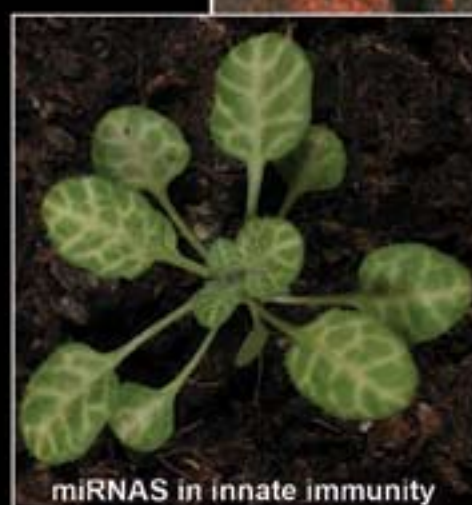
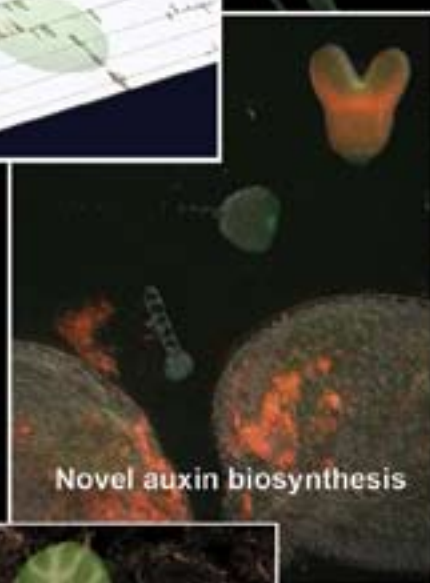
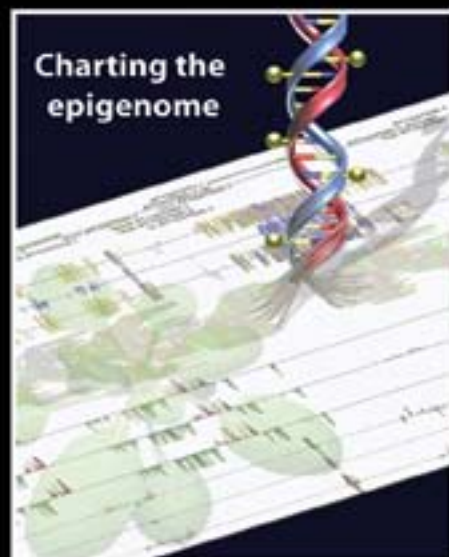


# The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project Annual Report 2009



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The Multinational Arabidopsis Steering Committee—June 2009

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**Charting the Epigenome**

Image credit: Ryan Lister and Joe Ecker (Salk Institute for Biological Studies, San Diego, CA, USA)

Lister R, O'Malley RC, Tonti-Filippini J, Gregory BD, Berry CC, Millar AH, and Ecker JR. Highly integrated single-base resolution maps of the epigenome in *Arabidopsis*. *Cell*, May 2 2008; 133(3): 523-36

**Novel Shoot Branching Inhibitor**

Image credit: Phil Brewer (ARC Centre of Excellence for Integrative Legume Research, University of Queensland, Brisbane, Australia)

Strigolactone inhibition of shoot branching. Gomez-Roldan V, Fermas S, Brewer PB, Puech-Pagès V, Dun EA, Pillot JP, Letisse F, Matusova R, Danoun S, Portais JC, Bouwmeester H, Bécard G, Beveridge CA, Rameau C, and Rochange SF. *Nature*, Sep 11 2008 455(7210): 189-94

**Novel Auxin Biosynthesis**

Image credit: Jose Alonso (N.C. State University, Raleigh, North Carolina, USA)

Stepanova AN, Robertson-Hoyt J, Yun J, Benavente LM, Xie DY, Dolezal K, Schlereth A, Jürgens G, and Alonso JM. TAA1-mediated auxin biosynthesis is essential for hormone crosstalk and plant development. *Cell*, April 4, 2008; 133: 177–91

**Genetic Incompatibility**

Image credit: Olivier Loudet (INRA, National Institute for Agronomical Research, Versailles, France)

Reference: Bikard D, Patel D, Le Metté C, Giorgi V, Camilleri C, Bennett MJ and Loudet O. Divergent evolution of duplicate genes leads to genetic incompatibilities within *A. thaliana*. *Science*, Jan 30 2009; 323(5914): 623-6

**miRNAs in Innate Immunity**

Image credit: Olivier Voinnet (IBMP-CNRS, Strasbourg Cedex, France)

Reference: Navarro L, Jay F, Nomura K, He SY, and Voinnet O. Suppression of the microRNA pathway by bacterial effector proteins. *Science*, Aug 15 2008; 321(5891): 964-7

**Unraveling Heavy Metal Tolerance**

Image credits: Josef Bergstein (Max Planck Institute of Molecular Plant Physiology, Golm, Germany) and Ute Kraemer (University of Heidelberg, Heidelberg, Germany)

Hanikenne M, Talke IN, Haydon MJ, Lanz C, Nolte A, Motte P, Kroymann J, Weigel D, and Krämer U. Evolution of metal hyperaccumulation required cis-regulatory changes and triplication of HMA4. *Nature*, May 15 2008; 453: 391-6

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# Foreword to the Report

This is the 2008/2009 MASC annual report on the status of the Functional Genomics Project. In 1990, an ad hoc committee composed of nine scientists from the United States, Europe, Japan and Australia prepared a report that outlined a plan for international cooperation in studies of the plant *Arabidopsis thaliana*. The goal of the Multinational *Arabidopsis thaliana* Genome Research Project was to understand, at the molecular level, the physiology, biochemistry, growth and development of a flowering plant. This goal would be addressed by determining the complete sequence of the *Arabidopsis* genome by the year 2000, concurrent with the development of vital resources and collaborations. The international community of scientists agreed to cooperate on several objectives including: the identification and characterization of the structure, function, and regulation of *Arabidopsis* genes; development of technologies for genome studies; establishment of biological resource centers; development of an informatics program to facilitate exchange of research results; development of human resources; and support of workshops and symposia. 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.

Owing to unprecedented multinational cooperation, the reference *Arabidopsis* genome was successfully completed and publicly released on schedule. Following this historic event, a committee of scientists representing the *Arabidopsis* research community met in 2001 to propose the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project, 'the second-phase of the far-reaching vision' by those who launched the Genome Project. This project had an even more ambitious goal: to determine the function for every *Arabidopsis* gene by the year 2010. The ultimate goal remains the same: a complete understanding of the biology of a flowering plant, using *Arabidopsis* as the experimental reference system.

