAUT1 is proteolytically cleaved *in vivo* in Arabidopsis, whilst its precursor could be detected in HEK293 cells. This cleavage however deprives GAUT1 of its transmembrane domain posing the question of how tethering of GAUT1 in the Golgi is achieved. A series of expression experiments with fluorescent fusions of GAUT1 and GAUT7 in tobacco leaves showed that GAUT1 accumulates in the Golgi in the presence of GAUT7, whereas the individual expression of GAUT1 leads to its secretion.

This study illustrates that GAUT1:GAUT7 complex is the catalytic core of a HG:GalAT complex and provides an example of how catalytic domains of plant cell wall glycosyltransferases can assemble into protein complexes to enable the synthesis of pectin. The findings contribute to our understanding of pectin synthesis in plants at the molecular level and could open up new ways of converting plants to biofuels.

Atmodjo MA, Sakuragi Y, Zhu X, Burrell AJ, Mohanty SS, Atwood JA 3rd, Orlando R, Scheller HV, Mohnen D. (2011) Galacturonosyltransferase (GAUT)1 and GAUT7 are the core of a plant cell wall pectin biosynthetic homogalacturonan:galacturonosyltransferase complex. PNAS (108) :20225-30.

Making your plants at EASE

By: Irene Lavagi, MASC Coordinator

A tool to accurately alter the genome of plants is currently lacking. The development of an efficient method to achieve this is therefore a key goal for plant molecular biology and crop breeding. The work by the group of Avraham Levy describes a technique for targeted mutagenesis or gene targeting that is tailored to the floral dip transformation of Arabidopsis through the use of GT-/TGM promoting proteins that are expressed in the egg cell (Even-Faitelson *et al.*, 2011). This in turn exploits the egg apparatus specific enhancer (EASE), which is a 77 bp enhancer sequence that controls specific gene expression in the egg apparatus of Arabidopsis.

A series of experiments using fluorescent protein reporters elegantly demonstrated that proteins expressed downstream of EASE become localized to the egg cell. A zinc finger nuclease (ZFN) expressed under EASE was found to induce targeted mutations that corresponded to genetically independent events. Furthermore it was found that the expression of the DNA repair and recombination 54 protein under EASE led to a 10-fold increase in the efficiency of gene targeting compared to wild type. The authors clearly make the case for EASE controlled gene expression being a key technique

for the engineering of the Arabidopsis genome through temporally and spatially controlled protein expression. EASE driven expression can be applied to a broad range of technologies such as ZFNs and TALENs and most importantly can be extended to assist in the development of similar approaches for crop breeding.

Even-Faitelson L, Samach A, Melamed-Bessudo C, Avivi-Ragolsky N, Levy AA (2011) Localized egg-cell expression of effector proteins for targeted modification of the *Arabidopsis* genome. *Plant J.* 2011 (68): 929-37.

Poplar growth improves with *Arabidopsis* kinase

By: Irene Lavagi, MASC Coordinator

Environmental stress is one of the most severe causes affecting plant growth and crop yields. Adaptations to environmental stress are generally believed to be the result of complex and polygenic traits. This makes it very difficult to enhance stress tolerance especially in economically and agriculturally significant crops and trees.

Nucleoside diphosphate kinases (NDPKs) are enzymes involved in a variety of physiological responses including oxidative stress signaling. They catalyze the exchange of phosphate groups between different nucleoside diphosphates and function to maintain an equilibrium between the concentrations of different nucleoside triphosphates. A recent publication furthered the understanding of the importance *Arabidopsis thaliana* NDPK2 in stress tolerance (Kim *et al.*, 2011). The group developed their previous findings in potato and sweetpotato plants with the demonstration that the level of *AtNDPK2* expression and activity in transgenic poplar is positively correlated with tolerance to methyl viologen mediated oxidative stress. *AtNDPK2* was expressed under the control of the oxidative stress-inducible SWPA2, with the expression of *AtNDPK2* leading to the activation of antioxidant enzymes in poplar. SWPA2 encodes an anionic peroxidase (POD). Researchers also observed that the expression of *AtNDPK2* in poplar leads to higher growth rate and importantly higher transcript levels of auxin response genes IAA2 and IAA5, which inevitably lends itself to the theory that enhanced *AtNDPK2* expression triggers an auxin-mediated gene induction response leading to improved plant growth.

It is known that *AtNDPK2* is a component of the H₂O₂ activated MAPK signaling pathway. It was previously observed that the overexpression of *NDPK2* in *Arabidopsis* leads to the increase expression of genes including those involved in signal transduction. In this more recent study the expression of antioxidant genes including POD, APX (ascorbate peroxidase) and CAT (catalase) were also found to be induced in poplar expressing *AtNDPK2*. Overexpression of *NDPK2* in potato and sweetpea also led to increased levels of H₂O₂ scavenging antioxidant enzymes. Taken together this data would indicate that *AtNDPK2* expression plays an important role in tolerance to environmental stress in monocot, dicots and woody plants.

The findings in the paper are particularly exciting as the indication is that the over expression of *NDPK2* in woody plants can be an efficient strategy for the production of biomass for the forestry, textile, paper industries and also the biomass-dependent generation of biofuels in natural environments.

Yun-Hee Kim, Myoung Duck Kim, Young Im Choi, Sung-Chul Park, Dae-Jin Yun, Eun Woon Noh, Haeng-Soon Lee, Sang-Soo Kwak (2011) Transgenic poplar expressing *Arabidopsis* *NDPK2* enhances

growth as well as oxidative stress tolerance. *Plant Biotech Journal* Volume (9): 334–347

Vitamin deficiencies in humans; Can Arabidopsis help?

By: Irene Lavagi, MASC Coordinator

A recent review in *The Plant Cell* draws our attention to the current understanding of plant vitamin metabolism and argues for the role that plant science can play in addressing the issue of malnutrition in the developing countries (Fitzpatrick et al., 2011). Although our current knowledge comes from efforts across the Plant Science community, for the purpose of this report the focus will be on Arabidopsis.

Vitamins are organic compounds that are essential in human nutrition and 13 compounds fall into this category. They are broadly divided into fat-soluble (A, D, E, K) and water-soluble (B1, B2, B3, B5, B6, B8, B9, B12 and C). Vitamin deficiencies are associated with a variety of diseases and conditions leading to poor health. Whilst in developed countries reasonable vitamin requirements are met through balanced and varied diets, in developing countries five billion people depend on a single staple crop for survival. The small amounts of specific vitamins in major food staple crops combined with the reliance on often a single species as food source has a detrimental effect on human health. Understanding the vitamin metabolic pathways at the molecular level in a multidisciplinary approach is crucial to enable the eradication of vitamin deficiencies.

Notable examples of Arabidopsis research on vitamin metabolic pathways include studies on Vitamin B3 (Niacin), Vitamin B6 (Pyridoxine), Vitamin B8 (Biotin), Vitamin B9 (Folate), Vitamin C (Ascorbate), Vitamin E (Tocopherol) and Vitamin K (Phylloquinone).

In humans, severe niacin deficiencies cause Pellagra, a disease which symptoms include diarrhea, skin lesions and eventually dementia. Recently niacin deficiency has been linked to mental disorders including apathy and depression. Niacin deficiencies are common in maize-based diets. Current research appears to suggest that plants are very sensitive to changes in the niacin biosynthetic pathway. In Arabidopsis, overexpression of the NAD⁺ synthase enzyme led to increased levels of niacin but also caused early senescence and negatively affected seed development (Shinnosuke et al., 2010). Loss of function of another niacin biosynthetic enzyme, quinolinate synthase, caused reduced NAD⁺ levels and early aging (Schippers et al., 2008). Further research will be needed to efficiently increase niacin levels in plants

Pyridoxine is involved in numerous metabolic and cellular processes. Deficiencies of pyridoxine are linked to various health problems including cardiovascular disease, blood pressure problems and pellagra. Studies in Arabidopsis have demonstrated that over-expression of the pyridoxine biosynthetic enzymes leads to successful increases of pyridoxine levels and larger organ size suggesting that this could be exploited to increase yield rates as well (Chen and Xiong, 2009; Leuendorf et al., 2010; Raschke et al., 2011).

Biotin is a cofactor for some of the enzymes involved in carbohydrate and fatty acid metabolism. The plant biotin synthetic pathway is believed to be very similar to biotin synthesis in bacteria and overexpression of biotin synthetic enzymes appears to complement *bio1* loss of function Arabidopsis mutant plants (Patton et al., 1996). A U.S. patent states that it is possible to increase biotin levels in *bio1* Arabidopsis mutants by expressing *E.coli* or Arabidopsis genes of the biotin synthetic pathway.

Folate is required for the biosynthesis of DNA bases and Vitamin B5. Folate deficiencies may cause serious diseases and birth defects including spina bifida and anacephaly. Expression of Arabidopsis folate biosynthesis enzymes in rice or wheat has been recently reported to lead to up to 100 fold increased folate levels (Storozhenko et al., 2007; Gillies et al., 2008).

Ascorbate deficiencies are known to cause scurvy. Healthy consumption of ascorbate appears to be important for the prevention of a variety of diseases including cardiovascular diseases and atherosclerosis. The expression of ascorbate biosynthetic enzymes in Arabidopsis resulted in increased Vitamin C content. Expression in other crop species including lettuce, potato and maize also resulted in increased Vitamin C levels with a 7-fold increase in lettuce expressing a rat Vitamin C biosynthetic enzyme. Expression of a kiwi Vitamin C biosynthetic enzyme was also reported to increase ascorbate levels by 4 fold (Bulley et al., 2009).

Tocopherol, Vitamin E, is synthesized by photosynthetic organisms. Tocopherol is involved in a variety of cellular processes including the body's defense against oxidative damage, signaling cascades and gene regulation. Humans cannot synthesize Vitamin E and must therefore acquire sufficient levels through their diet. Severe Vitamin E deficiencies can result in haemolytic anemia, neurological and ophthalmological disorders. Research in Arabidopsis played a major role in the elucidation of the tocopherol biosynthetic pathway starting with the cloning of first biosynthetic enzyme from this model plant in 1998. In the following years Arabidopsis was used once again to manipulate the expression of genes of the tocopherol biosynthetic pathway in leaves and seeds (DellaPenna and Pogson, 2006). The knowledge accrued in Arabidopsis has been readily transferred to crops by manipulating the orthologs identified by genome sequences searches leading to the successful increased Vitamin E accumulation in numerous crop species including maize and *Brassica napus* (canola) (Shukla and Mattoo, 2009). Comparative studies between Arabidopsis, sunflower, maize and tomato have also led to the identification of QTL explaining the differences in composition and content in Vitamin E in the different plant species (Gilliland et al., 2006; Hass et al., 2006; Chander et al., 2008; Schauer et al., 2006; Almeida et al., 2011).

Studies in Arabidopsis have and continue to underpin our advancements towards the understanding of the vitamin biosynthetic pathways in plants. Understanding how these pathways work will be key to alleviate malnutrition particularly in populations that rely on a single staple crop.

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Head blight disease; towards a chemical genomics approach

By: Irene Lavagi, MASC Coordinator

The fungus *Fusarium graminearum* causes head blight disease in cereal crops including wheat, barley, maize, oat and rye. Between 1990 and 2002, U.S. wheat and barley farmers lost over \$3 billion due to *Fusarium* head blight epidemics. Protection against pathogen attack is therefore a key goal for increasing crop yield. Despite numerous studies on the pathology of *Fusarium graminearum* infection in crops, the genetic complexity of polyploid cereal crops is often a barrier to the development of high throughput screens aimed at identifying strategies for crop protection. To try to overcome this problem researchers in Canada have developed a simple *Arabidopsis thaliana*-*F. graminearum* infection assay that has led to the identification of defense-activating small molecules both in *Arabidopsis* and wheat (Schreiber et al., 2011).

Typically *Fusarium* head blight disease develops in spring, when cereal crop plants flower. Infection occurs when flowers are fully open and is followed by invasion of floral tissues and neighboring spikelets, which in turn leads to necrosis of the infected tissues. In addition to lower yields, necrosis by head blight disease is accompanied by the accumulation of mycotoxins, including deoxynivalenol (DON), that inhibit protein translation and are harmful at high concentrations. To mimic this infection system in a way that would allow high throughput screening Schreiber and colleagues established liquid based assay in which *Arabidopsis* seedlings grown in 96-well plates were infected with *F. graminearum* and exhibited highly reproducible disease symptoms. Researchers were able to modulate the interaction between *Arabidopsis* and *F. graminearum* via the application of small molecules for example the well-established antifungal hygromycin was shown to protect *Arabidopsis* seedlings from *Fusarium* infection in this assay. Having established the efficiency of a liquid-based assay to assess *F. graminearum* infection of *Arabidopsis* seedlings, the group sought to screen novel compounds capable of preventing infection. Sulfanilamide-based compounds such as Sulfamethoxazole (Smex) and sulfanilamide (Snil) were tested. Pretreatment with Smex proved to protect *Arabidopsis* seedlings most efficiently. In addition 80 chemicals from a natural product collection were screened leading to the identification of the indole alkaloid gramine having the strongest protective effect. Most significantly, these results were confirmed in wheat. Co-application of Smex and *F. graminearum* reduced the infection from 97% to 43% of spikelets. DON accumulation was also reduced to 20% compared to the control. Snil and gramine treatment was less effective in protecting wheat spikelets from *F. graminearum* infection but significantly reduced DON accumulation.

Together these data provide evidence for *Arabidopsis* as a very powerful surrogate for studies on fungal pathology in more genetically complex plant hosts. Furthermore, it was demonstrated that information obtained from *Arabidopsis* studies can be readily translated to economically important crop species such as wheat.

Schreiber KJ, Nasmyth CG, Allard G, Singh J, Subramaniam R, Desveaux D. (2011). Found in translation: high-throughput chemical screening in *Arabidopsis thaliana* identifies small molecules that reduce *Fusarium* head blight disease in wheat. *Mol Plant Microbe Interact.* 24: 640–8.

Reports of the MASC Subcommittees

Bioinformatics

Prepared by Nicholas Provart (Chair, nicholas.provart@utoronto.ca) with input from MASC Bioinformatics Subcommittee members Tetsuro Toyoda (toyoda@base.riken.jp), and Christopher Town (cd-town@jcvi.org), and from Blake Meyers (meyers@dbi.udel.edu), Joanna Friesner (jfriesner@ucdavis.edu), and Dan Stanzione (dan@tacc.utexas.edu).

Several new *Arabidopsis* bioinformatics tools and data sets were published or released in 2011. The eagerly awaited comprehensive all-by-all interactome from the Braun and Vidal labs at Harvard was published by the *Arabidopsis* Interactome Mapping Consortium (2011) and provides a valuable data set for plant biology researchers. Data are accessible through the Interactome Mapping Consortium's own portal as well as from various other repositories, such as ANAP, an new integrated knowledge base for protein interaction network analysis (Wang *et al.*, 2012). A couple of tools for using next-generation sequence data for positional mapping and alternative transcript discovery were released, and these promise to accelerate the rate of gene discovery by eliminating the tedious fine mapping step required for positional cloning (NGM - Austin *et al.*, 2011), and to facilitate the identification of alternate transcripts (ARTADE2 – Kawaguchi *et al.*, 2012). The sequencing of *Arabidopsis* accessions as part of the 1001 Genomes project continues, and this past year saw the release of SNP data for 80 accessions (Cao *et al.*, 2011) and assembled genomes for 18 accessions by Gan *et al.*, (2011), as well as published (Huang *et al.*, 2010) and unpublished tools for exploring these and other 1001 Genomes data, such as the very useful Polymorph (<http://polymorph.weigelworld.org>; Fitz J, Ossowski S, Warthmann N, Clark RM, Schneeberger K and Weigel D, personal communication) and Ecker Laboratory (<http://signal.salk.edu/atg1001/>) sites. The iPlant Collaborative also released its easy-to-use web-based Discovery Environment for processing and analyzing large data sets from *Arabidopsis* and other plants, such as those produced by next-generation sequencing. See www.iplantcollaborative.org to try it out!