Since the Functional Genomics Project was proposed in 2001, international projects have generated vast datasets and resources and produced numerous breakthroughs in understanding the fundamental processes underlying plant growth and development. This is the result of the interplay of a variety of factors including the inherent properties of this remarkable organism, the synergistic development of a powerful set of tools in *Arabidopsis*, the easy access to various stocks and other key reagents, the openness and collegiality of the *Arabidopsis* community and the generous support from

various government programs. Indeed, we have entered a new era of plant biology research allowing questions to be addressed at an unprecedented scale, including studies at the level of the genome, transcriptome, proteome, metabolome and multiple other 'omic' approaches. This presents both unparalleled opportunities as well as important challenges that need to be met to continue to promote discovery in this reference plant. As the US 2010 project and other affiliated programs wind down, there needs to be funding mechanisms in place for support of large-scale projects, tool development, and computational modeling. 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. This is essential in order to fully leverage the impressive gains obtained thus far through *Arabidopsis* research and to maintain cutting edge research in plants.

This report details progress made over the last year by the international *Arabidopsis* functional genomics community including highlights from intensive efforts in basic research and advances in translating basic to applied research. When evaluating the success of *Arabidopsis* as a means of advancing applied research, as well as its future potential, it is important to keep the realities of public vs. private research and the relatively long timeframe from discovery to product in mind. 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. The importance of basic *Arabidopsis* research cannot be understated and it is clearly an invaluable reference to applied research efforts. 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.

**It is clear that advances in *Arabidopsis* research lay the foundation for the understanding of plant biology required to help meet the substantial challenges faced by agriculture in an environmentally sustainable manner. Success in acquiring a fundamental understanding of plant biology, and for translating basic plant knowledge to other systems, relies on maintaining strong global collaboration and funding streams. At this juncture, it is essential to maintain and strengthen support for both large-scale, high-throughput collaborative projects and more focused individual-lab studies in order to maximize the gains realized by the community and to ensure future success.**

The Multinational *Arabidopsis* Steering Committee

June 2009

# Executive Summary

The increasing demands of a growing, prosperous world for improved agricultural products including food, fiber and fuel, intensifies the need for a thorough understanding of the basic biology and ecology of plants. As the first plant to have its entire nuclear genome sequenced, *Arabidopsis thaliana* has become the most important model system for plant biology and a vital resource for the study of other multicellular organisms. Arabidopsis research has increasingly impacted our understanding of other plants and the intent has always been that the knowledge gained from this reference plant would serve to advance understanding about other plant species, particularly crop species, and thus translate into new or improved plant products and increased agricultural productivity. The transfer of knowledge from Arabidopsis to other plant species is accelerating due to the efforts of a vibrant research community and the leveraging of advances and resources made over the last 15 years especially that inform studies in plants of economic importance. Arabidopsis has shifted from model to reference organism - the plant in which the fundamentals are established and to which other plants are compared. Arabidopsis is now uniquely poised to address biological questions that range from the molecular to the ecosystem levels and resources currently available and under development will allow rapid experimentation to answer existing and future challenging questions. However, the utility of Arabidopsis extends far beyond the plant realm; researchers studying other organisms such as humans, flies, worms, fungi, and mice increasingly rely on the extensive collection of Arabidopsis resources and knowledge to inform their own research. Therefore, continued and expanded funding and international collaboration is critical to future success; maintaining and strengthening ties between researchers in all parts of the world, and between basic and applied scientists, are necessary to create the synergy needed to effectively meet the health and agricultural challenges of tomorrow.

The highly active and enthusiastic Arabidopsis community around the world continues to attract researchers; according to The Arabidopsis Information Resource (TAIR) there are currently about 19,000 Arabidopsis researchers in approximately 7,300 laboratories worldwide. 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 nine 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 research following more than two decades of increasing publication rates. 2,941 Arabidopsis peer-reviewed research papers were published in 2008, nearly a 10-fold rate increase over 1993 in which 306 peer-reviewed papers were published (Fig. 1, page 10), and an increase of more than 50-fold in the last 20 years.

This report includes summaries of just a few research highlights in the past year (pages 10-14) including:

- Discovery of a new mode of bacterial infection resistance with implications for human pathogenesis
- Identification of a long-sought novel plant hormone
- Discovery of the first paternal effect gene in plant embryogenesis
- Publication of in-depth maps of Arabidopsis epigenetic modifications
- Identification of a key component in a novel auxin biosynthesis branch
- Insights into genetic incompatibility with implications for speciation processes
- Improvements to genome annotation by proteogenomics
- Insights into modes of heavy metal tolerance and sequestration

## 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. Taking US utility patents as an example, the number of Arabidopsis patents continues to increase: in 2008 there were 788 utility patents referencing Arabidopsis compared to 18 in 1993, a nearly 45-fold increase (See Fig. 3, page 20). It has been estimated to take up to 12 years or more to navigate the commercialization pipeline from initial discoveries to agricultural products. Press releases from companies like Monsanto and SemBioSys reveal the usefulness of Arabidopsis to industry and suggest the upcoming decade will likely yield a number of commercial advances based on Arabidopsis studies (see Broader Impacts, page 19). In this report we have chosen to highlight just 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 19-23):

- Plant-based recombinant human insulin enters clinical trials
- Folate-fortified foods address nutrient deficiency
- Salt-tolerant bread wheat to cope with changing environments
- Higher water-use efficiency rice with increased biomass
- Genomic screens to identify stress-tolerance plant genes

### New Initiatives Announced This Year

- **The Netherlands-** The Dutch Government approved the second phase of the CBSG project which supports Arabidopsis research, including bioinformatics and enabling technologies, with €4.5 million.
- **UK-** BBSRC and industry partners have made a £27 million investment to establish a Sustainable Bioenergy Centre to make sustainable bioenergy an economically and socially viable alternative to fossil fuels. Arabidopsis researchers are involved in a number of the programs. BBSRC has also launched a new national Genome Analysis Centre to analyze plant, animal and microbial genomes.
- **China-** The National Science Foundation of China initiated a new 5 year initiative on epigenetics and stem cell research, including several Arabidopsis projects.

### Progress Towards The Goals Of The Multinational Coordinated Functional Genomics Project

Since 2004, 'thermometer' illustrations have provided a visual way to track progress and describe a function for every Arabidopsis gene (see Fig.2 pages 17-18). The availability of high-quality genetic resources will facilitate future studies and contribute to our expanding pool of knowledge. Current progress includes:

- Sequence-confirmed homozygous mutant plant lines: with two or more insertions = 8,763 genes; with one confirmed homozygous allele insertion = an additional 7,611 genes, giving a total of 16,374 unique genes, or 57%, with at least one confirmed homozygous insertion.
- As of May, 2009, seeds from 26,285 homozygous insertion lines have been received by ABRC; the first 8,889 lines were shipped to users in Spring, 2008 and 11,000 will be shipped in 2009. Pools of confirmed lines will be available in 2009.
- 26,896 of 28,523 (94%) unique Arabidopsis genes contain at least one sequenced insertion element. Newly procured since last year are an additional 12.5% of genes with two homozygous insertions and an additional 12.4% with one homozygous insertion.
- Isolation of full-length cDNAs for 20,821 (73%) of genes; clones of 19,799 are currently being distributed.
- Availability of fully-sequenced ORF clones for 16,127 (57%) genes and partially-sequenced clones for 1,136 more.

- 27,103 (95%) of 28,523 genes whose expression has been detected by cDNA, EST, MPSS, sage, microarray or smRNA data

### MASC Subcommittees

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

- **Clone-based Functional Genomics (ORFeomics)-** Progress towards obtaining full length cDNAs and open reading frame clones for all annotated Arabidopsis protein coding gene continues to be tabulated Table 1 (page 25). Recent goals include developing 'functional' clone sets for approaches like *in planta* overexpression and interactome mapping.
- **Proteomics-** Committee members published a report in the Journal of Proteome Research that provides a series of resources for plant proteome researchers. The Subcommittee held a Proteomics workshop at the 2008 Arabidopsis meeting (Montreal, Canada) and will hold another in 2009.
- **Systems Biology-** The committee chair organized the "Frontiers in Plant Systems Biology" workshop at the 2008 Arabidopsis conference (Montreal, Canada.)
- **Phenomics-** Subcommittee members continue to track progress by the various phenomics efforts underway worldwide including: amiRNAs, insertion lines, SNP sequencing, annotation/ontologies, meetings, phenotyping facilities, databases and phenotyping platforms.
- **Natural Variation and Comparative Genomics-** The most notable community advances continue to be in 'omics technology: whole genome draft sequence of *A. lyrata* has been released and many Arabidopsis accessions are currently being sequenced to determine variation in genomes and transcription patterns.

### MASC Recommendations And Short-Term Goals For The Next Year

- Work towards the completion of a reference collection of homozygous insertional lines for all Arabidopsis genes, ideally, including two alleles for all genes. Since genetic redundancy continues to pose significant limitations to genetic approaches, additional facile approaches are needed, such as the development of artificial microRNAs and RNAi resources to reduce the function of multiple target genes.
- Support projects that work towards obtaining detailed and dynamic patterns of gene expression and epigenetic modifications across spatial, developmental, and environmental variables.
- Continue to expand the large scale analysis of proteins, including the interactome, the description of changes in protein modifications such as phosphorylation and the analysis of the spatial and temporal pattern of expression of the proteome. These data need to be incorporated into accessible and compatible databases to enable system biology approaches.



- Continue to develop methods for high throughput analysis of metabolites across spatial, developmental, and environmental variables, ultimately including analysis at single cell resolution.
- Support the development of a complete, readily accessible collection of Arabidopsis Open Reading Frames (ORFs).
- Continue to address the roles of the large number of genes in Arabidopsis with relatively little functional information.
- Continue to develop large collections of transgenic lines expressing fluorescently-tagged proteins, or other methods to visualize the intracellular localization of all the proteins in Arabidopsis.
- Work towards the goal of improving curation approaches and making databases compatible; facilitate the storage and integration of phenotypic data, expression data etc.
- The community should continue to work with the iPlant Collaborative, and other similar groups, to develop the mathematical tools and informatics infrastructure necessary to enable new conceptual advances, integrative studies, and systems biology in Arabidopsis.
- Expand the collection of sequenced wild accessions and species closely related to Arabidopsis to at least several hundred.
- Continue to expand our understanding of the multitude of signaling pathways that act in plants and how these interact to modulate plant growth and development across various environmental contexts.

# Progress and Activities of Multinational Arabidopsis Functional Genomics Projects

## Progress and activities of the MASC in 2008/2009

In 2008, Joe Kieber (University of North Carolina-Chapel Hill, USA) succeeded Xing Wang Deng (Yale University, USA) to become the MASC chair and Keith Lindsey (Durham University, UK) became co-chair. Dr. Lindsey will become the new MASC chair when Dr. Kieber steps down following the annual International Conference on Arabidopsis Research (ICAR) in July, 2009. In 2006, MASC members recommended that The Arabidopsis Information Resource (TAIR) facilitate ICAR abstract submission to increase awareness of Arabidopsis genes under study and associate abstracts within TAIR to the genes listed, and to assist in the effort to monitor progress toward the 2010 initiative goal of understanding a function of all Arabidopsis genes. For the 2007 ICAR, 369 of 776 submitted abstracts contributed 1,722 distinct AGI codes, including 535 loci that were not already associated to literature in TAIR. In 2008, 336 of 628 submitted abstracts contributed 3,060 total distinct AGI codes including 926 loci that were not already associated to literature in TAIR at that time. The increasing contributions by conference attendees reflects the increased understanding of the functions of the genes in Arabidopsis and the ICARs provide the community with a forum to disseminate these results.

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, 2008 and March 1, 2009, 45 different MASC pages were viewed 11,565 times, an average of about 965 views a month. The top-viewed page (3,858 views) contains information on projects funded through the US NSF 2010 project ([www.arabidopsis.org/portals/masc/projects.jsp](http://www.arabidopsis.org/portals/masc/projects.jsp)). Another frequently viewed page was the Coordinator's Journal (described below) which received more than 2,000 views over the last year.

MASC subcommittees, proposed in 2002, were established to help track progress towards the goals outlined in the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. No new subcommittees were proposed over the last year, however, one subcommittee changed chairs: Systems Biology, previously chaired by Philip Benfey, is now co-chaired by Rodrigo Gutierrez and Andrew Millar. This report includes reports from 5 of 7 current MASC subcommittees: cDNAs and Clone-based Functional Proteomics (ORFeomics), Natural Variation and Comparative Genomics, Phenomics, Proteomics, and Systems Biology. No reports were submitted by Bioinformatics or Metabolomics due to lack of subcommittee activity. The structure and relevance of the MASC subcommittees will be up for discussion at the annual

MASC meeting in July, including proposals for reorganization or dissolution of those that remain inactive. Rodrigo Gutierrez, co-chair of Systems Biology, organized a workshop entitled 'Frontiers in Plant Systems Biology' that was held at the 19<sup>th</sup> ICAR in Montreal, Canada, July, 2008. The workshop goal was to bring together groups that produce, integrate and model data from a systems perspective. Harvey Millar and Klaas van Wijk, co-chairs of Proteomics, along with committee member Joshua Heazlewood, also organized a workshop at the ICAR entitled 'Plant Proteomics- Tools, Approaches, Standards and Breakthroughs in Studying the Proteome.' Proteomics plans to continue their annual workshops with another proposed for the 20<sup>th</sup> ICAR in Scotland this July. Subcommittee members published a joint report in the Journal of Proteome Research that provides a series of resources for plant proteome researchers. ORFeomics members continue to track clone-based functional resources in the public sphere and facilitate additions to collections. Similarly, Phenomics members continue to monitor development of phenomics-based resources. Further information can be found in the ORFeomics, Phenomics, Proteomics and Systems Biology subcommittee reports.