The announcement in 2009 of cuts to TAIR's funding resulted in the formation of an International *Arabidopsis* Informatics Consortium (2010). The first major IAIC *Arabidopsis* community meeting was held in a workshop at the ICAR in Madison (Wisconsin, U.S.A.) this past year. The IAIC will be an integral part of MASC's next 10 year vision for *Arabidopsis*, wherein this humble but very well researched plant will become a platform for systems biology modeling from "bench to bountiful harvests". Further progress towards developing a new "Arabidopsis Information Portal" (AIP) was made at a Design Workshop in Atlanta (Georgia, U.S.A.) in December 2011, attended by computer scientists, plant biologists, funding agencies, and other organismal database experts. Animated discussions and brainstorming helped to start to create the vision for what the AIP should be for users from different communities. A white-paper based on dis-

cussions from the Design Workshop is in preparation and should be available by the summer of 2012. See more information on IAIC in the Community Projects and Resources section of this report.

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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.

Recent activities

- To achieve these goals, we aimed to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. This subcommittee website was launched in 2011 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.
- In addition, a MASCM (Multinational Arabidopsis Steering Committee Metabolomics) gator portal is under development. The webinterface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases in a way comparable to that offered by the MASCP (MASC Proteomics) gator portal (<http://gator.masc-proteomics.org/>).

Recent and upcoming meetings

- The Metabolomics 2011 meeting in Cairns, Australia, June 27 – 30, 2011 <http://www.metabolomics2011.org/> was organized by Ute Roessner. Metabolomics studies in Arabidopsis was one of the major topics of this meeting.
- The Metabolomics 2012 meeting will take place in Washington, DC, US, from June 25 - 28, 2012 <http://www.metabolomics2012.org/>

Metabolomics funding news

- Based on the joint NSF (US) and JST (Japan) workshop for 'Identifying Potential Collaborative Research Opportunities in Metabolomics' held in May 6-7, 2010, at the University of California, Davis, a joint research program between NSF and JST has been launched in the winter of 2011 http://www.nsf.gov/news/news_summ.jsp?org=NSF&cntn_id=122045&preview=false, http://www.jst.go.jp/pr/announce/20111107/index_e.html.
- Four joint U.S. and Japanese research teams have been awarded funding totaling about \$12 million (about Yen 960 million) to develop new environmentally-friendly techniques to increase the production of renewable biofuel and reduce pesticide use based on cutting-edge metabolomics research.
- Two project teams (Lloyd Sumner/Kazuki Saito, Oliver

Fiehn/Masanori Arita), which focus on metabolite and gene annotation of Arabidopsis and bioinformatics have been granted by this joint program. Discussions about setting up similar US-German programs have been initiated and look promising.

Updates

Arabidopsis metabolome expression databases 'AtMetExpress development' (1) and 'AtMetExpress 20 ecotypes' (2) have been established 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 publicized (3,4). Mass spectral databases, MassBank <http://www.massbank.jp/index.html?lang=en> (5) and ReSpect for Phytochemicals <http://spectra.psc.riken.jp/> have been publicly available. The Madison-Qingdao metabolomics consortium database (<http://mmcd.nmrfaam.wisc.edu/>) has emphasis on Arabidopsis and contains both NMR and MS data of metabolites

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2. Matsuda F, Nakabayashi R, Sawada Y, Suzuki M, Hirai MY, Kanaya S and Saito K (2011) Mass spectra-based framework for automated structural elucidation of metabolome data to explore phytochemical diversity. *Front. Plant Sci.* 2:40. doi: 10.3389/fpls.2011.00040.
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4. Quanbeck SM, Brachova L, Campbell AA, Guan X, Perera A, He K, Rhee SY, Bais P, Dickerson JA, Dixon P, Wohlgemuth G, Fiehn O, Barkan L, Lange I, Lange BM, Lee I, Cortes D, Salazar C, Shuman J, Shulaev V, Huhman DV, Sumner LW, Roth MR, Welti R, Ilarslan H, Wurtele ES and Nikolau BJ (2012) Metabolomics as a hypothesis-generating functional genomics tool for the annotation of *Arabidopsis thaliana* genes of "unknown function". *Front. Plant Sci.* 3:15. doi: 10.3389/fpls.2012.00015.
5. Horai H., et al. (2010) MassBank: a public repository for sharing mass spectral data for life sciences. *J Mass Spectrom.* 45:703-14.

ORFeomics

Prepared by Joe Ecker (Co-chair, ecker@salk.edu) and Motoaki Seki (Chair, mseki.psc.riken.jp)

The ORFeomics subcommittee keeps tracking progress made towards the production of full length cDNAs and open reading frame clones for all annotated Arabidopsis protein coding genes (Table1). New clones include additional 606 ORF associomics clones (Frommer *et al.*), 1,600 ORF clones from AIST/RIKEN, 635 Y1H ORFs from Gaudiner and Sihoban, and 12,069 HALO tagged ORF clones from SALK/Promega.

Phenomics

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

Subcommittee goals

The Sub-Committee plans to develop concrete steps to each of the 4 priorities:

- Strong interaction with scientists and workgroups providing genetic resources as well as new technological opportunities.
- Integrate plant phenotyping into studies on natural variation of Arabidopsis and link them to environmental cues
- Integrate the phenotyping activities into the overall pipeline of knowledge generation and data bases
- Contribute to the IAIC developments

Progress on previously stated goals and recommendations of the subcommittee

Examples for the interaction and development with genomic resources;

- For Genome to Phenome, information of location of T-DNA in the genome is available for RIKEN Arabidopsis Activation Tagging lines (<http://amber/gsc.riken.jp/act/top.php>) (Minami Matsui collaboration with NEC Soft co Ltd.) and RIKEN Ac/Ds transposon lines (<http://rarge.gsc.riken.jp/phenome/>) (<http://rapid.psc.database.riken.jp/>) (Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki). Around 10,000 Full-length cDNA information integrated in Arabidopsis FOX (Full-length cDNA over-eXpressing) lines are available (Contact Minami Matsui).
- A Database SciNetS (<https://database.riken.jp>) has been developed to provide an integrated access point for RIKEN data Tetsuro Toyoda). By this database phenotype information of Activation tagging lines, Ac/Ds transposon lines and FOX lines are available.
- The Chloroplast Function Database (<http://rarge.psc.riken.jp/chloroplast>) provides the phenotype and segregation data of Arabidopsis Ds/Spm and T-DNA-tagged mutants of nuclear genes encoding chloroplast proteins information of more than 200 morphological mutants and the homozygous lines generated in this project are also available each of the Arabidopsis stock centers (Fumiyoshi Myouga and Kazuo Shinozaki).
- The Salk Institute: has re-sequenced the entire SALK and SAIL collection using a next-generation sequencing method for index T-DNA inserts which have been developed. The director of the project (Ronnan OMalley) reports that they have identified ~130,000 new T-DNA insertions providing coverage for many genes which previously had only one or no insertion allele. With

this expansion of the T-DNA collection an additional ~4500 homozygous mutants have been genotyped bringing them much closer to the goal of a collection of two homozygous alleles for all Arabidopsis genes. These new homozygous lines and the entire set of new insertion sites will be made available early 2012.

Development of novel technological opportunities for plant phenotyping:

- 2011 has seen the commissioning of a number of image based phenotyping systems for Arabidopsis researchers in Australia. Trayscan, a system co-developed by Photon Systems Instruments in the Czech Republic and the High Resolution Plant Phenomics Centre in Canberra, has been constructed and two units commissioned across the Australian National University and CSIRO in Canberra. These units are part of the national facility and are available on a cost recovery basis to researchers in Australia and internationally. Trayscan consists of an equilibration conveyor holding 16 trays of Arabidopsis plants in individual pots which can be illuminated in a temperature controlled environment at irradiances of up to 500 umolm-2s-1. Trays move from this conveyor into a far infrared thermal imaging station then a pulse modulated chlorophyll fluorescence and colour imaging station. When the plants bolt, they can be imaged in individual pots from the top and side. Throughput is 3000 plants per day in tray mode and the system is currently being used to screen for stomatal response mutants and for osmotic tolerance. CabScan, a growth cabinet based 3-D growth analysis system for Arabidopsis has also been commissioned at the Phenomics Centre, allowing 120 plants per unit to be imaged continuously in 3-D in Conviron PGFlex cabinets and acquiring thermal images simultaneously.
- Growth facilities for Arabidopsis research in Australia have increased by more than 3 fold with major infrastructure investments being made in growth cabinet facilities in Canberra, Adelaide, Melbourne, Brisbane and Perth. Many of these facilities are integrating their growth environments with investments in genomics, transcriptomics, proteomics, metabolomics and Phenomics.
- In Germany (Jülich Plant Phenotyping Center JPPC) the capacity for root system phenotyping have been significantly increased and expanded to more environmental cues. In parallel automated systems for shoot structure in 2D and 3D (including biomass, growth, compactness, leaf numbers, etc.) and function (photosynthetic, thermal and spectral imaging) have been set up and developed to a robust, routine system.

Meetings related to the subcommittee and its goals held in the past year

- In September 2011 the 2nd International Plant Phenotyping Congress was held in Jülich and saw almost 250 participants discussing about technological advances, applications and information technology developments. The congress was organized by Forschungszentrum Jülich (hosted by one of the chairs of the MASC committee as member of the International Plant Phenotyping Network (IPPN)).
- In December 2012 plant phenotyping options were presented by Ulrich Schurr at the Cold Spring Harbour Conference Conference “Plant Genomes – what’s next?” co-organized by one of the members of the subcommittee (Detlef Weigel) with significant resonance from the research community.

Table 1: Arabdopsis ORF and cDNA clone repositories

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP consortium & Salk Institute	Univector pUNI51		Full sequence	14,398	signal.salk.edu/cdnastatus.html http://methyloome.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methyloome.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	http://interactome.dfc.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.psu.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/sheenweb/category_genes.html	ABRC
Steve Clouse	Gateway expression	N-terminal Flag tagged kinases		782	http://www4.ncsu.edu/~scclouse/Clouse2010.htm	ABRC
Frommer et al.	Gateway entry, no stop	Membrane protein genes	5' and 3' seq. (long reads)	2,706	http://associomics.org	ABRC
AIST/RIKEN	Gateway entry	Transcription factor	Full sequence	1,600		BRC
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	pIX-HALO vector			12,069		ABRC
cDNA clones						
RIKEN/SSP/Salk Institute	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	25,000	www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/Arabidopsis	CNRGV

Stock centres distributing Arabidopsis clone repertoires

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

Recent efforts to establish international collaborations in area(s) of interest to subcommittee

- In January 2012 the European Plant Phenotyping Network (EPPN - <http://www2.fz-juelich.de/icg/icg-3/eppn>) was started. This EU project provides transnational access based on calls to phenotyping facilities in a number of different institutions in Europe for European and associated countries. The first calls will be publically announced in March 2012. In addition the project covers intensive networking activities to discuss and develop a plant phenotyping community around the European

and Australian plant phenotyping facilities. EPPN will establish new technology and implement adequate solutions into phenotyping platforms and set standards for phenotyping experiments as well as information technology. Existing phenotyping centres will be adapted to the needs of the community and EPPN will foster the generation of new phenotyping activities and thus meet the future challenges. The cornerstone of the project focuses on the provision of Transnational Access of a diverse user community to the EPPN plant phenotyping facilities across Europe. Additionally, to enhance interaction with

potential users and to promote discussions about the opportunities of plant phenotyping a number of events such as conferences, summer schools and workshops will be organized.

New recommendations from the subcommittee

- Australia is proud to host the 24th ICAR meeting in Sydney in 2013 in which we will have a strong Phenomics presence, including a session sponsored by the Australian Plant Phenomics Facility. For more information see <http://www.sallyjayconferences.com.au/icar2013/>
- EPPN will become active in providing access to state-of-the-art plant phenotyping facilities to the science community.

Goals of the Phenomics Subcommittee towards the 2020 From Bench to Bountiful Harvests Roadmap

Plant Phenotyping is a central part of understanding plant development and plant environment interaction. Thus the Sub-Committee has the following specific goals:

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

- Continue to coordinate phenotyping of Arabidopsis genome wide knockouts to allow genome-phenome linkages to occur.
- Digital image based growth analysis and functional high throughput non-destructive measurements coordinated to allow growth and development models to be populated with gene specific data.

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

- Continue to coordinate phenotyping of re-sequenced Arabidopsis ecotype collections to allow genome-phenome linkages to occur and growth and development models to be populated with gene-specific data.
- Link environmental phenotypic response and plasticity of Arabidopsis to natural environments and collection sites.

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

- Establish a Minimum Information for Plant Phenomics Experiments (MIPPE) data standard to provide uniform data on growth conditions and experimental metadata to enable modelling and extrapolation of controlled environment information to the field.

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

- Provide open access to the Arabidopsis research community to PODD and other ontology-driven database tools developed within the International Plant Phenotyping Network (IPPN).
- Via agreement on MIPPE and the Plant Phenomics Investigation Ontology (PPIO), promote the widespread adoption of uniform vocabularies and machine-readable formats for describing and computing experimental data and metadata.

E) Deepen International Cooperation and Coordination

- Through development of the International Plant Phenotyping Network (IPPN) the (re-)use of public phenotyping data toward building models and meta-analytical compendia as well as user community access to existing image and data analysis software, and experimental methodologies.

Proteomics

Prepared by Joshua Heazlewood (Co-chair, jlheazlewood@lbl.gov) and Wolfram Weckwerth (Co-chair, wolfram.weckwerth@univie.ac.at) with contributions from subcommittee members.

The past year has seen an update in the subcommittee's objectives as the Arabidopsis 2010 Functional Genomics Program ends and MASC develops a new roadmap to address the important translation of Arabidopsis research into agricultural outcomes. As a consequence MASC has developed a new set of objectives and goals to directly support the five major thrusts of this new program, Arabidopsis 2021: From bench to a bountiful harvest. The specific objectives to support this roadmap can be found at the MASC website (<http://www.masc-proteomics.org/masc/index.php/Goals>). These updated goals for MASC will support the development of an Arabidopsis predictive model through the development of proteomic applications in Arabidopsis e.g. AtSRM Atlas; develop tools to enable the exploitation of Arabidopsis accessions through proteomics e.g. 1001 Proteomes; support translational linkages by connecting the progress in Arabidopsis proteomics research with other plant systems e.g. INPPO; assist in the development of the IAIC through maintenance and expansion of proteomic resources in Arabidopsis e.g. MASC Gator; and develop linkages with other proteomic communities and systems e.g. iMOP.

Recent Activities:

MASC has developed a new set of goals and objectives to specifically support the MASC 2021 roadmap 'from bench to a bountiful harvest'. These objectives are available at <http://www.masc-proteomics.org/>.

- A MASC subcommittee workshop was held at ICAR 2011 (Madison, Wisconsin) in an effort to better engage with the Arabidopsis community and articulate the objectives of MASC and its scientific subcommittees. The activities and objectives of the proteomics subcommittee were highlighted by Katja Bärenfaller. Major points included an overview of proteomic data resources that members of the subcommittee have been developing and how these are being integrated into the MASC Gator.
- MASC showcased Arabidopsis as a model system for proteomics at the Human Proteome Organization (HUPO) initiative on Model Proteomes (iMOP) session during the 2011 HUPO Congress (Geneva, Switzerland). The presentation was made by Joshua Heazlewood and highlighted the development of the MASC Gator to the wider international proteomics community. An iMOP workshop will be held in March 2012 (Kiel, Germany) with several MASC iMOP representatives in attendance.
- As the iMOP representatives of MASC, both Steve Briggs and Klaas van Wijk are speaking in the 'Engineering Proteins in the Plant World' session at the US HUPO congress in March 2012 (San Francisco, USA).
- MASC anticipates a proteomics workshop will be held at the ICAR 2012 (Vienna, Austria) and the subcommittee will also contribute to a MASC workshop/information session at this meeting.
- A proteomics workshop will be organized this year (2012) at the XV International Congress on Molecular Plant-Microbe Interactions (Kyoto, Japan) by Alex Jones and Hirofumi Nakagami. The workshop will provide an overview of proteomics

approaches to understand plant-microbe interactions and discuss methods that can be used to decipher defense-related signaling pathways.

- Members of MASCP have continued to develop and maintain public online proteomic resources. Recent examples include the gel-based proteomic resource GelMap from the group of Hans-Peter Braun. The GelMap resource provides digital versions of 2-DE and BN-PAGE with hyperlinks to identified proteins and MS/MS data. Recently, this resource was integrated into the MASCP Gator along with the P3DB plant phosphorylation database developed by Jay Thelen. The inclusion of these two proteomic repositories brings the total number of resources to 10 through the MASCP Gator.
- A number of MASCP members have been directly involved in the development of a new journal, *Frontiers in Plant Proteomics*, which is a specialty area of *Frontiers in Plant Science*. The journal is part of the Frontiers organization and is a not for profit open access journal with a unique interactive review process. A number of MASCP members are coordinating Research Topics in the proteomics specialty area including Sub-cellular proteomics (Nicolas Taylor and Harvey Millar), Mechanisms regulating immunity in plants (Alex Jones) and Protein phosphorylation in plants (Joshua Heazlewood and Jay Thelen).

There were a number of contributions published in the past year (2011-2012) that significantly advanced proteomics in *Arabidopsis* and these include:

- Klodmann J, Senkler M, Rode C, Braun HP (2011) Defining the protein complex proteome of plant mitochondria. *Plant Physiology* (157): 587-598. *The study demonstrates the power of enabling digital reference gel maps (2DE and BN-PAGE) to mine and analyze proteomes arrayed using these techniques.*
- Li L, Nelson CJ, Solheim C, Whelan J, Millar AH. (2012) Determining degradation and synthesis rates of *Arabidopsis* proteins using the kinetics of progressive ^{15}N labeling of 2D gel-separated protein spots. *Mol Cell Proteomics*. 2012 Jan 3. [Epub ahead of print]. *This study shows the potential for analysis of the kinetics of progressive ^{15}N labeling to determine both the synthesis and degradation rates of protein in plant cells. It shows the more than 50-fold difference in degradation rates of different classes of proteins and provides a pipeline for targeted analysis of specific proteins of interest through analysis of 2D gel separation of labeled proteomes.*
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- O'Brien JA, Daudi A, Finch P, Butt VS, Whitelegge JP, Souda P, Ausubel FM, Bolwell GP. (2012) A Peroxidase-Dependent Apoplastic Oxidative Burst in Cultured *Arabidopsis* Cells Functions in MAMP-Elicited Defence. *Plant Physiol*. 2012 Feb 7. [Epub ahead of print] PMID: 22319074.
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PMID: 22247251.

- Both papers emphasize the central role of peroxidases in the apoplastic oxidative burst elicited by MAMPs as a central component of pattern-triggered immunity. Proteomics demonstrated that knockdown of PRX33/PRX34 led to the depletion of various MAMP-elicited defence-related proteins and increases in enzymes involved in cell wall remodeling.

In the past, MASCP has used this report to highlight the current proteomic coverage in *Arabidopsis* i.e. the number of proteins that have been identified by various proteomic surveys of *Arabidopsis*. Previous years have seen considerable expansion in the number of proteins identified by mass spectrometry. This is due to a number of large scale proteogenomic analyses undertaken by research teams involving MASCP members (Steve Briggs and Katja Bärenfaller). Currently, the number of identified or validated proteins stands at 21,916 and represents approximately 62% of the potential *Arabidopsis* proteome (TAIR10). This represents a minor increase in numbers over this time last year. The identification of a protein by mass spectrometry is influenced by a variety of factors including protein properties. The grand average of hydrophilicity index (GRAVY) is a value that can be attributed to a protein based on its amino acid composition. A positive score indicates a hydrophobic protein (such as a membrane protein) while a negative score would be indicative of a soluble protein. We analyzed the distribution of GRAVY indexes for all potential proteins from TAIR10 and compared this with the collection of 21,916 proteins that have been identified through mass spectrometry (Figure 1). As can be seen from their distributions, current proteomic techniques are capable of identifying both hydrophobic and hydrophilic proteins but proteins in the middle of the distribution are over-represented. Interestingly, both highly hydrophobic (positive score) and hydrophilic (negative score) are under-represented. This reduction in the identification of hydrophobic proteins could indicate technical limitations in sample solubilization resulting in precipitation and/or reduced access by proteases, thus limiting resultant peptides and identifications. While, when attempting to identify very hydrophilic proteins, the resultant hydrophilic peptides may not be efficiently captured by reverse phase chromatography techniques prior to analysis by mass spectrometry. Thus, improved or targeted technical methods are essential when attempting to fully characterize a complex proteome containing proteins with extreme properties, such as in the case of membrane proteins.

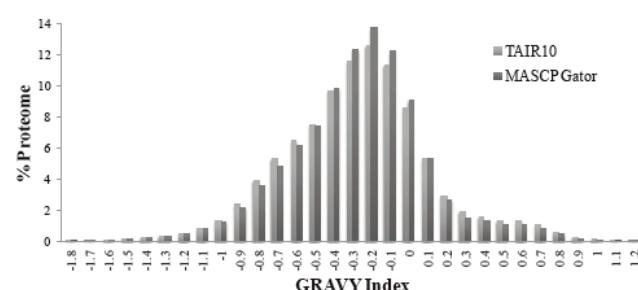


Figure 1. A comparison in the distribution of the GRAVY index between all proteins potentially coded by *Arabidopsis* (TAIR10) and those currently identified by proteomic surveys (collected in the MASCP Gator). Note: positive GRAVY (hydrophobic), negative GRAVY (hydrophilic).

Goals of the Proteomics Subcommittee towards the 2020 From Bench to Bountiful Harvests Roadmap

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

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

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

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

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

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

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

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

E) Deepen International Cooperation and Coordination

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

Natural Variation and Comparative Genomics

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

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

Natural Variation

Accomplishments:

Several major breakthroughs were made in 2011 in the field of Natural Variation. Primarily, this includes generating the genome sequences of the first ~100 genomes of the Arabidopsis 1001 genome project (e.g., Cao *et al.*, 2011; Gan *et al.*, 2011; Schneeberger *et al.*, 2011). In addition to genomes, natural variation was explored in the epigenomic realm (e.g., Becker *et al.*, 2011; Schmitz *et al.*, 2011).

Needs:

Creating improved and “user friendly” resources are a major area where the Natural Variation community should invest future efforts. It is important to develop web-based resources that make sequence data (as well as the raw data) easily available for researchers to re-utilize. For example, much of these sequencing data have been generated under the expectation of their usefulness for genome-wide association (GWA). Many labs would therefore greatly benefit from developing web-based interfaces that allow easy access and friendly GWA analysis of these data. There have been some encouraging and positive developments in this area including Huang *et al.*, 2011, and the various ongoing efforts to integrate the Arabidopsis 1001 genomes (e.g., EU transPLANT project (www.transplantdb.eu/)). However, fostering open-source public availability of web resources and data remains paramount if this data and others are to be made available in a useful form to the larger community.

Another area of current need is that of the collection of site metadata and sample provenance, which has proved valuable (Hancock, 2011; Fournier-Level 2011) and problematic (Anastasio *et al.* 2010). It is essential that work in this area continues to research solutions to current barriers.

Ongoing Justification:

One goal of plant biology has been to link variations in natural populations to genotypic variation, with the aim of understanding evolution within a species and moving beneficial traits into plants of agricultural importance. Arabidopsis has proven to be an efficient plant model for evolutionary analyses because of the ease of manipulation, breadth and depth of understanding, of genetic and biochemical pathways and its abundance of natural variation. Combined, these attributes have allowed the largest number of genes and nucleotide polymorphisms underlying natural variation to be uncovered in Arabidopsis compared to any other plant species. However, it still remains a considerable challenge to map genotype to phenotype. In part this is because we observe results from complex, quantitative, multi-gene traits, which are greatly influenced by environmental factors. However, providing access to this unexploited wealth of variation, Arabidopsis researchers can begin to link phenotypic differences with genotypic variations on a global scale. In

addition to variation in DNA sequence, large data sets from other ‘omic’ technologies such as proteomics, metabolomics, ionomics, and epigenomics are also being used to assess the variation that exists at different levels of biological organization and molecular regulation. By combining large scale ‘omic’ data sets obtained across populations it is possible to bring the power of systems biology to quantitative genetics and environmental genomics. This approach can be used to construct and infer biologically meaningful regulatory networks that can reveal the molecules that contribute to systems robustness, plasticity and the survival and adaptation of species.

Comparative Genomics

Accomplishments:

Several major breakthroughs were made in 2011 in the field of Comparative Genomics. Primarily, this includes generating the genome sequences for *Arabidopsis lyrata* (Hu *et al.*, 2011), *Brassica rapa* (The *Brassica rapa* Genome Sequencing Project Consortium, 2011), and the extremophile *Thellungiella parvula* (Dassanayake *et al.* 2011). Dozens of other genomes are in progress, including species from these genera of Brassicales: *Aethionema*, *Arabis*, *Batis*, *Biscutella*, *Boechera*, *Brassica*, *Cardamine*, *Caulanthus*, *Cleome*, *Euclidium*, *Leavenworthia*, *Sisymbrium*, and *Thlaspi*. The Brassicales Map Alignment Project (BMAP) has a centralized list of species being sequenced in the Brassicales (which is updated semi-annually on brassica.info). The DOE JGI Community Sequencing Program recently funded a BMAP proposal to sequence 20 genomes: 7 species are being sequenced in a pilot study and 13 additional species will be chosen by January 2013.

In addition, Brassibase (Koch *et al.* 2012) has been created, which is an online-accessible knowledge and database system for Brassicaceae taxonomy, systematics and evolution. The database includes chromosome numbers, character traits, germplasm resources, and accurate enumeration of all species, genera and tribes. Biological knowledge of the mustard family is exponentially increasing; however, biological material and resources, either collected directly in the wild or held in germplasm collections, have often been misidentified; and only very rarely has the material been further characterized and documented.

A DFG funded knowledge base (priority programme Adaptonics 1529) has also recently been established entitled “Evolutionary plant solutions to ecological challenges / Molecular mechanisms underlying adaptive traits in the Brassicaceae”(see <http://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html>). The project centers on the Brassicaceae and aims to obtain fundamentally novel, comprehensive and increasingly predictive insights into the molecular solutions that plant species develop to match local environmental demands.

Needs:

The integration of population genomics and comparative genomics is ongoing in *Arabidopsis*, *Brassica*, and other plant species. As outlined by the International Arabidopsis Informatics Consortium (IAIC)(2010, 2012), the major strategic challenges include not only gathering high-throughput data, but also organizing and integrating the data into broadly accessible bioinformatics platforms. Current investigations examine both within-species comparisons of natural variation and cross-species comparative -omics. However, the ability to retrieve a specific region of the genome across a large set of Ara-

bidopsis accessions, let alone to other species, is not a simple task. It is essential that any future informatics platform integrate data, tools and resources for comparative studies. For example Phytozome (Goodstein *et al.*, 2012), Gramene (Youens-Clark *et al.*, 2011), CoGe (<http://genomevolution.org/CoGe/>), and PLAZA (Van Bel *et al.*, 2012) could all act as providers for a comparative module of the AIP.

The current idea is to replace the centralized TAIR database with the centralized Arabidopsis Information Portal (AIP) that would connect to multiple databases, tools and resources. It is fundamental that the AIP serves not only *Arabidopsis*, but also related plant species such as the crop Brassicas. Indeed, the portal will need to be flexible enough in design to work for any species. The design of the AIP should provide core functions whilst remaining flexible to encourage constant innovation from multiple contributors. We would recommend that the community portal include these basic components: databases for genomic and molecular stocks, gold standard genome annotations, curation of functional data, transcriptome (expression level, e.g., Movahedi *et al.* 2012), epigenomics (including small RNAs), proteomics, protein-protein interactome, metabolomics, and phenomics. The AIP should also contain search engines that can integrate cross-species information, such as PosMed-plus (Makita *et al.* 2009). Data made accessible via the AIP should be linked and attached to literature to permit data mining and meta analyses. For example, ranking candidate genes to prioritize experimentation can be accomplished by connecting phenotypic keywords to genes through linked data of biological interactions. Representatives from the Brassicales Map Alignment Project (BMAP), Multinational Brassica Genome Project (MBGP), MASC, IAIC, and Brassibase will be coordinating efforts with each other and emerging international partners to ensure that the new platform meets the needs of the plant community.

Ongoing Justification:

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

There is ongoing debate whether the *Arabidopsis* networks are under neutral evolution, dosage constraints, or selection (*Arabidop*

sis Interactome Mapping Consortium, 2011; Bekaert *et al.* 2011) and investigating networks in the context of copy number variation in *Arabidopsis* and additional whole genome duplications (e.g., *Arabidopsis suecica*, *Brassica* and *Camelina*) should add insight into network evolution.

By combining the power of emerging technologies with the extensive knowledge base that has built up in previous decades, the community of researchers investigating *Arabidopsis*, *Brassica* and other species in the Brassicales communities are poised to lead the way in the utilization of natural variation, systems biology and comparative –omics to understand how sequence variation affects biological and evolutionary processes and inform crop improvement efforts.

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

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

- Build predictive models with insights from natural variation within Arabidopsis and comparisons to other related species of plants.
- Use information gained from other species to enhance our knowledge of Arabidopsis; for example, whole genome duplications in Brassica increase the resolution of conserved non-coding region detection.
- Develop systems biology and ‘omics resources parallel to those available in Arabidopsis in crops like Brassica and Camelina and phylogenetically related model species that exhibit traits not present in Arabidopsis (e.g., both C3 and C4 photosynthesis in *Cleome*, woodiness in *Caper*).

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

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

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

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

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

- Integrate -omics data and informatics infrastructure in Arabidopsis with other species.
- Develop international standards for population genomics (Arabidopsis 1001 genomes, Brassica 100 genomes) and comparative genomics (BMAP 100 genomes) to maintain high-quality reference genomes and re-sequenced genomes.
- Develop open access ontology-driven database tools and promote the adoption of uniform vocabularies and machine-readable formats for describing experimental data and metadata.