A full-time MASC Coordinator position, established in 2002, has been supported for 6 of the last 7 years by the NSF (US) and for one year by the DFG (Germany). The current Coordinator, Dr. Joanna Friesner (University of California, Davis), is funded by an NSF grant through fall, 2009. At that time, a new UK-based MASC Coordinator will begin after successful funding of a GARNet (Genomic Arabidopsis Resource Network) grant was obtained by GARNet members. In 2007, Joanna established the 'Coordinator's Journal' webpage as part of the MASC pages, in order to provide additional outreach and communication. The Journal relays information of interest and relevance to the Arabidopsis community ([www.arabidopsis.org/portals/masc/journal.jsp](http://www.arabidopsis.org/portals/masc/journal.jsp)). The MASC Coordinator provides help and coordination to the MASC, the North American Arabidopsis Steering Committee (when the Coordinator is US-based), and the larger Arabidopsis functional genomics research community. Specific duties include (1) serving as the executive secretary of the MASC, (2) organizing and raising funds for the annual International Conference on Arabidopsis Research, including grant-writing and obtaining external sponsorship, (3) writing and editing the annual MASC progress report with input from MASC members, (4) serving as a liaison between members of the MASC, the international research community, funding agencies, and databases and stock centers, and (5) maintaining and updating the functional genomics MASC website together with TAIR to inform the global research community about various opportunities, collaborations, large-scale activities and research progress.

## Scientific Highlights of the Past Year

Following a 20 year trend, the annual rate of peer-reviewed publications involving Arabidopsis research steadily increased over the last year. The availability of a wide range of resources within the Arabidopsis community greatly facilitates a large body of cutting-edge research that allows for rapid advances in plant biology. Highly-utilized resources include: mutant insertion collections, including homozygous T-DNA insertion mutant lines; RNAi resources, including recently-developed artificial microRNAs; cDNA and ORF clones; large-scale microarray data; and RILs and other mapping populations. Resources that are more recent additions include expanded information about the Arabidopsis proteome, metabolome, and methylome, and the natural diversity found in Arabidopsis accessions. Web-based databases and browsers are also proliferating, reflecting the need to manage the vastly increasing number of datasets put forth by the many worldwide Arabidopsis research groups.

Arabidopsis lends itself exceptionally well to studying most aspects of 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 continents. With the release of the reference sequence in 2000, the 'genomic era' of Arabidopsis research truly began, allowing a rapid increase in discoveries and publications (Figure 1).

(Figure 1). Nearly 3,000 peer-reviewed Arabidopsis publications were produced in the past year, many of which contain exciting new breakthroughs that will no doubt have impacts on studies in plants and other species.

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

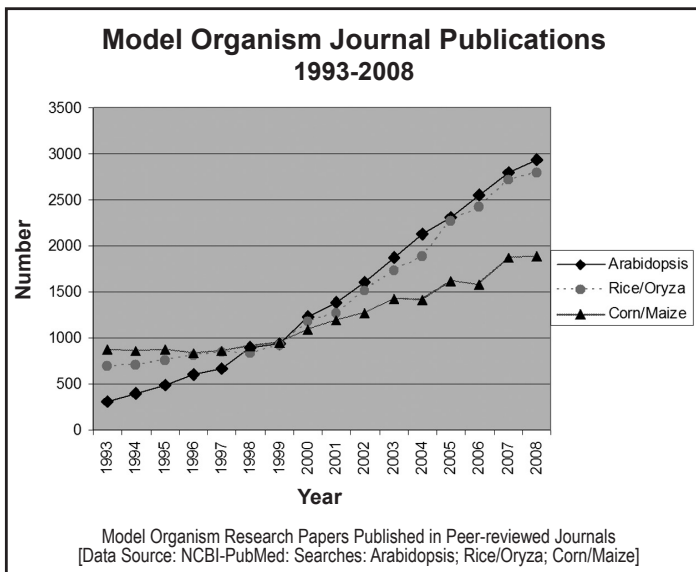
## miRNAs Protect Against Bacterial Infection

By: Joanna Friesner, MASC Coordinator

RNA silencing, a critical mechanism used by plants to resist viral infection, involves the processing of viral RNA molecules into small RNAs (sRNAs). Subsequently, viruses may evolve to combat plant resistance by suppressing the host RNA silencing machinery. Plant cells detect pathogen-associated molecular patterns (PAMPs) displayed on the surface of bacterial pathogens and invoke an immune response. A subset of sRNAs, the microRNAs (miRNAs), are known to be differentially regulated following PAMP detection although their contribution to PAMP-triggered immunity (PTI) is not clear. A recent publication by Navarro et al. examines the role of miRNAs in innate immunity and provides evidence that they are a key part of plant basal defense against pathogenic and non-pathogenic bacteria. Their findings suggest that bacteria, like viruses, can change to suppress plant host RNA silencing which may contribute to synergistic infections observed by some bacteria and viruses.

A crippled version of the virulent *Pseudomonas syringae* bacterial strain *Pto* DC3000 *brcC*<sup>-</sup>, which elicits but fails to suppress the plant immune response, was applied to wild-type and mutant *Arabidopsis thaliana* plants defective for siRNA or miRNA accumulation. The *brcC*<sup>-</sup> bacteria grew poorly on wild-type and siRNA-deficient plants while growth on miRNA-deficient *dcl1* and *hen1* mutants was enhanced. Several other bacterial strains not typically pathogens of Arabidopsis, including *E. coli*, similarly sustained growth on *dcl1* and *hen1* mutants and induced phenotypes consistent with virulent infection. The authors went on to show that a number of *P. syringae* secreted effectors suppress the plant miRNA pathway at several points. Interestingly, they also showed that bacterial and viral challenges may act synergistically against plant defenses; pre-infection by a virus that suppresses siRNA and miRNA functions promoted infection by non-pathogenic bacteria on wild-type Arabidopsis plants. These results provide strong evidence that miRNAs are important for plant basal defense and anti-bacterial protection. The authors also suggest that miRNA responses to bacteria and viruses may be responsible for observed synergistic interactions between the two types of organisms. Finally, they note parallels between plant and human miRNA involvement in innate immunity and disease induction caused by pathogenic bacteria.