E) Deepen International Cooperation and Coordination

- Undertake a coordinated analysis of natural variation and comparative ‘omics with the international Brassicales Map Alignment Project (BMAP), Multinational Brassica Genome Project (MBGP), International Arabidopsis Informatics Consortium (IAIC), and Brassibase.
- Continue to offer BMAP workshops at international conferences to coordinate efforts, share expertise, and develop -omics standards and comparative ontologies. Share information on standards, lists of species being sequenced, and emerging international white papers (posted at brassica.info semi-annually)

The International Arabidopsis Functional Genomics Community

Country Highlights

Argentina

- Several new Arabidopsis research grants have been awarded by the Agencia de Promoción Científica y Tecnológica.
- Notable published highlights include; Velasquez, S.M., Ricardi, M.M., Gloazzo Dorosz, J., Fernandez, P.V., Nadra, A.D., Pol-Fachin, L, Egelund, J., Gille, S., Harholt, J., Ciancia, M., Verli, H., Pauly, M., Bacic, A., Olsen, C.E., Ulvskov, P., Petersen, B.L., Somerville, C., Iusem, N.D., Estevez, J.M. (2011) O-Glycosylated Cell Wall Proteins Are Essential in Root Hair Growth. *Science* 332, 1401-1403

Australia and New Zealand

- Arabidopsis 2013 – The 24th International Conference on Arabidopsis research will be held in Sydney, Australia, 24th-28th June. www.sallyjayconferences.com.au/icar2013/

Austria

- New research network: "Metabolic reprogramming by induction of transcription" (MERIT): an EU-funded Marie-Curie Initial Training Network, coordinated by the University of Utrecht with participation from the University of Vienna (Markus Teige, Wolfram Weckwerth) and partners in Belgium, The Netherlands, Germany, Spain, and Portugal
- Arabidopsis 2012 – The 24th International Conference on Arabidopsis research will be held at the Hofburg Palace in Vienna, 3-7 July 2012. www.icar2012.org/

Czech Republic

- New joint research centers are being developed at Olomouc and Brno. The "Centre of the Region Hana for Biotechnological and Agricultural Research" in Olomouc combines researchers from Palacky University, the Crop Research Institute and Institute of Experimental Botany ASCR with many links with the commercial sector. The "Central European Institute of Technology (CEITEC)" in Brno includes a big unit devoted to genomics and proteomics of plant systems. Both centers are currently opening new labs and recruiting new researchers.

Finland

- Notable published highlights include; Blomster *et al.* (2011) Apoplastic reactive oxygen species transiently decrease auxin signaling and cause stress-induced morphogenic response in Arabidopsis. *Plant Physiol* 157:1866-83.

India

- India (represented by Jitendra P. Khurana and R. Srinivasan, New Delhi) has joined MASC and submitted a report which contains an overview of the laboratories involved in Arabidopsis research in India.
- Published highlights include; Pattanayak GK, Tripathy BC

(2011) Overexpression of protochlorophyllide oxidoreductase C regulates oxidative stress in Arabidopsis. *PLOS one* (6) DOI: 10.1371/journal.pone.0026532

Ireland

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

Israel

- Only one grant proposal employing Arabidopsis has been funded by BARD in 2011.
- Tel Aviv University hired Dr. Itay Mayrose, a bioinformaticist, from the labs of Sally Otto and Lauren Rieseberg in Vancouver, Canada.

Italy

- A British-Italian partnership on "Tailoring the composition of cell wall polymers to improve processing of biomass" has been set up.
- Notable published highlights include the plant oxygen sensor; Licausi F, Kosmacz M, Weits DA, Giuntoli B, Giorgi FM, Voesenek LA, Perata P, van Dongen JT (2011) Oxygen sensing in plants is mediated by an N-end rule pathway for protein destabilization. *Nature*, 479:419-422
- An RNAseq service for Arabidopsis has been established at the Filarete Foundation in Milan.

Japan

- A new 3-year project, "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society", started in 2011 with support from the Strategic Japanese-US Joint Research Program (JST in Japan and NSF in US), PIs are Kazuki Saito of RIKEN, Japan, and Lloyd Sumner of Noble Foundation, US.

The Netherlands

- Two prestigious ERC-Starting Grants were awarded to Dolf Weijers (Wageningen University) and to Roberta Groce (Free University Amsterdam). Roberta Groce was also awarded a senior NWO-VICI grant entitled: 'Harvesting the sun safely'. An NWO-VENI junior innovation grant was awarded to the Arabidopsis project of Martijn van Zanten (Utrecht University).

Sweden

- In the last year two new initiatives for strengthening experimental plant research in Sweden have started up; The Linnean Centre for Plant Biology in Uppsala and The Plant Link in Lund.
- Researchers from SciLifeLab and Umeå Plant Science Centre are about to complete the sequencing and analysis of the >20Gbp genome of Norway spruce

Switzerland

- Arabidopsis research resulted in nearly 100 publications in 2011 reporting research on a variety of topics .
- pep2pro database available at <http://www.pep2pro.ethz.ch>, featuring quantitative information for nearly 15,000 Arabidopsis proteins in different organs (Baerenfaller *et al.*, Integrative Biology 3:225, 2011).
- The 8th Tri-National Arabidopsis Meeting (TNAM, Austria-Germany-Switzerland) in 2012 will be hosted by Switzerland at the University of Lausanne.

United Kingdom

- A new European Commission-funded network will coordinate plant science research across Europe and beyond. The network, (ERA-NET for Coordinating Action in Plant Sciences - ERA-CAPS) will be coordinated by the UK Biotechnology and Biological Sciences Research Council (BBSRC) and will run until 2014.
- Published highlights include Daniel J. Gibbs (2011) Homeostatic response to hypoxia is regulated by the N-end rule pathway in plants. *Nature* doi:10.1038/nature10534

United States

- In 2012 the NAASC election will follow the Vienna ICAR; NAASC members will use the meeting for networking to try and increase voter participation.
- The 2011 ICAR was held in Madison, Wisconsin and was attended by 825 participants.
- The International Arabidopsis Information Consortium (IAIC) was formed following two international community workshops held in 2010, which considered the future bioinformatics needs of the Arabidopsis community and other science communities that depend vitally on Arabidopsis resources. A Design Workshop was held in December 2011 to initiate an international community discussion on the design of the Arabidopsis Information Portal (AIP). Blake Meyers (NAASC) was nominated to lead the development of the IAIC and a Research Coordination Network proposal to the NSF was submitted and funded (6/15/2011). Support is intended to foster collaborations, including across international boundaries, and encourage collaborative technologies and development of community data and meta-data standards, among other goals.

Argentina

http://www.arabidopsis.org/info/2010_projects/Argentina.jsp

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New Grants from the Agencia Nacional de Promoción Científica y Tecnológica (www.agencia.gov.ar), which support Arabidopsis research:

- Molecular mechanism of flowering time and circadian rhythm regulation by methyl transferase. Marcelo J. Yanovsky, Fundación Instituto Leloir, Buenos Aires.
- Structure and function of TCP plant transcription factors. Daniel González, Universidad Nacional del Litoral, Province of Santa Fe.
- Temporal integration of light signals controlling growth in plants. Jorge J. Casal, Fundación Instituto Leloir, Buenos Aires.
- Nitric oxide activation of phosphatases C and D in plants. Ana María Laxalt, Universidad Nacional de Mar del Plata, Province of Buenos Aires.
- New photomorphogenic mechanisms affecting plant physiology. Hernán Esteban Boccalandro, IBAM, Province of Mendoza.
- Regulation of auxin receptors by Nitric oxide. María Cecilia Terriente, Universidad Nacional de Mar del Plata, Province of Buenos Aires.
- Isoforms of starch synthases. Mariana Martín, CEFOBI, Rosario, Province of Santa Fe.
- O-glycoproteins in Arabidopsis. Jose Manuel Estevez, IFIBYNE, Buenos Aires.
- Plant aquaporins as multimeric channels. Karina Edith Alleva, Universidad de Buenos Aires, Buenos Aires.
- Identification of new proteins in Light signal transduction. María Agustina Mazzella, INGEBI, Buenos Aires.
- Function of microARN mir396 and GRF transcription factors in *Arabidopsis thaliana*. Ramiro Esteban Rodríguez Virasoro, IBR, Rosario, Province of Santa Fe.
- Genome stability in Arabidopsis. Claudia Spampinato, CEFOBI, Rosario, Province of Santa Fe.
- Mitochondrial proteins in the response to stress. Elina Welchen. Universidad Nacional del Litoral, Province of Santa Fe.

Noteworthy breakthroughs published in 2011:

- Velasquez, S.M., Ricardi, M.M., Gloazzo Dorosz, J., Fernández, P.V., Nadra, A.D., Pol-Fachin, L., Egelund, J., Gille, S., Harholt, J., Ciancia, M., Verli, H., Pauly, M., Bacic, A., Olsen, C.E., Ulvskov, P., Petersen, B.L., Somerville, C., Iusem, N.D., Estevez, J.M. (2011) O-Glycosylated Cell Wall Proteins Are Essential in Root Hair Growth. *Science* 332, 1401-1403

Australia & New Zealand

http://www.arabidopsis.org/info/2010_projects/Australia.jsp
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We warmly invite you to be a part of the 24th International Conference on Arabidopsis Research (ICAR), the largest annual international scientific conference devoted to *Arabidopsis thaliana* – a model plant worked with by an estimated 16,000 labs around the world. Experiments performed in *Arabidopsis* often underpin plant research in general and *Arabidopsis*-driven research leads the way with technologies and concepts.

The conference will be held in the recently refurbished Sydney Convention and Exhibition Centre. With its prime Darling Harbour waterfront location and being walking distance to the city and harbour bridge the Sydney Convention and Exhibition Centre is an ideal setting for a meeting. It is adjacent to a wonderful array of restaurants to suit everyone's budget, and within close walking distance of a variety of hotels, motels and apartments. Sporting and cultural events and shopping opportunities are a major part of life in Sydney and the integrated transport network of trains and buses make it easy and comfortable to get around. The city itself is 15 minutes from the airport.

A particular feature of the program will be more speakers and sessions for presentations by world leading and early/mid career investigators. In addition to 25 plenaries and keynotes, there will be 24 invited seminars and 36 talks selected from Abstracts. Thus, the program will be a mix of cutting-edge *Arabidopsis* research from leading researchers around the world, topical keynotes, translational biology and early career seminars.

We hope you will take this unique opportunity to enjoy four days of plant science in Sydney, together with tours on the harbour and around Australia. We look forward to welcoming you "Down Under"
Barry Pogson
Chair, ICAR 2013
on behalf of the ICAR 2013 Local Organizing Committee

www.icar2013.com.au
[or www.sallyjayconferences.com.au/icar2013/](http://www.sallyjayconferences.com.au/icar2013/)

**24th International Conference on
Arabidopsis Research**
24 – 28 June 2013
Sydney Convention Centre, Darling Harbour, Sydney, Australia



Austria

http://www.arabidopsis.org/info/2010_projects/Austria.jsp
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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; GWA <http://arabidopsis.gmi.oeaw.ac.at:5000/DisplayResultsGene/geneForm>

Systems biology:

- Wolfram Weckwerth (www.univie.ac.at/mosys/wolfram_weckwerth.html). Co-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/kriha): telomeres and genome stability
- Peter Schlägelhofer (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/botwww/botwww-forschung/botwww-arbeitsgruppe/botwww-molephys.htm): 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): Signaling events in the plant stress response

Epigenetics:

- Antonius and Marjori Matzke (www.gmi.oeaw.ac.at/research-groups/amatzke): RdDM, nuclear architecture
- Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/oms.htm): epigenetic changes in polyploids
- Hisashi Tamari (www.gmi.oeaw.ac.at/research-groups/htamaru): 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 Schlägelhofer) (www.mfpl.ac.at/index.php?cid=647).
- "Signaling to plant immunity responses" (PathoNet) is an ERANet PG project with members from Austria, Germany and United Kingdom (www.gen-au.at/archiv/projekt.jsp?id=117)
- "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-Univ. 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, with members of the GMI
- "MeioSys-Systematic analysis of factors controlling meiotic recombination in higher plants", a collaborative project funded by the EU (FP7) with partners from Austria (Peter Schlägelhofer), 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. www.esf.org/activities/eurocores/running-programmes/euroeefg/collaborative-research-projects/epicol.html
 - "Metabolic reprogramming by induction of transcription" (MERIT): an EU-funded Marie-Curie Initial Training Network, coordinated by the University of Utrecht with participation from the University of Vienna (Markus Teige, Wolfram Weckwerth) and partners in Belgium, The Netherlands, Germany, Spain, and Portugal. (<http://theory.bio.uu.nl/MERIT/html/index.html>)

Conferences:

- **Arabidopsis 2012** – The 23th International Conference on Arabidopsis Research (ICAR) will be held at the Hofburg Palace in Vienna, 3-7 July 2012. www.icar2012.org/
- **Viennese Plant Network meetings** – biannual minisymposia of all plant Institutes of the Viennese area.
- **Plant RNA Workshop** – 8-9 July 2012 www.icar2012.org/Satellite%20Meetings/Plant-RNA
- **Plant Vascular Development 2012** – 1-2 July 2012 www.icar2012.org/Satellite%20Meetings/plant-vascular-development-2012

Public Relations- Education:

- **Lange Nacht der Forschung** 27.4 2012 www.lnf2012.at/index.php?option=com_content&view=article&id=53&Itemid=153
- **Fascination of Plants Day** 18.5.2012 www.plantday12.eu/
- **Dialog Gentechnik** www.dialog-gentechnik.at/, 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:** www.projects.mfpl.ac.at/mfpl-phd-selection/
- **PhD School "Chromosome Dynamics".** Coordinated by Peter Schlägelhofer. <http://gscd.gmi.oeaw.ac.at/>
- **VBC Summer School** is a ten week research and teaching programme for undergraduates from around the world (www.vbc-summerschool.at)

Czech Republic

http://www.arabidopsis.org/info/2010_projects/Czech%20Republic.jsp
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Arabidopsis studies are focused on the three major fields in the Czech republic – plant phytohormones biology, genome biology and cell biology. Along with traditional centers at the institutes of the Academy of Sciences of the Czech Republic, universities and especially new joint research centers are abruptly developing in Moravian cities Olomouc and Brno. “Centre of the Region Hana for Biotechnological and Agricultural Research” (<http://www.cr-hana.eu/en/index.html>) in Olomouc combines researchers from Palacky University, Crop Research Institute (VURV) and Institute of Experimental Botany ASCR with many links with the commercial sphere and “Central European Institute of Technology (CEITEC)” (<http://www.ceitec.eu/>) in Brno includes big unit devoted to genomics and proteomics of plant systems (see also this year publication highlight from CEITEC). Both of these centers are currently opening new labs and recruiting new researchers from across the globe. In 2011 Czech plant biologists published about 20 papers related to Arabidopsis – in many cases contributing as members of international author collectives.

Highlights 2011

- Pekárová B, Klumpler T, Tíšková O, Horák J, Jansen S, Dopitová R, Borkovcová P, Papoušková V, Nejedlá E, Sklená V, Marek J, Zídek L, Hejátko J, Janda L. Structure and binding specificity of the receiver domain of sensor histidine kinase CKI1 from *Arabidopsis thaliana*. (2011) *Plant J.* 67:827-39.

Tools and resources

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

Funding sources

Both major funding agencies for basic research – Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR) – support regularly projects based on the use of Arabidopsis as a model plant.

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

Both institutions support bilateral projects with selected countries.

Finland

http://www.arabidopsis.org/info/2010_projects/Finland.jsp

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Arabidopsis tools developed in the last year

Inducible control of symplastic communication (icals3m); Vaten *et al.* (2011) Callose biosynthesis regulates symplastic trafficking during root development. Dev. Cell 21:1144-55.

Notable published highlights

Using ozone as a tool for studying apoplastic reactive oxygen species (ROS) signaling it was shown that ROS rapidly and transiently decrease auxin signaling. Furthermore, analysis of various auxin mutants treated with ozone suggested that ROS together with auxin is a crucial regulator of stress induced changes in plant growth. The cell death program activated by ozone is also regulated by a balance between the antioxidant ascorbic acid and the redox regulated signaling protein NPR1. Progress was also made in understanding the role of the multifunctional protein RCD1. Identification of amino acid residues required for interaction between RCD1-DREB2A led to the discovery of new protein-protein interaction motifs.

Blomster *et al.* (2011) Apoplastic reactive oxygen species transiently decrease auxin signaling and cause stress-induced morphogenic response in Arabidopsis. Plant Physiol 157:1866-83.

India

http://www.arabidopsis.org/info/2010_projects/India.jsp
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Arabidopsis research groups in India

At present, there are a few groups in India, where work is being carried out using Arabidopsis as a system.