Reference: Navarro L, Jay E, Nomura K, He SY, and Voinnet O, Suppression of the microRNA pathway by bacterial effector proteins. *Science*, Aug 15 2008; 321(5891): 964-7



**Figure 1**

Considered alongside classic model organisms such as corn, the Arabidopsis publication record is 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 1993 and 2008, the number of peer-reviewed Arabidopsis publications increased nearly 10-fold, while rice and corn publications increased about 4-fold and 2-fold, respectively

## Of Weeds and Peas: Identification of a Novel Plant Hormone

By: Joanna Friesner, MASC Coordinator

Over 10 years ago, studies of pea and petunia mutants revealed that an unidentified graft transmissible signal was capable of reversing a highly branched mutant phenotype. A recent publication by Gomez-Roldan et al., using pea and *Arabidopsis*, provides evidence that strigolactones are a novel plant shoot hormone and strong candidates for the long-sought signal (1). To identify the shoot branching inhibitor the authors analyzed the highly-branched *rms1* and *rms5* pea mutants. Candidate signaling compounds were suggested by *Arabidopsis* genes orthologous to *RMS5* and *RMS1*: carotenoid cleavage dioxygenases 7 and 8 (*CCD7* and *CCD8*), encoded by the shoot branching genes *MAX3* and *MAX4*, respectively. The authors focused on *CCD8* (*P. sativum rms1*) in the study, and although its precise role in plants is unclear, previous bacterial studies suggest it is involved in  $\beta$ -carotene cleavage. Studies of *Arabidopsis* *MAX3* provided additional evidence that the shoot-branching signaling compound may be carotenoid-derived.

Strigolactones, a carotenoid-derived compound, have been found in shoots and roots and are thought to be involved in both symbiotic and parasitic plant-interactions where they may function as a recognition signal. Gomez-Roldan et al. detected two strigolactones present in wild-type root exudates that were absent in *ccd8* exudates. Further analysis of *ccd8* root exudates revealed significantly decreased ability to promote symbiotic fungal hyphae branching and parasitic plant seed germination, suggestive of largely reduced strigolactone activity. Adding a synthetic strigolactone analog to the mutants restored wild-type shoot branching and microbial interaction responses. While *ccd8* plants appear defective in strigolactone production this isn't the case for *rms4/max2* shoot-branching mutants which are insensitive to the branching inhibition signal and fail to restore branching upon application of exogenous strigolactone. The responses of *Arabidopsis* branching mutants to exogenous strigolactone confirmed the pea findings and strongly suggest that strigolactones, or a closely related compound, are a novel plant hormone responsible for shoot branching inhibition in plants. In addition, the pea data support additional roles for strigolactones in plant-microbe interactions.

A side-by-side publication focusing on highly-branched rice mutants similarly demonstrated an important role for strigolactones in shoot development and interactions with parasitic plants (2). These results may lead to the development of economically important plant varieties with greater resistance to parasitic infection.

### References:

- (1) Gomez-Roldan V, Fermas S, Brewer PB, Puech-Pagès V, Dun EA, Pillot JP, Létisse F, Matusova R, Danoun S, Portais JC, Bouwmeester H, Bécard G, Beveridge CA, Rameau C, and Rochange SF, Strigolactone inhibition of shoot branching. *Nature*, Sep. 11 2008; 455(7210):189-94
- (2) Umehara M, Hanada A, Yoshida S, Akiyama K, Arite T, Takeda-Kamiya N, Magome H, Kamiya Y, Shirasu K, Yoneyama K, Kyoizuka J, and Yamaguchi S, Inhibition of shoot branching by new terpenoid plant hormones *Nature*, Sep. 11 2008; 455(7210): 195-200

## How to Tolerate Heavy Metal

By: Joanna Friesner, MASC Coordinator

The closely-related species *Arabidopsis thaliana* and *Arabidopsis halleri* differ vastly in their ability to accumulate and tolerate high levels of heavy metals; *A. halleri* is a metal hyperaccumulator while *A. thaliana* is not. Several candidate genes have emerged from transcriptional profiling and comparative genomic approaches to determine the cause(s) underlying this difference. A recent publication by Hanikenne et al. provides evidence that very high expression of the *HMA4* plasma membrane metal pump gene is necessary for metal hyperaccumulation and metal hypertolerance, findings that may contribute to improved strategies for bioremediation and biofortification.

*A. halleri* preferentially stores zinc (Zn) and cadmium (Cd) in shoots over roots while the opposite occurs in *A. thaliana* and in virtually all other plants. This study showed that the *AhHMA4* gene sequence is present in triplicate copy, with 88% identity to the *A. thaliana* sequence, and is more highly expressed in *A. halleri* than *A. thaliana* resulting in more efficient metal transfer from roots to shoots. RNAi directed against *HMA4* gene expression in *A. halleri* gave a 55-90% reduction of *HMA4* transcript levels and 65-88% lower Zn levels in shoots compared to controls; levels similar to those found in wild-type *A. thaliana*. Zn distribution differs in wild-type and *HMA4*-deficient *A. halleri* roots where it is found prominently in the xylem in the former, and in the pericycle in the latter, suggesting that reduction in the *AhHMA4* metal pump interferes with Zn transport into the xylem. Gene expression analysis in *AhHMA4* RNAi plants indicates that high expression of *AhHMA4* in *A. halleri* leads to de-regulation of expression of several other genes. Thus, *AhHMA4* acts as a "physiological master switch" in metal hyperaccumulation. Furthermore, *AhHMA4* contributes to Cd and Zn hypertolerance; root elongation in the presence of these metals was reduced 32-40% in wild-type and 63-97% in *HMA4* RNAi *A. halleri*, when compared to untreated controls.

Promoter strength comparison of the three *AhHMA4* and the single *AtHMA4* genes revealed the *A. thaliana* promoter was weaker than each of the *A. halleri* promoters, which in turn, were each similar to the constitutive CaMV 35S promoter. To determine whether increased expression of *AhHMA4* affects metal accumulation and tolerance in *A. thaliana*, the authors transformed *A. thaliana* with a construct carrying an *AhHMA4* cDNA driven by the *AhHMA4-1* promoter. Transgenic *A. thaliana* lines had moderately elevated *HMA4* transcript levels (2.4-2.8 fold increase) and imaging suggested that Zn was localized to the xylem rather than the pericycle, similar to wild-type *A. halleri*. However, the story remains incomplete: *AhHMA4*-transgenic *A. thaliana* lines were no more tolerant of toxic concentrations of Zn or Cd than non-transgenic controls suggesting additional genes are required for metal detoxification, in particular, for the detoxification of metals delivered to the shoot at high rates in *HMA4*-expressing *A. thaliana*. This work provides insights into adaptations that enable plants to grow in extreme environments.