- Jiten Khurana and Sudip Chattopadhyay at University of Delhi South Campus and National Institute of Technology, Durgapur, respectively, work on the role of light and hormone signalling in plant growth and development. Some of the mutants characterized by Khurana's group earlier, *viz.* *bls1* and *cnr1*, are defective in light, hormone and sugar signalling. A few more mutants identified based on their constitutive photomorphogenic phenotype (in dark) also display altered response to plant hormones.
- The group of Sudip Chattopadhyay has cloned and functionally characterized several transcription factors (Z-box binding factors or ZBFs) and regulatory proteins (such as SHW1 and EHY1) that play important roles from early seedling stage to floral development. Presently, his laboratory is investigating the interaction of ZBFs among themselves and with other regulatory proteins in regulating seedling development.
- Ashverya Laxmi at National Institute of Plant Genome Research, New Delhi, is exploring the interactive effects of glucose and hormones in regulating plant growth and development. Her group has recently shown that glucose can also influence root directional responses by modulating hormone response pathways.
- Imran Siddiqui's group at Centre for Cellular and Molecular Biology, Hyderabad, is interested in understanding the regulation of female meiosis and gametogenesis. They have shown that mutation of an Arabidopsis gene, *DYAD/SWI1* known to be involved in meiotic chromosome organization, leads to apomeiosis, a major component of apomixis.
- Utpal Nath's laboratory at IISc, Bangalore, has isolated several mutants with altered leaf shape and size. His group has focused on two mutants where leaf serration and surface curvature are altered. In addition, Utpal's lab has obtained mutant lines from ABRC in two homologous genes that are thought to interact with the *TCP* genes and their double mutant lines are delayed in flowering.
- Ashis Nandi from Jawaharlal Nehru University (JNU), New Delhi, is trying to understand the mechanism of systemic acquired resistance in Arabidopsis; his group has reported the identification of a novel recessive mutant *cdd1* that shows enhanced disease resistance and constitutive salicylic acid signalling.

- Ashwani Pareek, also from JNU, and co-workers have identified and characterized glyoxalase genes from Arabidopsis with respect to their role in abiotic stress response. Their group also demonstrated that during salt stress the expression of ABA responsive genes involves induction of several transcription factors in Arabidopsis roots.
- At Calcutta University A. Lahiri has carried out comparative analysis of cis-regulatory elements and identified a novel regulatory element that is strongly associated with ABA signalling-mediated transcription repression.
- Arabidopsis is also being used as a system to understand the effect of heat stress on state transition in photosystems, akin to the effect of light, R. Subramanyam, University of Hyderabad.
- At JNU, the group of B.C. Tripathi has demonstrated that over-expression of protochlorophyllide oxidoreductase C regulates oxidative stress in Arabidopsis.
- K.P. Das's group at Bose Institute, Kolkata, has established the role of DNA polymerase lamda in repair of UV-B-induced DNA damage in the dark using a mutant deficient in its activity.
- R. Srinivasan and SR Bhat at the National Research Centre on Plant Biotechnology, New Delhi, are using T-DNA promoter trap and activation tagging to identify tissue specific and environmental signal specific promoters and to identify genes of agronomic importance, respectively. This group at NRCB has also shown that using a fusion of an Arabidopsis promoter of peroxidase 18 and a mitochondrial orf108 of Brassica associated with cytoplasmic male sterility could be useful in devising a novel transgene containment system particularly relevant to clonally propagated plants.
- In addition to the work described above that is specifically being carried out on Arabidopsis as a system, there are several other groups in India which make use of Arabidopsis as an experimental tool to validate the functions of genes from other species, specially those that are not amenable for genetic transformation.

Highlights of publications

- 1 Aggarwal P, Padmanabhan B, Bhat A, Sarvepalli K, Sadhale P, Nath U (2011) Biochem. Biophys. Research Commun. (410): 276–281
- 2 Choudhury A, Lahiri A (2011) Comparative analysis of abscisic acid-regulated transcriptomes in Arabidopsis. Plant Biol. (13): 28–35
- 3 Kumar, P Vasupalli, N Srinivasan, R Bhat, SR (2012) An evolutionarily conserved mitochondrial orf108 is associated with cytoplasmic male sterility in different allotetraploid lines of *Brassica juncea* and induces male sterility in transgenic *Arabidopsis thaliana*. J Expt. Bot., doi:10.1093/jxb/err459
- 4 Kushwah S, Jones AM, Laxmi A (2011) Cytokinin interplay with ethylene, auxin and glucose signaling controls Arabidopsis seedling root directional growth. Plant Physiol. (156): 1851–1866

- 5 Kushwah S, Jones AM, Laxmi A (2011) Cytokinin-induced root growth involves actin filament reorganization. *Plant Signaling Behavior* (6): 1848-1850
- 6 Nallaepalli S, Mekala NR, Zsiros O, Mohanty P, Subramanyam R (2011) Moderate heat stress induces state transition in *Arabidopsis thaliana*. *Biochim. Biophys. Acta* (1807): 1177-1184
- 7 Kushwah S, Jones AM, Laxmi A (2011) Cytokinin interplay with ethylene, auxin and glucose signaling controls *Arabidopsis* seedling root directional growth. *Plant Physiol.* (156): 1851–1866
- 8 Nallaepalli S, Mekala NR, Zsiros O, Mohanty P, Subramanyam R (2011) Cytokinin-induced root growth involves actin filament reorganization. *Plant Signaling Behavior* (6): 1848-1850
- 9 Nallaepalli S, Mekala NR, Zsiros O, Mohanty P, Subramanyam R (2011) Moderate heat stress induces state transition in *Arabidopsis thaliana*. *Biochim. Biophys. Acta* (1807): 1177-1184
- 10 Pattanayak GK, Tripathy BC (2011) Overexpression of protochlorophyllide oxidoreductase C regulates oxidative stress in *Arabidopsis*. *PLOS one* (6) DOI: 10.1371/journal.pone.0026532
- 11 Roy S, RoyChaudhury S, Singh SR, Das KP (2011) AtPol λ A homolog of mammalian DNA polymerase λ in *Arabidopsis thaliana*, is involved in the repair of UV-B induced DNA damage through the dark repair pathway. *Plant Cell Physiology* (52): 448-467
- 12 Sarvepalli K, Nath U (2011) Hyper-activation of the TCP4 transcription factor in *Arabidopsis thaliana* accelerates multiple aspects of plant maturation. *Plant J.* (67): 595-607
- 13 Singh K, Singla-Pareek SL, Pareek A (2011a) Genome-wide analysis of rice and *Arabidopsis* identifies two glyoxalase genes that are highly expressed in abiotic stresses. *Functional Integrative Genomics* (11): 293-305
- 14 Singh K, Singla-Pareek SL, Pareek A (2011b) Dissecting out the crosstalk between salinity and hormones in roots of *Arabidopsis*. *OMICS* (15): 913-24

Arabidopsis genomics tools and resources

As of now, there is no national repository for *Arabidopsis* resources developed in India. The resources developed or mutants isolated/characterized are available with the respective PIs and can be accessed by contacting them personally.

Major funding sources

- The research work on *Arabidopsis* in India is supported primarily by the funding received from the Government of India through the Department of Biotechnology (DBT), the Department of Science and Technology (DST), the Council of Scientific and Industrial Research (CSIR), and the Indian Council of Agricultural Research (ICAR), with the headquarters of all these organizations based in New Delhi.
- Most of the work being done on *Arabidopsis* India is in the form

of individual efforts with grants received from Government of India in the competitive mode. However, there are some international collaborations but more so at the personal level.

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 currently no private sector institutions working with *Arabidopsis thaliana* in Ireland.

Plant Research Ireland Website:

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

Irish *Arabidopsis* research groups

The following 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.
- Dr. Fuquan Liu, School of Biological Sciences, Queens University Belfast, Northern Ireland.

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

Irish scientific highlights

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

- 1 Alden KP, Dhondt-Cordelier S, McDonald KL, Reape TJ, Ng CK, McCabe PF, Leaver CJ. (2011) Sphingolipid long chain base phosphates can regulate apoptotic-like programmed cell death in plants. *Biochem Biophys Res Commun.* 410:574-80.
- 2 Ali SS, Khan M, Fagan B, Mullins E, Doohan FM. (2012) Exploiting the inter-strain divergence of *Fusarium oxysporum* for microbial bio-processing of lignocellulose to bioethanol. *AMB Express.* 2:16.
- 3 Donoghue MT, Keshavaiah C, Swamidatta SH, Spillane C. (2011) Evolutionary origins of Brassicaceae specific genes in *Arabidopsis thaliana*. *BMC Evolutionary Biology* 11:47.
- 4 Hectors K, van Oevelen S, Guisez Y, Prinsen E, Jansen MA. (2012) The phytohormone auxin is a component of the regulatory system that controls UV-mediated accumulation of flavonoids and UV-induced morphogenesis. *Physiol Plant.* 2012 Feb 3.
- 5 Hogg BV, Kacprzyk J, Molony EM, O'Reilly C, Gallagher TF, Gallois P, McCabe PF. (2011) An *in vivo* root hair assay for determining rates of apoptotic-like programmed cell death in plants. *Plant Methods.* 13:7:45.
- 6 Islam MN, Jacquemot MP, Coursol S, Ng CK. (2012) Sphingosine in plants more riddles from the Sphinx? *New Phytol.* 193:51-7.
- 7 Jacques E, Hectors K, Guisez Y, Prinsen E, Jansen MA, Verbelen JP, Vissenberg K. (2011) UV radiation reduces epidermal cell expansion in *Arabidopsis thaliana* leaves without altering cellular microtubule organization. *Plant Signal Behav.* 6:83-5.
- 8 Köhler C, Wolff P, Spillane C. (2012) Epigenetic Mechanisms Underlying Genomic Imprinting in Plants. *Annu Rev Plant Biol.* Jan 30.
- 9 Liu F, Bakht S, Dean C. (2012) Cotranscriptional role for Arabidopsis DICER-LIKE 4 in transcription termination. *Science.* 335:1621-3.
- 10 McKeown PC, Laouie-Duprat S, Prins P, Wolff P, Schmid MW, Donoghue MT, Fort A, Duszynska D, Comte A, Lao NT, Wennblom TJ, Smart G, Köhler C, Grossniklaus U, Spillane C. (2011) Identification of imprinted genes subject to parent-of-origin specific expression in *Arabidopsis thaliana* seeds. *BMC Plant Biology* 11:113
- 11 Newell CA, Natesan SK, Sullivan JA, Jouhet J, Kavanagh TA, Gray JC. (2012) Exclusion of plastid nucleoids and ribosomes from stromules in tobacco and Arabidopsis. *Plant J.* 69:399-410.
- 12 Ng CK, Coursol S. (2012) New insights into phospholipase d and sphingosine kinase activation in Arabidopsis. *Front Physiol.* 3:67.
- 13 Rae L, Lao NT, Kavanagh TA. (2011) Regulation of multiple aquaporin genes in Arabidopsis by a pair of recently duplicated DREB transcription factors. *Planta.* 2011 Apr 21.
- 14 Smyth EM, McCarthy J, Nevin R, Khan MR, Dow JM, O'Gara F, Doohan FM. (2011) In vitro analyses are not reliable predictors of the plant growth promotion capability of bacteria; a *Pseudomonas fluorescens* strain that promotes the growth and yield of wheat. *J Appl Microbiol.* 111:683-92.
- 15 Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, Donoghue MT, Azam S, Fan G, Whaley AM, Farmer AD, Sheridan J, Iwata A, Tuteja R, Penmetsa RV, Wu W, Upadhyaya HD, Yang SP, Shah T, Saxena KB, Michael T, McCombie WR, Yang B, Zhang G, Yang H, Wang J, Spillane C, Cook DR, May GD, Xu X, Jackson SA. (2011) Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature Biotechnology.* 30:83-9.

- 16 Wendt T, Doohan F, Mullins E. (2011) Production of *Phytophthora infestans* resistant potato (*Solanum tuberosum*) utilising Ensifer adhaerens OV14. *Transgenic Res.* Sep 13.
- 17 Wendt T, Doohan F, Winckelmann D, Mullins E. (2011) Gene transfer into *Solanum tuberosum* via *Rhizobium* spp. *Transgenic Res.* 2011 20:377-86.
- 18 Wolff P, Weinhofer I, Seguin J, Roszak P, Beisel C, Donoghue MT, Spillane C, Nordborg M, Rehmsmeier M, Köhler C. (2011) High-resolution analysis of parent-of-origin allelic expression in the Arabidopsis Endosperm. *PLoS Genetics* 7(6):e1002126.

Israel

<http://www.arabidopsis.org/portals/masc/countries/Israel.jsp>

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In 2011, ~50 research articles employing Arabidopsis were published from groups in Israel. 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 projects 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. As a result only one grant proposal employing Arabidopsis has been funded in 2011. The Israel Science Foundation and European Community remain the major source of funding for basic research employing Arabidopsis.

Returning young scientists

Tel Aviv University hired Dr. Itay Mayrose, a bioinformaticist, from the labs of Sally Otto and Lauren Rieseberg in Vancouver, Canada.

Italy

<http://www.arabidopsis.org/portals/masc/countries/Italy.jsp>

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Newly awarded *Arabidopsis* projects:

- Among the most relevant newly funded projects, the groups of F.Cervone/G.de Lorenzo and of P.Tavladoraki/R.Angelini (Roma Tre University) are the recipient of a new grant on perception and response to damage-associated molecular patterns in plants from the Italian Ministry of Research and Education.
- The group F.Cervone/G.De Lorenzo has also started a British-Italian partnership on "Tailoring the composition of cell wall polymers to improve processing of biomass".
- The group of I.Ruberti (CNR, Rome) has been awarded a grant on Agronanotechnology funded by the Italian Ministry of Agriculture and Forestry.

Current *Arabidopsis* Projects:

Several longer term projects are still ongoing.

- The group of M.Cardarelli/P. Costantino (CNR/Sapienza University, Rome) and of N.Marmiroli (University of Parma) are involved in two different COST actions, on plant reproduction for crop improvement, and on mineral-improved crop production for healthy food and feed, respectively.
- The groups of G.Serino/P.Costantino (Sapienza University, Rome) and G. Frugis (CNR, Rome), are continuing their collaboration on protein degradation in plants stress response and development with Q. Xie (CAS, China) and L.J. Qu (Peking University), funded 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, and by two grants from the Italian Ministry of Agriculture and Forestry.
- The group of C. Tonelli is being supported by a grant on the use of *Arabidopsis* as a model system to investigate stomatal control over water use efficiency and pathogens penetration from the Umberto Veronesi Foundation (Milan, Italy).
- The ERA-NET Plant Genomics Projects project "Multiple stress response and adaptation" (participants P.Costantino and I.Ruberti) was completed in 2011.

Relevant *Arabidopsis* genomics tools and resources:

- C. Tonelli and M. Galbiati (University of Milan) have established an RNAseq service for *Arabidopsis* at the Filarete Foundation in Milan.
- Several new *Arabidopsis* mutants have been identified and characterized, among which two mutants lines tolerant to lethal

concentrations of CdS nanoparticles (N.Marmiroli).

- Transcriptomic data obtained for these mutants using the Affymetrix GeneChip Array is also available from N.Marmiroli group.
- The group of M.Cardarelli/P. Costantino developed transgenic lines over-expressing the phytochelatin biosynthetic gene AtPCS1, tolerant to toxic concentrations of Cd.
- A collection of single and multiple combinations of mutants in the HD-Zip II g and d subfamily genes have been identified by the I.Ruberti group. The same group has also developed transgenic plants carrying translational fusions for the HD-Zip II g and d subfamily genes.
- The P.Tavladoraki/ R.Angelini have generated loss-of-function T-DNA insertional mutants as well as reporter genes fusions for CuAO (Copper Amine Oxidase) and PAO (Polyamine Oxidase).