Reference: Hanikenne M, Talke IN, Haydon MJ, Lanz C, Nolte A, Motte P, Kroymann J, Weigel D, and Krämer U, Evolution of metal hyperaccumulation required cis-regulatory changes and triplication of *HMA4*. *Nature*, May 15 2008; 453: 391-6



## Reproductive Barriers Between Arabidopsis Accessions

By: Joanna Friesner, MASC Coordinator

Genetic incompatibility arising through inter-specific crosses is a major obstacle in plant breeding. It has been hypothesized that such incompatibilities are due to functional divergence of genes that, when combined, give progeny with reduced phenotypic robustness including sterility. A recent study by Bikard et al. provides new evidence that divergent evolution of recently duplicated genes within a species can result in widespread genetic incompatibility, findings that may provide insight into the speciation process.

Genotype analysis of recombinant inbred lines derived from crosses between *Arabidopsis thaliana* accessions Columbia (*Col*) and Cape Verde Islands (*Cvi*) revealed unlinked genes that failed to segregate independently thus displaying linkage disequilibrium (LD). The authors determined that a particular combination of *Col* and *Cvi* alleles at each locus of one of the gene pairs, termed LD1, was embryo-lethal. Fine-mapping of the LD1 incompatible interaction produced a candidate gene pair encoding the HPA protein which participates in biosynthesis of histidine, an essential amino acid. The *HPA* paralogs present in *Col*, LD1.1 and LD1.5, appear to be from a recent gene duplication event giving dispersed loci on chromosomes 1 and 5, respectively. LD1.1 and LD1.5 coding sequences differ by two synonymous single nucleotide polymorphisms and only LD1.5 is expressed in *Col*. In contrast, only the LD1.1 locus is expressed in *Cvi* and LD1.5 appears to have been deleted. The two accessions have evidently undergone reciprocal gene loss such that only one functional *HPA* sequence is present in each. The homozygous combination of the silenced *Col* LD1.1 allele and the *Cvi* LD1.5 deletion allele leads to defective embryo development and seed abortion, presumably due to insufficient histidine biosynthesis. Another combination of LD1 alleles gave normal embryo development but defective root growth which was quantitatively rescued by exogenous histidine supplementation.

These results, and additional allelic complementation tests, suggest that epistasis at LD1 is most likely explained by allelic variation at *HPA* and that the *Col/Cvi* incompatibility is due to intraspecific divergence of a duplicate gene pair. The authors examined LD1.1/LD1.5 genetic incompatibilities further and found that divergence of the *HPA* gene pair was widespread among 30 natural accessions suggesting that rapid evolution of a single gene can quickly lead to incompatibilities within species.

Reference: Bikard D, Patel D, Le Metté C, Giorgi V, Camilleri C, Bennett MJ and Loudet O, Divergent evolution of duplicate genes leads to genetic incompatibilities within *A. thaliana*. *Science*, Jan 30 2009; 323(5914): 623-6

## Charting the Epigenome

By: Joanna Friesner, MASC Coordinator

The epigenetic modifications found in many eukaryotes provide cellular instructions beyond those encoded in the DNA alone. For example, X-chromosome inactivation in human female cells is partly achieved through non-coding RNAs (ncRNAs) and DNA methylation. DNA methylation is also important in plants and is known to be involved in regulation of gene expression, development, and for maintaining silenced transposons. Plant ncRNAs, especially small RNAs (smRNAs) also play significant regulatory roles. Therefore, a deep understanding of gene function and regulation requires more than genomic DNA sequences. A recent study takes the closest, most comprehensive view to date of the *Arabidopsis thaliana* floral epigenome and develops highly integrated maps of epigenetic modifications. Data are displayed in the AnnoJ Genome Browser (<http://neomorph.salk.edu/epigenome.html>) which should be a useful resource.

Lister et al. improve on previous efforts to map epigenetic modifications in the *Arabidopsis* floral genome by employing direct sequencing-by-synthesis of whole genome cytosine methylation (C-methylome), transcription (transcriptome), and the small RNA transcriptome at single-base resolution in wild-type *Col-0* and mutants defective in DNA methyltransferase or demethylase activity. New regions of genome methylation were discovered and it was determined that local sequence context affects the distribution of methylation. Sequencing of mutants defective for methylation establishment, maintenance, or demethylation, revealed both the effects of each class of genes on C-methylation and allowed for identification of their genomic targets. Strikingly, comparison of the smRNA transcriptome with the C-methylome showed that sequences matching smRNAs were nearly 26 times more likely to be C-methylated than non-smRNA sequences. These data suggest that smRNAs are important for targeting the genome for DNA methylation, perhaps primarily for the one-third of the methylated genomic loci associated with smRNAs. The impressive sequencing effort performed in this study provides important pictures of the epigenetic states in floral tissue from *Col-0* and several important mutants. The real challenge now is addressing the dynamic nature of epigenomes that can be highly variable depending on external and internal environments.

Reference: Lister R, O'Malley RC, Tonti-Filippini J, Gregory BD, Berry CC, Millar AH, and Ecker JR, Highly integrated single-base resolution maps of the epigenome in *Arabidopsis*. *Cell*, May 2 2008; 133(3): 523-36



## A New Path to Auxin

By: Joanna Friesner, MASC Coordinator

Plants, sessile organisms unable to relocate in response to environmental fluctuations, possess sensitive and complex mechanisms for sensing external inputs and responding rapidly. The ability of plants to respond to environmental cues, including light quality, is critical to their survival and involves modulating development and growth through hormone signaling. Two recent back-to-back publications by Tao et al. and Stepanova et al. identify the Arabidopsis *TAA1* gene and show that it catalyzes the first step in a previously proposed, but uncharacterized, branch of auxin biosynthesis. Importantly, the authors provide new insights on the link between responses to environmental cues, including shade avoidance, and hormonal crosstalk in plant development.

*TAA1*, initially named *sav3* by Tao et al. and *wei8* by Stepanova et al., was identified through genetic screens by both groups. Tao et al. screened for mutant seedlings unable to elongate after being moved from growth in continuous white light to simulated shade while Stepanova et al. screened for mutants displaying specific root ethylene defects. After positional cloning and further characterization of the allelic mutants, the groups renamed the locus *TAA1* for its role in catalyzing the conversion of L-tryptophan to indole-3-pyruvic acid (IPA), an intermediate in auxin biosynthesis. Tao et al. characterized *sav3* plants and found they had only about 60% of wild-type levels of free auxin and failed to normally upregulate auxin in response to internal (high temperature) or external (shade) cues. In addition, they showed that a number of genes induced by auxin in wild-type plants had decreased expression in *sav3* and *in silico* computational modeling, based on the TAA1 protein crystal structure, suggested that L-Trp is the preferred substrate for TAA1 with IPA the expected product. Stepanova et al. found that *wei8* plants displayed root-specific ethylene insensitivity with longer than wild-type roots in the presence of the ethylene precursor ACC. Exogenous auxin (IAA) rescued the root phenotype of *wei8* although addition of Trp did not, pointing to a function for TAA1 downstream of Trp. Through *in vitro* assays both groups demonstrated that recombinant wild-type TAA1 catalyzed the conversion of L-Trp into IPA. Stepanova et al. further showed that mutant TAA1 recombinant proteins lacked wild-type aminotransferase activity and failed to convert L-Trp into IPA.

These studies provide strong evidence that the IPA-dependent pathway for auxin biosynthesis is present in higher plants and that TAA1 acts to catalyze the formation of IPA from L-Trp. The research also demonstrates the importance of auxin biosynthesis throughout the plant in response to environmental cues, such as light quality and phytohormones, and adds to the growing body of knowledge on hormonal crosstalk in plants.

### References:

Tao Y, Ferrer J, Ljung K, Pojer F, Hong F, Long J, Li L, Moreno J, Bowman M, Ivans L, Cheng Y, Lim J, Zhao Y, Ballare CL, Sandberg G, Noel JP, and Chory J. Rapid synthesis of auxin via a new Tryptophan-dependent pathway is required for shade avoidance in plants. *Cell*, April 4, 2008; 133: 164–76  
Stepanova AN, Robertson-Hoyt J, Yun J, Benavente LM, Xie DY, Dolezal K, Schlereth A, Jürgens G, and Alonso JM. TAA1-mediated auxin biosynthesis is essential for hormone crosstalk and plant development. *Cell*, April 4, 2008; 133: 177–91

## SSP: the First Paternal Effect Gene in Plant Embryogenesis

By: Joanna Friesner, MASC Coordinator

In Arabidopsis, embryogenesis follows fertilization of the female gametophyte by the male gametophyte, pollen. The pollen contains two sperm cells, one which fuses with the egg cell to give the zygote, and another which fuses with the central cell to give rise to the zygote-supporting endosperm. Asymmetric growth of the newly-formed Arabidopsis zygote results in a small apical pro-embryonic cell and a large basal cell that establishes the suspensor which provides nutrition to the embryo, analogous to a mammalian umbilical cord. Several examples of maternal control in plant embryogenesis are known including methylation-sensitive gene imprinting where a gene's activity depends on its parental origin; typically the paternal allele is silent while the maternal allele is expressed. A recent landmark publication by Bayer et al. provides evidence for the first paternal effect gene in plant embryogenesis.

The authors identified *ssp* mutants whose zygotes make small, abnormal basal cells, fail to elongate, and display various suspensor defects. Cloning the *SSP* gene sequence revealed it was a member of a particular kinase family and mutation of a protein domain predicted to mediate stable plasma membrane association rendered the protein non-functional. However, key kinase active site residues are absent indicating it may not possess enzymatic kinase function. Atypical *ssp* phenotype segregation led to reciprocal genetic crosses which revealed that embryonic phenotype strictly depends on paternal inheritance. If *ssp* plants were used as the pollen donor for *SSP* recipients, all embryos were abnormal and had the *ssp* phenotype; conversely, if *SSP* pollen was crossed with *ssp* recipients, all embryos were normal. The paternal effect appears not to have an epigenetic basis, such as via gene imprinting, as *SSP* function was insensitive to global changes in DNA methylation. Strikingly, the authors found that *SSP* appears to be expressed exclusively in mature pollen and transcripts only are translated into protein following fertilization. They propose that protein accumulation within the zygote activates the known *YDA* signaling pathway to promote zygote and suspensor maturation. Therefore, paternally-derived *SSP* can act as the 'molecular cue' that initiates the steps required for regulating the first asymmetric division of the plant embryo.

Reference: Bayer M, Nawy T, Giglione C, Galli M, Meinnel T, and Lukowitz W. Paternal control of embryonic patterning in *Arabidopsis thaliana*. *Science*, March 13 2009; 323: 1485-8

## Revising and Refining the Arabidopsis Genome Through Proteomics

By: Joanna Friesner, MASC Coordinator

The annotated Arabidopsis reference genome is an integral part of the majority of molecular biology studies involving Arabidopsis. Therefore, it is of utmost importance to have correct genome annotation of exons, introns, pseudogenes, and coding sequence boundaries. In the last eight years following the initial release of the reference genome, a number of studies have contributed to refining and redefining the genome using techniques such as genome tiling arrays and more sophisticated bioinformatic prediction programs. Proteogenomic approaches, which use proteomics to annotate genomes, are particularly useful as they can unambiguously determine characteristics of protein-coding sequences. A recent study by Castellana et al. achieves deeper sampling to expand on previous proteogenomic efforts to refine the Arabidopsis genome, including the identification of novel genes and the improvement of existing gene models.

By employing a particular type of tandem mass spectroscopy (MS/MS), the authors obtained 21 million mass spectra and 144,070 distinct peptides from 45 MS/MS runs. Samples were obtained from roots, leaves, flowers, siliques, and cell culture. Cell culture samples were enriched specifically for phosphopeptides which allowed for sampling of the typically under-represented phosphoproteome. Peptides were compared to three databases including the TAIR7 annotated genome release. 126,055 of the peptides mapped to the existing TAIR database confirming 12,769 proteins, or roughly 40% of the annotated genome. 18,024 peptides did not match TAIR7; using bioinformatic analysis, the authors identified 778 new protein coding genes, 280 of which were previously unidentified and the remaining 498 had been described as pseudogenes. It will be interesting to see if functional studies, such as examining T-DNA insertion lines, provide support to these new gene models identified in what was previously annotated as pseudogenes or intergenic space. The peptide data also contributed to refining the annotation of 695 existing gene models, including identifying novel exons, boundary changes, and changes in exon length.

The most recent annotated genome release, TAIR8, incorporates just 52 (3%) of the novel peptides identified in this study suggesting that proteogenomic datasets complement existing genome annotation strategies and that future updates will contain significant modifications as new data become available. All peptides from the study can be uploaded as a track in TAIR8; files are available at: <http://peptide.ucsd.edu>.

*Reference: Castellana NE, Payne SH, Shen Z, Stanke M, Bafna V and Briggs SP. Discovery and revision of Arabidopsis genes by proteogenomics. PNAS, Dec 30 2008; 105(52):21034-8*

## Community Arabidopsis Projects and Resources

### The Arabidopsis Information Resource (TAIR, [www.arabidopsis.org](http://www.arabidopsis.org))

By: Eva Huala, TAIR Director

#### Curation of gene function data:

In the past year TAIR curators have added gene function information based on experimental data to 2,718 genes that previously lacked annotations of this type. These new annotations resulted from curation by TAIR staff of 951 published research articles in the last year as well as direct submission of data to TAIR by the research community. The total number of Arabidopsis genes with direct experimental data for biological process, molecular function or cellular compartment is now 8,622. If experimental data on gene expression patterns is also included, 20,283 genes (71% of all TAIR8 genes excluding transposon genes and pseudogenes) now have experimental annotations in TAIR.