Highlights of groundbreaking *Arabidopsis* journal articles:

- Licausi F, Kosmacz M, Weits DA, Giuntoli B, Giorgi FM, Voesenek LA, Perata P, van Dongen JT (2011) Oxygen sensing in plants is mediated by an N-end rule pathway for protein destabilization. *Nature*, 479:419-422
*A collaboration between the Sant'Anna, Pisa and the Potsdam Max Planck Institute in Germany. This article reports the identification of the mechanism that senses reduced oxygen levels in *Arabidopsis*. The study shows that oxygen sensing in plants is mediated by an N-end rule pathway, and opens up new possibilities for improving flooding tolerance in crops.*
- Skirycz A, Vandenbroucke K, Clauw P, Maleux K, De Meyer B, Dhondt S, Pucci A, Gonzalez N, Hoeberichts F, Tognetti VB, Galbiati M, Tonelli C, Van Breusegem F, Vuylsteke M, Inzé D. (2011) Survival and growth of *Arabidopsis* plants given limited water are not equal. *Nat Biotechnol* 29:212-214
*A study in collaboration with Ghent University, Belgium, aimed at determining the survival and growth of *Arabidopsis* plants given limited water.*
- Galbiati M, Matu JT, Francia P, Rusconi F, Cañón P, Medina C, Conti L, Cominelli E, Tonelli C, Arce-Johnson P (2011) The grapevine guard cell-related VvMYB60 transcription factor is involved in the regulation of stomatal activity and is differentially expressed in response to ABA and osmotic stress. *BMC Plant Biol* 11:162
- Rizza A, Boccaccini A, Lopez-Vidriero I, Costantino P and Vittorioso P (2011) Inactivation of the *ELIP1* and *ELIP2* genes affects *Arabidopsis* seed germination. *New Phytologist* 190: 896–905
- Galletti R, Ferrari S, De Lorenzo G (2011). *Arabidopsis MPK3* and *MPK6* play different roles in basal and oligogalacturonide- or flagellin-induced resistance against *Botrytis cinerea*. *Plant Physiology* 157: 804-814
- Savatin DV, Ferrari S, Sicilia F, De Lorenzo G. (2011) Oligogalacturonide-auxin antagonism does not require posttranscriptional

- gene silencing or stabilization of auxin response repressors in Arabidopsis. *Plant Physiology* 157:1163-74
- De Lorenzo G, Brutus A, Savatin DV, Sicilia F, Cervone F. (2011) Engineering plant resistance by constructing chimeric receptors that recognize damage-associated molecular patterns (DAMPs). *FEBS Letters* 585:1521-1528
 - Brunetti P, Zanella L, Proia A, De Paolis A, Falasca G, Altamura M,M, Sanità Di Toppi L, Costantino P, Cardarelli M. (2011). Cadmium tolerance and phytochelatin content of Arabidopsis seedlings over-expressing the phytochelatin synthase gene AtPCS1. *JExBot* 62 (15): 5509-19.

Conferences and awards

- G.Frugis and G.Serino were the organizers of a workshop on “Control of protein degradation in plant development and environmental response”, held in Rome on November 7, 2011.
- N.Marmiroli was the organizer of the COST meeting “What's for lunch? Nutrients and minerals in every day food”, held in Venice, Italy, November 2011.
- C. Tonelli was the organizer of the 7th conference on the Future of Science, held in Venice on September 18-20, 2011.
- Paolo Costantino (Rome), Chiara Tonelli (Milan) and Ida Ruberti are coorganizers of the EMBO Conference “Plant Development and Environmental Interactions” to be held in Matera, Italy, May 27-30, 2012.
- G.De Lorenzo was a recipient of a Sapienza University award for Excellence in Research for her studies on cell wall in plant immunity and development.
- A call of the Italian Ministry of Instruction, University and Research is now open and the groups of S.Sabatini/P.Costantino and of I.Ruberti are in the process of developing a network proposal on regulatory circuits controlling root growth.

Japan

<http://www.arabidopsis.org/portals/masc/countries/Japan.jsp>

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Advances

In 2011 Plant Science in Japan started several projects to support advanced plant research (Japan Advanced Plant Science Research Network and NC-CARP). These programs strengthen the “omics” platform developed by institutes and universities. RIKEN Plant Science Center (PSC) and the Kazusa DNA Research Institute support the platforms of plant metabolome. PSC supports platform of hormonome. RIKEN, the National Institute of Basic Biology (NIBB) and the Nara Institute of Science and Technology (NAIST) support transcriptome and epigenome platforms based on high-through-put sequencing. NAIST and PSC support proteome platform.

Activities of the individual centers

RIKEN PSC (<http://www.psc.riken.jp/english/index.html>)

- Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi). PSC established the Arabidopsis metabolomics platform (<http://prime.psc.riken.jp/>), which consists of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics. The publicly-available platform resources include Arabidopsis metabolome expression database AtMetExpress (<http://prime.psc.riken.jp/lcms/AtMetExpress/>); Arabidopsis MS/MS spectral tag (MS2T) viewer (<http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html>); standard spectrum search (http://prime.psc.riken.jp/?action=standard_index), ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (<http://spectra.psc.riken.jp/>); Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index); Drop Met (http://prime.psc.riken.jp/?action=drop_index); Annotation of metabolites by NMR from ¹³C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search).
- Hormonome platform and RIKEN Plant Hormone Research Network; (<http://hormones.psc.riken.jp/>)(Hitoshi Sakakibara and Yuji Kamiya)
- Transcriptome platform using tiling array in collaboration with RIKEN BASE (<http://omicspace.riken.jp/gps/>) (Motoaki Seki, Tetsuro Toyoda, Kazuo Shinozaki)
- Proteome platform (<https://database.riken.jp/sw/links/en/ria1021i>). PSC (Hiroyuki Nakagami, Ken Shirasu) and Keio University (Yasushi Ishihama, Naoyuki Sugiyama) developed a high-through-put shotgun phosphoproteomics tool for plants and phosphorylation site databases (<http://phosphoproteome.psc.database.riken.jp>, <http://pepbase.iab.keio.ac.jp>)
- Phenome platform (<http://amber/gsc.riken.jp/act/top.php>) RIKEN Activation tagging lines Database and Full-length-cDNA-overexpressing (FOX) Arabidopsis lines (contact to Mi

- nami Matsui), Ds-transposon tagged lines (<http://large.gsc.riken.jp/phenome/>)(Takashi Kuromori, Tetsuya Sakurai, Kazuo Shinozaki).
- Chloroplast gene phenotype (Fumiyo Miyouga, Kazuo Shinozaki).
- The Chloroplast Function Database (<http://large.psc.riken.jp/chloroplast>)
- Analysis of small Open Reading Frame (Kousuke Hanada, Minami Matsui, Motoaki Seki)
- Mass Bank (Masanori Arita, Kazuki Saito) The public repository of mass spectral data for sharing them among scientific research community. MassBank data are useful for the chemical identification and structure elucidation of chemical compounds detected by mass spectrometry. (<http://www.massbank.jp/en/about.html>)

RIKEN BRC

- Experimental Plant Division (Masatomo Kobayashi, kobayashi@rtc.riken.jp) collects, preserves and distributes Arabidopsis resources developed in Japan through National BioResource Project (NBRP). The project includes not only Arabidopsis but also other plant resources such as rice, wheat, barley, legume, tomato, chrysanthemum, morning glory and algae collected in universities and research institutes. From April 2012, the 3rd term of NBRP will be launched, and the improvement of quality and information of the resources is expected during next five years (<http://www.brc.riken.go.jp/lab/epd/Eng/>).

RIKEN BASE

(Tetsuro Toyoda) (<http://www.base.riken.jp/>)

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

KAZUSA DNA RESEARCH INSTITUTE

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

New Projects

- MEXT, Environmental sensing of plants: Signal perception, processing and cellular responses (2010-2015), Headed by Akira Nagatani, Kyoto University
- MEXT, Integrated Analysis of Strategies for Plant Survival and Growth in Response to Global Environmental Changes (2010-2015), Headed by Jian Feng Ma, Okayama University, Institute of Plant Science and Resources
- Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project on "Metabolomics for Low Carbon Society". Research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and Kazuki Saito (RIKEN PSC). Research led by Oliver Fiehn (Univ. of California at Davis) and Masanori Arita (Univ. of Tokyo)
- ERATO Higashiyama Live-Holonics Project (2010-2015) Headed by Tetsuya Higashiyama, Nagoya University. This project aims to study intercellular signaling in multicellular organisms with complete control of cells and molecules under the microscope, by developing new technologies for live-cell analysis.
- BMEP (Biomass Engineering Program) (www.riken.jp/bmep/english/index.html) RIKEN started BMEP in 2010. This program is focusing on the establishment and innovation for plant biomass production and renewable chemical materials and Bioplastics. Brachypodium as a model of grass biomass is used besides Arabidopsis in this program. This interdisciplinary program is organized by cooperation of chemists and plant biologists.
- Japan Advanced Plant Science Research Network has been started in 2011. In this program nine centers of excellence take roles to support plant researches for green innovation. Tohoku Univ.; Tracer analysis system using stable radioactive compounds. Univ. of Tsukuba; Transformation platform. Univ. of Tokyo; Ionome analysis, Metabolite analysis, Cell sorting and Photosynthesis measurement. RIKEN; Metabolome, Hormonone, Epigenome and Transcriptome analyses, Nagoya Univ.; Cell imaging, National Institute of Basic Biology; Next generation sequencing, Image analysis, NAIST; Cell signaling and Proteome analysis, Kyoto Univ.; Light and CO₂ controlled growth room, Okayama Univ.; Multi-Stress evaluation system.
- NC-CARP (as a program in GRENE ;Green Network of Excellence). A new program "Network of Centers of Carbon Dioxide Resource Studies in Plants: NC-CARP (organizer: Professor Hiroo Fukuda)" started from 2011 as a 5-year project. This program aims at innovation of plant biomass technology by collaboration among Plant Science, Agriculture, Engineering and Chemistry, and at education of this new area. The centers include Kobe University and The National Institute of Advanced Industrial Science and Technology (AIST) in addition to the nine centers belonging to the Japan Advanced Plant Science Research Network.
- JST-NSF (http://nsf.gov/funding/pgm_summ.jsp?pims_id=503558). A new 3-years project, "Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society", started from 2011 by the support of the Strategic Japanese-US Joint Research Program (JST in Japan and NSF in US), PIs are Kazuki Saito of RIKEN, Japan, and Lloyd Sumner of Noble Foundation, US.

Arabidopsis genome tools and resources

RIKEN resources and tools

- Resources from RIKEN (<http://www.brc.riken.go.jp/lab/epd/Eng/>) BRC
- PSC. RPIMe (<http://prime.psc.riken.jp/>); AtMetExpress (<http://prime.psc.riken.jp/lcms/AtMetExpress/>); Arabidopsis MS/MS spectral tag (MS2T) viewer (<http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html>); Standard Spectrum Search (http://prime.psc.riken.jp/?action=standard_index); ReSpect (RIKEN MSn Spectral Database for Phytochemicals) (<http://spectra.psc.riken.jp/>)
- Widely-targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index); Drop Met (http://prime.psc.riken.jp/?action=drop_index); Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search)
- RIKEN Plant Hormone Research Network (<http://hormones.psc.riken.jp/>); The Chloroplast Function Database (<http://large.psc.riken.jp/chloroplast/>); RIKEN Arabidopsis Activation Tagging Line Database (<http://amber.gsc.riken.jp/act/top.php>); RIKEN Arabidopsis Genome Encyclopedia (RARGE) (<http://rarge.psc.riken.jp/>); Phenome Analysis of Ds transposon-tagging line in Arabidopsis (RAPID).(<http://rarge.gsc.riken.jp/phenome/>); RIKEN Plant Phosphoproteome Database (RIPP-DB) (<http://phosphoproteome.psc.database.riken.jp>)
- BASE. OMICSPACE (<http://omicspace.riken.jp/gps>)
- KAZUSA resources and tools; Kazusa Metabolomics Database KOMICS (<http://www.kazusa.or.jp/komics/>); The KaPPA-View4 (<http://kppv.kazusa.or.jp/>); MassBase (<http://webs2.kazusa.or.jp/massbase/>); KomicMarket (<http://webs2.kazusa.or.jp/komics/>); MS-MS Fragment Viewer (<http://webs2.kazusa.or.jp/msmsfragmentviewer/>); KAGIANA (<http://pmnedo.kazusa.or.jp/kagiana/index.html>); Cop (<http://webs2.kazusa.or.jp/kagiana/cop/>); The regulatory network research RnR (<http://webs2.kazusa.or.jp/kagiana/rnr/>); MFSearcher (<http://webs2.kazusa.or.jp/mfsearcher/>)

Current grants

- RIKEN is supported by MEXT.
- Kazusa projects are supported by Chiba-Prefecture.
- (Grants-in-Aid for Science from MEXT, (www.jsps.go.jp/english/egrants/grants.html)
- CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
- Program of Promotion of Basic Research Activities for Innovative Biosciences (www.brain.go.jp/welcome-e.html)
- ALCA (Advanced Low Carbon Technology Research and Development Program)(<http://www.jst.go.jp/alca/en/index.html>)

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

The Netherlands

<http://www.arabidopsis.org/portals/masc/countries/Netherlands.jsp>
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New Arabidopsis grants

Two prestigious ERC-Starting Grants were awarded to Dolf Weijers (Wageningen University) who studies the establishment of stem cells in the Arabidopsis embryo and to Roberta Groce (Free University Amsterdam), to investigate the biophysical principles of thylakoid membranes in relation to acclimation to light. Roberta Groce was also awarded a senior NWO-VICI grant entitled: 'Harvesting the sun safely' to understand how plants can protect themselves from too much light and still maintain active photosynthesis. An NWO-VENI junior innovation grant was awarded to the Arabidopsis project of Martijn van Zanten (Utrecht University), studying genes that control leaf position as a means to control heat effects.

Scientific Highlights for the Netherlands

Overall Dutch Arabidopsis scientists published 114 papers in the past year. Notable highlights include:

- Krüger TP, Wientjes E, Croce R, van Grondelle R. (2011) Conformational switching explains the intrinsic multifunctionality of plant light-harvesting complexes. <http://www.ncbi.nlm.nih.gov/pubmed/21808044> Proc Natl Acad Sci U S A. 108(33):13516-21.
- Prasad K, Grigg SP, Barkoulas M, Yadav RK, Sanchez-Perez GF, Pinon V, Blilou I, Hofhuis H, Dhonukshe P, Galinha C, Mähönen AP, Muller WH, Raman S, Verkleij AJ, Snel B, Reddy GV, Tsiantis M, Scheres B. (2011) Arabidopsis PLETHORA transcription factors control phyllotaxis. <http://www.ncbi.nlm.nih.gov/pubmed/21700457> Curr Biol. 21(13):1123-8.

Sweden

<http://www.arabidopsis.org/portals/masc/countries/Sweden.jsp>

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Plant research in Sweden

Plant research in Sweden is focused on various aspects of plant biology ranging from ecology and adaptation in the evolutionary context as well as physiology, to epigenetic regulation and biotechnology. Arabidopsis is model of choice for a vast part of the community along side crop model species for Agricultural and Forestry applications.

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.

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.

Research institutes and new initiatives

- In the last year two new initiatives for strengthening experimental plant research in Sweden have started up; in Uppsala and Lund in the south of Sweden. The Linnean Centre for Plant Biology in Uppsala (<http://lcpu.se/>). The Plant Link (www.plantlink.se).
- The Science for Life Laboratory (SciLifeLab, <http://www.scilifelab.se>) a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala.
- The Umeå Plant Science Centre is the largest Centre for plant science in Sweden and for example maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis (<http://www.upsc.se>, "resources").

Research updates and meetings

- Researchers from SciLifeLab and Umeå Plant Science Centre are about to complete the sequencing and analysis of the >20Gbp genome of Norway spruce (<http://www.congenie.org>). Large RNAseq analysis of the expressed genes will further aid and make significant contribution to the comparative and functional genomics, enabling comparisons from the annual herbaceous Arabidopsis to the deciduous angiosperm hybrid aspen

and the gymnosperm Norway spruce.

- The 1st International Conference on Plant Proteases; From biology to biotechnology took place in Hemavan, Sweden, April, 2011. About hundred scientists participated and at least half of them work with Arabidopsis as a model system. The next conference is expected to take place in 2013.

Research highlights

The last year about 60 experimental papers using Arabidopsis as a model system was published by Swedish research groups and their international collaborations, for example:

- Roszak P and Köhler C (2011) Polycomb group proteins are required to couple seed coat initiation to fertilization. PNAS (108) 20826-20831.
- Gendre D, Oh J, Boutté Y, Best JG, Samuels L, Nilsson R, Uemura T, Marchant A, Bennett MJ, Grebe M, Bhalerao RP (2011) Conserved Arabidopsis ECHIDNA protein mediates trans-Golgi-network trafficking and cell elongation. PNAS (108) 8048-8053.
- Vattén A et al (2011) Callose Biosynthesis Regulates Symplastic Trafficking during Root Development. Developmental Cell (21) 1144-1155.

Major collaborations

UPRA is a European Open Laboratory between the UPSC (Umeå Plant Science Centre in Umeå, Sweden) and the research center of INRA (National Institute for Agricultural Research). The dedicate complementarities of both Research Centers in different topics of systems biology and plant genomics has naturally led to the creation of this European open laboratory. Emphasis is put on transfer of knowledge and tools on a model genetic species, Arabidopsis, and *Populus* and through this network training of young scientists. Agreements are also established with Riken, Japan and Max Planck Institutes, Germany and Royal Veterinary and Agricultural University of Denmark.

Swedish Arabidopsis resources

- The Science for Life Laboratory (SciLifeLab, <http://www.scilifelab.se>) a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala.
- The Umeå Plant Science Centre 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 Royal Academy of Science (<http://www.kva.se>) and The Royal Academy of Agriculture and Forestry (<http://www.ksla.se>)
- The Swedish Foundation for Strategic Research (<http://www.strateresearch.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 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; <http://erc.europa.eu/>) and the European Union fund several projects using Arabidopsis.
- Funding of exchange on postdoctoral level between Sweden and other countries where research using Arabidopsis may be funded, can be found among the funded research of "Major funding sources", above. For example The Swedish Foundation for Strategic Research (SSF) is participating in a joint programme with the Japan Society for the Promotion of Science (JSPS) aimed at stimulating young Swedish researchers to conduct cooperative research activities with leading Japanese research groups. For information on JSPS, see www.jsps-sto.com.

Recent awards

- ERC recently awarded Dr Claudia Köhler at Swedish University of Agricultural Sciences in Uppsala, a "Starting Grant" for a project that aims to elucidate epigenetic regulation using Arabidopsis.
- The Swedish Research Council supports outstanding research in Sweden and a large part of the funded plant biologist use Arabidopsis. Their last (2011) call included support to studies of for example the circadian clock, photosynthesis, regulation of the endosperm development, senescence as well as genetic and hormonal control root vascular development.

Switzerland

<http://www.arabidopsis.org/portals/masc/countries/Switzerland.jsp>
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Arabidopsis research in Switzerland remains strong as indicated by the nearly 100 publications in 2011 reporting research on topics ranging from ecology and evolution to regulation of physiological processes, epigenetic regulation, chloroplast biology, light-regulated growth and development, molecular aspects of symbiosis and pathogenesis, cell wall formation, transport processes and vitamin biosynthesis.

Swiss Plant Science Web (SPSW)

The Swiss Plant Science Web (SPSW), which was established in 2010 (<http://www.swissplantscienceweb.ch>), is now fully operational, including the associated technology platforms that support 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). SPSW has become very active in coordinating educational and training activities in plant sciences, including the organization of summer schools for Master and PhD students. The 2012 Summer School focuses on "Modeling Development in Plant Sciences" and is jointly organized by SPSW and SystemsX.ch (<http://www.swissplantscienceweb.ch/education/phd-summer-school/2012/>). SPSW continues to be a good entry point to learn more about Arabidopsis research and plant sciences 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, <http://www.cti.admin.ch/index.html?lang=en>), which supports technology development and transfer to the commercial sector.
- The Swiss systems biology initiative SystemsX.ch also continues to support 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.agronomics.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. Several of these prestigious research grants have been awarded to Swiss plant scientists.

- In 2011 the Zurich-Basel Plant Science Center was also awarded a large grant from the European Commission for the International Postdoctoral Fellowship program "Plant Fellows" that will start later in 2012 (http://www.plantsciences.ch/research/fellowships/postdoc_fellowship/KICK_OFF_PLANT_FELLOWS_2012.pdf).

Research Breakthroughs:

- Swiss Arabidopsis researchers continue to use functional genomic tools and approaches widely to gain new mechanistic insights into plant development and function, but only a few examples of the more than 100 publications related to Swiss Arabidopsis research can be highlighted here.
- Significant progress has been made in understanding auxin regulation in development and viral response (e.g., Ding *et al.*, *Nature Cell Biology*, 2011; Santuari *et al.*, *Current Biology*, 2011; Jay *et al.*, *PLoS Pathogens*, 2011).
- Understanding epigenetic regulation of developmental processes remains a strong focus of Arabidopsis research in Switzerland (e.g., Autran *et al.*, *Cell*, 2011; Dumbliauskas *et al.*, *EMBO Journal*, 2011; Gutzat *et al.*, *Development*, 2011), but increasingly regulation of plant functions by small RNAs are taking center stage as well (e.g., Ito *et al.*, *Nature*, 2011, see also <http://www.swissplantscienceweb.ch/newsletter-spsw/spsw-newsletter-211/onson-a-jumping-gene>: Si-Ammour *et al.*, *Plant Physiology*, 2011)
- A major breakthrough was made with the identification of proteins involved in Caspary strip formation in root endodermis. This research was reported by Prof. Niko Geldner, who is also recipient of an ERC Junior Award (Roppolo *et al.*, *Nature*, 2011).
- Progress continues to be made in understanding the synthesis and signaling function of jasmonate (e.g., Gfeller *et al.*, *Plant Physiology*, 2011) and differentiation processes (Peaucelle *et al.*, *Current Biology*, 2011).
- Major highlights also included the transcriptome analysis of the Arabidopsis megasporangium mother cell that uncovered the importance of RNA helicase for plant germline development (Schmidt *et al.*, *PLoS Biology*, 2011), the positive effect of vitamin B6 overproduction on plant growth (Raschke *et al.*, *Plant Journal*, 2011), and that loss of the major Toc159 import complex protein has no significant effect on the composition of the chloroplast proteome (Bischof *et al.*, *Plant Cell*, 2011).
- Progress has also been made in plant innate immunity (e.g., Roux *et al.*, *Plant Cell*, 2011) and other plant processes associated with pathogen defense (L'Haridon *et al.*, *PLoS Pathogens*, 2011).

Arabidopsis Meetings

The 8th Tri-National Arabidopsis Meeting in 2012 will be hosted by Switzerland at the University of Lausanne (<http://www3.unil.ch/wpmu/tnam12/>).

Tools and Resources

- The AGRON-OMICS consortium in collaboration with Affymetrix developed the AGRONOMICS1 Arabidopsis genome tiling array that continues to be available to the Arabidopsis community (Rehrauer *et al.*, Plant Physiology, 2010; http://www.agron-omics.eu/index.php/resource_center/tiling-array). The AGRONOMICS1 array is commercially available from Affymetrix and the Functional Genomics Center Zurich (<http://www.fgcz.ch/>) has strong expertise in array processing and data analysis.
- 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 7,100 Arabidopsis microarray experiments but also gene expression data from other plants, human, animals, yeast and E.coli. In addition, Genevestigator can now be used with RefGenes (<http://www.refgenes.org/rg/>) , 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).
- Another major resource for the Arabidopsis proteome is the pep2pro database available at <http://www.pep2pro.ethz.ch>, which features quantitative information for nearly 15,000 Arabidopsis proteins in different organs (Baerenfaller *et al.*, Integrative Biology 3:225, 2011). Quantitative Arabidopsis protein data in pep2pro and transcript level data in Genevestigator are linked so that Arabidopsis researchers can immediately obtain full gene expression information. pep2pro and other proteome databases relevant for Arabidopsis research can now be accessed through MASCP Gator at <http://gator.masc-proteomics.org/> (Joshi *et al.*, Plant Physiology 155: 259, 2011).

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 the BBSRC remit.
- A new European Commission-funded network launched at the end of January 2011 will coordinate plant science research across Europe and beyond. The network, (ERA-NET for Coordinating Action in Plant Sciences - ERA-CAPS) will be coordinated by the UK Biotechnology and Biological Sciences Research Council (BBSRC). It will run until 2014 and is expected to fund two calls for collaborative research projects as well as organising strategic workshops for identifying common priorities and activities around data sharing and open access. The collaborative projects are expected to investigate fundamental plant biology and science that may have applications including improved crops for food, energy and industrial biotechnology. Projects funded by the network will involve scientists from three or more partner nations with each country funding researchers from their own national institutions.
- The European Commission has published its proposals for the next European Framework Programme for Research and Innovation, called "Horizon 2020". This will run from 2014 to 2020 with a proposed total budget of EUR 80 billion. Horizon 2020 will consist of three specific pillars, with the European Research Council (ERC) as part of the first pillar (called "Excellent science") together with Marie Curie funding, Future and Emerging Technologies (FET) and Research Infrastructures.
- A special initiative between BBSRC and the Scottish Government entitled 'Food security and living with environmental change' was launched in 2011.

- 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.

UK Arabidopsis Research Network

- GARNet represents UK Arabidopsis researchers via a committee of 10 elected members and two ex-officio members, Prof Sean May and Dr Sabina Leonelli. Each year new members are elected to the GARNet committee as others rotate off. In December 2011 John Doonan, Anthony Hall, Heather Knight and Cyril Zipfel were elected to the committee for a three year term to join the current committee of Malcolm Bennett, Jim Beynon, Juliet Coates, Smita Kurup, Ian Moore, Jim Murray and Nick Smirnoff. GARNet is currently chaired by Jim Murray (since 1st January 2011).
- GARNet can be found online at www.garnetcommunity.org.uk/
- 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 (2009-2012) at the University of Warwick.

UK Plant Science Federation (UKPSF)

The UK Plant Sciences Federation was established in late 2011. It includes representatives of a number of stakeholders, including plant research communities (MONOGRAM, UK-Brassica Research Community/OREGIN, UK-Solanaceae and GARNet), learned societies, industrial groupings and plant science educationalists with the aim to provide 'one voice for UK Plant Science' in order to help build a stronger UK plant research base.

UKPSF Member Organisations are listed online <http://www.societyofbiology.org/aboutus/special-interest-groups/ukpsf/ukpsfmembers>

The UKPSF is a special interest group of the Society of Biology (<http://www.societyofbiology.org/aboutus/special-interest-groups/ukpsf>)

The aims of the UKPSF are

- Increase the understanding and perceived importance of Plant Science amongst government, funders, industry and society in general
- Formulate a coordinated strategy and vision for Plant Science in the UK that can be utilised to inform policy

- Help to improve the general funding environment for UK Plant Science Research and Education
- Create a forum for debate that is independent and inclusive
- Provide a focus and contact point for UK Plant Science
- To educate and inspire the next generation of Plant Scientists

In early 2012 the Executive Committee of the UKPSF was established. Members include;

Jim Beynon, GARNet/University of Warwick

Ian Crute, Agriculture and Horticulture Development Board

Sandy Knapp, Linnean Society/Natural History Museum, London

Celia Knight, Gatsby Plants Summer School

Penny Maplestone, British Society of Plant Breeders

Ginny Page, Science and Plants for Schools

Sarah Perfect, Syngenta

A UKPSF operates with financial support from the Society for Experimental Biology and The Gatsby Charitable Foundation

The UKPSF can be found online at '-PlantSci' at www.plantsci.org.uk. The website aims to support Plant Scientists in their day to day research by providing the latest funding opportunities, news and information all under one leaf. PlantSci is also trying to embrace modern technology to help achieve its goals and has a presence on twitter (twitter.com/plantscience)!

UK Meetings

Upcoming Meetings

- 'Making data accessible to all'. In collaboration with the Social Sciences ESRC genomics centre at the University of Exeter, GARNet will hold a 2-day workshop to address the issues surrounding data donation, publication and use from the viewpoint of plant biologists, with the aim to produce a series of recommendations about the problems involved in data dissemination in plant science, which could be used to inform funders/publishers' policies.

Past Meetings

- UK Plant Science Meeting, 18-19th April, John Innes Centre, Norwich. This was the first meeting of the Federation of Plant Science and showcased the wealth of UK Plant Science.
- 'Next generation Sequencing in Arabidopsis - Research Workshop, 17th April 2012 John Innes Centre was organised by the BBSRC Genome Analysis Centre and aimed to outline the Next Generation Sequencing platforms and pipelines at The Genome Analysis Centre (TGAC) and how they can further Arabidopsis research.
- Centre for Plant Integrative Biology (CPIB) study group, 3-6th January 2012, Nottingham. Mathematicians worked along with biologists for three days to mathematically model plant biology process.
- 6th and 7th September 2011, GARNet Meeting entitled 'Dynamic biology - New Levels and New Dimensions of Regulation'

'was held at the University of Cambridge. Thanks to a collaboration with the Journal of Experimental Botany video recordings of the talks are available at www.lancs.ac.uk/other/bsajxb/JXB/

Notable Research Breakthroughs in the UK

- Angel A, Song J, Dean C, Howard M (2011) A Polycomb-based switch underlying quantitative epigenetic memory. *Nature* 476:105-8.
- Daniel J. Gibbs (2011) Homeostatic response to hypoxia is regulated by the N-end rule pathway in plants. *Nature* doi:10.1038/nature10534
- Jun Fan, Casey Crooks, Gary Creissen, Lionel Hill, Shirley Fairhurst, Peter Doerner, and Chris Lamb (2011). *Pseudomonas* sax Genes Overcome Aliphatic Isothiocyanate-Mediated Non-Host Resistance in *Arabidopsis*. *Science* 1185-1188. [DOI:10.1126/science.1199707]
- M. Shahid Mukhtar, Anne-Ruxandra Carvunis, Matija Dreze, Petra Epple, Jens Steinbrenner, Jonathan Moore, Murat Tasan, Mary Galli, Tong Hao, Marc T. Nishimura, Samuel J. Pevzner, Susan E. Donovan, Lila Ghamsari, Balaji Santhanam, Viviana Romero, Matthew M. Poulin, Fana Gebreab, Bryan J. Gutierrez, Stanley Tam, Dario Monachello, Mike Boxem, Christopher J. Harbort, Nathan McDonald, Lantian Gai, Huaming Chen, Yijian He, European Union Effectoromics Consortium, Jean Vandenhoute, Frederick P. Roth, David E. Hill, Joseph R. Ecker, Marc Vidal, Jim Beynon, Pascal Braun, Jeffery L. Dangl (2011) Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. *Science* (333): 596-601

United States

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

NAASC (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 (e.g. the 2011 meeting at the University of Wisconsin-Madison.) NAASC's community service efforts include: (1) fundraising to support ICAR including participation by young scientists, under-represented scientists, and others, (2) serving on relevant advisory committees and boards, (3) acting as leaders and participants for community-related initiatives, and (4) acting as liaison between researchers, funders and other relevant groups such as MASC.

1 NAASC members serve four-year terms and are elected by the community with two of eight members rotating off annually. In 2012 the NAASC election will follow the Vienna ICAR; NAASC members will use the meeting for networking to try and increase voter participation. Mark Estelle and Jane Glazebrook conclude their terms at the 2012 ICAR. Continuing members include: Xinnian Dong (Duke University), Blake Meyers (University of Delaware), Wolf Frommer (Carnegie Institution for Science), Dominique Bergmann (Stanford University), Nick Provart (University of Toronto, Canada), and Jose Alonso (NC State University.) Blake Meyers will be the new NAASC president and NAASC representative to MASC for 2012-2013.

2 Community support obtained by NAASC in the past year: Xinnian Dong secured an NSF grant in support of ICAR 2011 for participation by early career scientists, under-represented minorities, faculty at HBCUs and MSIs, and several invited speakers. Blake Meyers received awards from the U.S. Departments of Agriculture (USDA) and Energy (DOE) in support of ICAR 2011 for participation by early career scientists and several invited speakers. Blake Meyers also was awarded a four-year grant from the NSF to support development of the International Arabidopsis Informatics Consortium (IAIC, see below for details.)

3 NAASC Honors, Awards, and Distinctions: (1) 15 plant scientists (including 8 current or former NAASCCers) were selected to receive the first Howard Hughes Medical Institute/Gordon and Betty Moore Foundation (HHMI-GBMF) awards which provide 5 years of significant funding to boost innovative fundamental plant biology research (with the possibility of a 5 year renewal). Current NAASC members among the awardees are Dominique Bergmann, Xinnian Dong, and Mark Estelle. Former NAASC member awardees: Philip Benfey (Duke University), Xuemei Chen (UC Riverside), Jeff Dangl (UNC-Chapel Hill), Joe Ecker (Salk Institute), and Elliot Meyerowitz (CalTech) <http://www.hhmi.org/news/plantscience20110616.html>. (2)

New Fellows of the American Association for the Advancement of Science (AAAS): Xinnian Dong (current NAASC), Xuemei Chen and Rick Amasino (former NAASC) were elected as Fellows of AAAS in November 2011. (3) Genetics Society of America: Joe Ecker received the 2011 George W. Beadle award and Joanne Chory received the 2012 GSA medal. Both are former NAASC members.

- 4 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 IAIC (see below).
- 5 2011 ICAR (Wisconsin, USA): NAASC organized last year's main Arabidopsis meeting at the University of Wisconsin-Madison. This was the first North American ICAR since Montreal in 2008. The meeting was quite successful (see below for a meeting summary.)
- 6 2012 ICAR (Austria): Dominique Bergmann submitted a proposal to NSF requesting support for six under-represented minorities, ten early career scientists, and four invited speakers for the 'MASC: Emerging topics in Arabidopsis research' session. The award decision was made recently and NSF awarded the full request.
- 7 Committee service: Mark Estelle and Jane Glazebrook co-chaired the ICAR 2011 conference organizing committee which included the remaining NAASC members and the NAASC Coordinator. Jose Alonso, Nick Provart, and Blake Meyers serve on the Arabidopsis Biological Resource Center (ABRC) advisory committee.

The 2011 International Conference on Arabidopsis Research at the University of Wisconsin-Madison

The 2011 ICAR returned to Madison, Wisconsin, a site of historical significance to the Arabidopsis community. This was the 9th ICAR in Madison (counting from 1995 when ICARs became annual events) and included 825 participants. It was due in large part to the significant efforts of NAASC members (with service starting in 1992) and the generous support of U.S. funding agencies, (especially the National Science Foundation) that an annual ICAR has been achieved. In 2007 the Multinational Arabidopsis Steering Committee (MASC) decided to move to a 3-year schedule to diversify meeting effort, location, and costs, and facilitate participation by scientists in other regions. The ICAR now rotates between North America, Europe, and Asia/Pacific Rim. The 22nd ICAR conference co-chairs were Mark Estelle and Jane Glazebrook; Joanna Friesner, NAASC Coordinator, acted as lead organizer and the rest of NAASC served on the organizing committee. Details and the program can be found at: <http://arabidopsis.org/news/abstracts.jsp>

ICAR 2011 highlights

- 1 825 participants; 16 platform symposia; 40 Invited Speakers (in 2 keynote lectures, 6 plenary and 10 concurrent sessions); 50 Speakers selected from abstracts; 7 community-organized workshops (with 42 additional talks); 510 posters in 3 poster sessions; 21 exhibitors, 14 sponsors, and 6 advertisers. Keynote Lectures by Joanne Chory (Salk Institute, USA) and Sophien Kamoun (Sainsbury Lab, John Innes Centre, UK). Presentation of the 2011 Genetics Society

of America George W. Beadle award to Joe Ecker (Salk Institute, USA) by Elliot Meyerowitz (Cal Tech, USA).

- 2 First ICAR 5K Run/Walk: the 'Weed Stampede' took place on the shores of Lake Mendota on the final morning of the conference. First place male/female: Fabrice Besnard (France) and Katie Greenham (USA); Second place male/female: Josh Steffen (USA) and Brittany McDaniel (USA); third place male/female: Chris Van Schie (USA) and Siobhan Brady (USA); fourth place male/female: Thomas Altmann (Germany) and Louse Lieberman (USA), and fifth place male/female: Adan Colon-Carmona (USA) and Magdalena Weingartner (Germany).
- 3 'Born to be Wild-Type' Arabidopsis World Tour Conference T-shirt
- 4 Conference banquet at the new Union South 'Sett hall'- karaoke, open bar, dancing, iPad2 giveaway, bowling, pool, video games, rock-climbing, and lots of networking and fun.

The International Arabidopsis Informatics Consortium (IAIC) - Update and Progress

The IAIC is a community consortium that was initiated in response to growth in the size and complexity of Arabidopsis data, combined with an expected reduction in funding for TAIR, the primary Arabidopsis information database. The goal of the IAIC is to develop a novel, integrated, international framework with which to address the informatics needs of the Arabidopsis community, while providing a smooth transition from the current TAIR-based central database structure to this stable, long-term structure. The composition and design of this resource are underway and will require significant input from members of the international Arabidopsis community.)

1. IAIC Update

- Scientific Advisory Board, confirmed in February 2012. Initial members, serving staggered terms (to be determined at ICAR 2012) are:
 - i. Gloria Coruzzi- US
 - ii. Kazuki Saito- Japan
 - iii. Magnus Nordborg- Austria
 - iv. Mark Estelle- US
 - v. Mark Forster- UK
 - vi. Paul Kersey- UK
 - vii. Xuemei Chen- US
- Community input via the Steering Committee (SC), established in June 2010. Current members are: Blake Meyers (Interim IAIC Director), Ruth Bastow, Jim Beynon, Volker Brendel, Rion Dooley, Erich Grotewold, Nick Provart, Dan Stanzione, and Doreen Ware (Jim Carrington, an original SC member, had to step down due to new commitments.)
- Community website: www.arabidopsisinformatics.org/
- Community presentations at: (1) 2010 ICAR in Yokohoma, Japan, (2) PAG 2011 in San Diego, CA; (3) PAG 2012 in San Diego, CA. Upcoming: ASPB 2012 (Austin, Texas) and ICAR 2012 (Vienna, Austria)

- Organization of the IAIC Design Workshop (DW) in December 2011 to initiate an international community discussion on the design of the Arabidopsis Information Portal (AIP). This AIP will be the primary interface providing dynamic access to core and key non-core resources, and links to 'boutique databases'. It will be the central hub for coordination of Arabidopsis informatics that defines standards for data storage, access, and inter-connectivity. It is expected to integrate and continue the key functions provided by TAIR, while going beyond those core activities to address a broad range of informatics challenges. (Further Design Workshop details are at the IAIC webpage.)

Goals for the Design Workshop

- Understand the need for the AIP, and how it will address the needs of the Arabidopsis community.
- Identify and prioritize the technical challenges in building the AIP and the data that we must integrate.
- Learn what we can leverage from existing, planned and other funded resources.
- Start to identify teams and collaborators who could work together to build parts of the AIP, including core and non-core components.
- Prepare ideas and identify funding opportunities that could lead to grant proposals in the near term.
- Start to develop the standards to allow boutique databases to "plug in" to the AIP architecture.

Presentations at the DW to provide critical background, planning, or present projects as models

- Three IAIC "Working Groups" presented the results of discussions held in advance of the Design Workshop: Engineering/Architecture/Infrastructure; Modules/Use Cases; Standards/Ontologies
- Francis Ouellette (Ontario Institute for Cancer Research, Canada), Mark Forster (Syngenta, UK), Dan Stanzione (iPlant Collaborative, USA) and Magnus Nordborg (University of Southern California, USA and Gregor Mendel Institute, Austria)

Desired outputs of the DW

- From an engineering perspective, what is the minimal number of design options on which the AIP can coalesce?
- Identification of one or possibly two teams to lead AIP development. Timeline: AIP development of paramount importance (goal to develop a plan between Dec. 2011 and July, 2011) followed by core modules and guidelines for their development.
- White paper (ideally disseminated in a journal publication) aimed at an audience of biologists and funders that relates the process, positions and outcomes of the DW.
- Describe the technical requirements for the AIP that would be useful to teams interested in building the AIP.
- Community engagement via the SC and the new Scientific Advisory Board (SAB) to drive forward AIP development.

2. Rationale for development of the IAIC: Arabidopsis informatics needs are growing quickly with new data types and a rapidly increas-

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

3. IAIC Initiation: The IAIC was formed following two international community workshops held in 2010, which considered the future bioinformatics needs of the Arabidopsis community and other science communities that depend vitally on Arabidopsis resources. Of the 50+ participants, Blake Meyers (NAASC) was nominated to lead the development of the IAIC. To support this effort, Meyers (and other key workshop participants) submitted a Research Coordination Network proposal to the NSF (funded: 6/15/2011). Support is intended to foster collaborations, including across international boundaries, and encourage collaborative technologies and development of community data and meta-data standards, among other goals.

Key Deliverables from the workshops

- Publication: An international bioinformatics infrastructure to underpin the Arabidopsis community. Plant Cell 2010 22(8):2530-6 (www.ncbi.nlm.nih.gov/pubmed/20807877)
- NSF proposal submitted by Blake Meyers and funded for four years to develop the IAIC. Award Abstract #1062348. RCN: An International Arabidopsis Informatics Consortium

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

- 2011 Plant Science Program HHMI-GBMF Investigators: Philip Benfey, Dominique Bergmann, Simon Chan, Jeff Dangl, Xinnian Dong, Joe Ecker, Mark Estelle, Rob Martienssen, Elliot Meyerowitz, Craig Pikaard, Keiko Torii
- Election to the National Academy of Sciences (NAS) 2011- Steve Jacobsen, Sakis Theologis
- Election to the American Association for the Advancement of Science (AAAS) 2011- Z. Jeffrey Chen, Richard M. Amasino, Xuemei Chen, Xinnian Dong, Sheng Yang He, Sheila McCormick, Jack C. Schultz, Steve Rodermeier, Gretchen Hagen, and Greg Howe
- The Genetics Society of America (GSA): 2011 George W. Beadle Award: Joe Ecker. 2012 GSA Medal: Joanne Chory
- The American Society of Plant Biologists (ASPB): Sean Cutler: 2011 Charles Albert Shull Award; Steve A. Kay- 2011 Martin Gibbs Medal. Ravi Maruthachalam: 2011 Early Career Award

Highlights from US Arabidopsis Research Groups

Several research advances over the last year deserve special mention. These include large scale, multi-investigator and multidisciplinary projects with impacts on the research capabilities of many in the scientific community, as well as work from individual groups that overturned long-held ideas; studies that revise our ideas of maternal control, highlight ways in which exploiting plant and animal systems

together lead to breakthroughs that eluded each field alone or conversely, demonstrate ways in which assumptions about behavior derived from animal experiments proved to be misleading.

- First, a recent report using hybrid Arabidopsis accessions and a zygotic reporter provides compelling evidence that in Arabidopsis, the maternal and paternal genomes contribute about equally to the early embryonic transcriptome and that zygotic gene products primarily control early embryogenesis (1). These results were unexpected given the paradigm from animal embryogenesis (and supported by an earlier Arabidopsis publication (2)), in which maternal gene products predominantly control the process. By taking advantage of sequenced ecotypes and reciprocal crosses, Nodine and Bartel were able to control for the contributions of maternally-derived seed coat mRNA which masked the roughly equal parental contributions.
- Chen, Frommer, and colleagues used an interesting technique to shed light on a longstanding plant mystery: how sucrose is relocated from the site of production (mesophyll cells) to the site of translocation throughout the plant (phloem cells). Taking advantage of an apparent lack of sucrose transporters in human cells, the authors developed a FRET-sensor heterologous expression system in human embryonic kidney cells to screen a number of candidate membrane genes, including the previously identified SWEET family of sucrose transporters (3). The screen revealed that one clade, AtSWEET10 to 15, specifically permit the accumulation of sucrose. Mutant, expression, and localization data further demonstrated that AtSWEET11 and 12 proteins are sucrose-specific transporters involved in sucrose efflux into phloem cells, and confirmed the sucrose transport results using rice orthologs of SWEET proteins.
- Genome wide association studies (GWAS) have become a popular approach in human genetics because they take advantage of the genetic and phenotypic variation present in existing populations. Recent side-by-side publications provide evidence for a genetic basis for climate adaptation in Arabidopsis. Hancock, Bergelson, and colleagues examined GWA for 107 phenotypes and 13 climate variables in a collection of ~1000 accessions genotyped for 215,000 SNPs (4). They identified a number of candidate genes potentially involved in adaptation to climate and their analysis allowed them to predict the reproductive success of 147 accessions grown in a common garden. Fournier-Level, Wilczek, and colleagues examined GWA for a set of Arabidopsis lines grown at four sites across Europe and genotyped for ~ 213,000 SNPs (5). The authors evaluated survival and reproductive success across geography and found that climate significantly influences the alleles present in local populations. These studies suggest that GWAS will be of considerable value in ecological and evolutionary genetic studies of Arabidopsis.
- Finally, we would like to draw attention to a recent publication describing the first large-scale experimental interactome protein-protein interaction map for *Arabidopsis thaliana* (6). Binary interactions were tested using a high throughput yeast two-hy-

brid system for approximately 8000 open-reading frames representing ~ 30% of predicted Arabidopsis protein-coding genes. Analyses by the Interactome Consortium reported about 6200 interactions between ~ 2700 proteins. Considering a number of parameters, the authors estimate the size of the complete Arabidopsis interactome to be 299,000 (+/- 79,000) binary protein-protein interactions. Thus, even though the current report of about 2% of estimated interactions is just the tip of the protein interaction iceberg, these data are exciting because they significantly increase the body of knowledge of plant protein interactions, facilitate systems analyses, and provide fodder for new experiments. We can expect an increase in the characterization of the many Arabidopsis proteins whose functions are currently unknown.

- 1 Nodine, M.D. and Bartel, D.P. Maternal and paternal genomes contribute equally to the transcriptome of early plant embryos. (2012) *Nature* 482, 94-97.
- 2 Autran, D. *et al.* Maternal epigenetic pathways control parental contributions to Arabidopsis early embryogenesis. (2011) *Cell* 145, 707-719.
- 3 Chen, L-Q. *et al.* Sucrose efflux mediated by SWEET proteins as a key step for phloem transport. (2012) *Science* 335, 207-211.
- 4 Hancock, A.M. *et al.* Adaptation to climate across the Arabidopsis thaliana genome. (2011) *Science* 334, 83-86.
- 5 Fournier-Level, A. *et al.* A map of local adaptation in Arabidopsis thaliana. (2011) *Science* 334, 86-89.
- 6 Arabidopsis Interactome Mapping Consortium. Evidence for network evolution in an Arabidopsis Interactome map. (2011) *Science* 333, 601-607.

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