#### Collaboration with journals

The new TAIR-Plant Physiology collaboration aims to gather Arabidopsis gene function data directly from authors whose articles have just been accepted for publication. This partnership has resulted in direct author submission of function or expression information for 9,160 genes drawn from 55 articles published in Plant Physiology over the last 10 months (May 08 – February 09). However, the initial rate of data submission was lower than expected with only 21% of authors providing their data after the first request. This submission rate increased to 79% when repeated followup data requests were sent to a small subset of authors. We contacted authors that didn't initially submit data to explore how the submission rate could be improved and found that many authors were uncertain about which types of data should be submitted. To mitigate this problem we changed the wording of the data request and added specific examples illustrating the types of data appropriate for submission. The submission rate will be re-evaluated in mid-2009 to verify that the wording changes have had the desired effect. In addition, plans are underway to expand the collaboration to include The Plant Journal and to test the concept of providing a more structured web interface for authors to submit gene function data.

#### Curation of gene structures and genome assembly:

The May 2009 TAIR9 genome release contains 27,379 protein coding genes (an increase of 144 over the TAIR8 release), 4827 pseudogenes and transposable element genes (an increase of 68) and 1312 ncRNAs (an increase of 24). In all, the new release contains 33,518 genes. Fourteen percent of Arabidopsis genes (4626) now have annotated splice variants. Updates were made to 1254 gene models of which 774 had CDS updates; a total of 1144 exons were modified and 1056 new exons incorporated. There were 13 gene splits and 46 gene merges. We also developed a ranking system for this release that attributes confidence scores to all exons and gene models based on different types of experimental and computational evidence. The new confidence ranking will, for example, allow researchers to identify a set of

gold standard confirmed structures or identify sets of exons where both donor and acceptor splice sites are supported.

In addition to gene structure updates the TAIR9 release included corrections to the chromosome assemblies, including 227 single nucleotide substitutions, 341 insertions or deletions, and adjustment to a standard length of 100 nt for 14 regions in which vector, *E. coli* or rice sequences had been removed and replaced by runs of N in a previous release. A reference genome policy has been developed with community input to set quality standards for corrections to the reference assembly, and the standards described in the policy have been put into effect beginning with the new TAIR9 release. More information on the reference genome update policy is available at [http://www.arabidopsis.org/doc/portals/genAnnotation/gene\\_structural\\_annotation/ref\\_genome\\_sequence/11413](http://www.arabidopsis.org/doc/portals/genAnnotation/gene_structural_annotation/ref_genome_sequence/11413).

#### **Metabolic pathway data:**

Two AraCyc metabolic pathway releases were produced by the AraCyc team in the past year (AraCyc 4.5 in June 2008 and AraCyc 5.0 in March 2009). The AraCyc 5.0 release contains a total of 332 pathways, with 1970 unique genes assigned to the pathways, and 87% of these pathways have been experimentally confirmed. A new project affiliated to TAIR, the Plant Metabolic Network (<http://www.plantcyc.org/>), was launched in June 2008 to provide a general metabolic pathway database for all plants (PlantCyc) as well as several new species-specific databases. The most recent PlantCyc release, PlantCyc 2.0, contains 581 pathways (excluding superpathways), 8558 enzymes, 2464 compounds, and over 300 plant species.

#### **Other new data and tools:**

In the past year TAIR has added a large number of new tracks to its GBrowse genome browser, including aligned Brassica sequences (ATIDB), methylation plots (Ecker et al., 2006), orthologs (Inparanoid), plant gene families (Phytozome), MPSS data (Lu et al., 2005), proteomics data (Baerenfaller et al. 2008), polymorphic regions (Zeller et al., 2008), promoter elements (PlantPromoterDB, Yamamoto et al., 2008), transposable elements and their genes, mRNAs (Col-0) and smRNAs (Col-0) (Lister et al., 2008; Gregory et al., 2008), gaps, genome corrections and more. In addition, through a collaboration with staff at WormBase a new text mining tool, Textpresso, has been made available for over 17,000 Arabidopsis full text research articles (<http://www.textpresso.org/arabidopsis/>). A synteny viewer displaying aligned genomes of *Arabidopsis lyrata* and *A. thaliana* will be released in late spring 2009.

### **The Arabidopsis Biological Resource Center (ABRC, [www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm](http://www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm))**

By Randy Scholl, ABRC Director

The Arabidopsis Biological Resource Center (ABRC) collects, preserves and distributes seed and DNA resources of Arabidopsis and related species. Current ABRC seed stock holdings include insertion lines covering 25,000 genes, the 10,000+ lines of the Arabidopsis TILLING service, 360 natural accessions which are genetically fingerprinted, 21 recombinant inbred populations, a set of near-isogenic lines, new Wisconsin Ds-Lox T-DNA lines, RNAi lines, and related species. DNA resources at ABRC

include full-length ORF and cDNA clones for about 16,000 genes, BACs covering the entire genome, BACS of nine related species, the AGRICOLA GST entry clones, various sets of expression clones and 8,000 amiRNA clones. The present collection of vector constructs represents a rich and diverse set of resources for investigation of gene expression. The distribution of seed and DNA stocks exceeded 90,000 in 2008.

ABRC is presently conducting a stock donation campaign with emphasis on improvement of the published mutant collection. Toward this end, we have greatly streamlined the donation process. The new simplified form and procedure can be found at [http://arabidopsis.org/submit/abrc\\_submission.jsp](http://arabidopsis.org/submit/abrc_submission.jsp). We encourage everyone to participate by sending their published mutant stocks. Donations of other seed stocks as well as clones are welcome. ABRC continues to focus on functional genomics. The J. Ecker laboratory (Salk Institute, <http://signal.salk.edu/gabout.html>) is genetically purifying to homozygosity 50,000 T-DNA insertion knockout lines. To date, 26,285 of these lines have been received. The stocks being utilized for this project include the J. Ecker (SALK) population plus lines from Syngenta (SAIL), B. Weissshaar (GABI-Kat) and P. Krysan/R. Amasino/M. Sussman (Wisconsin Ds-Lox). Initial members of sets of the confirmed SALK T-DNA lines have been distributed to laboratories for forward screening. The first 8,889 lines of this collection were shipped to users in Spring, 2008 and 11,000 will be shipped in 2009. Pools of confirmed SALK lines will be available in 2009. Receipt and distribution of Entry and Expression full length/ORFeome clones remains a priority. ORF clones lacking a stop codon are being received from members of the Arabidopsis Membrane Interactome Project, with 1,530 received to date. The extensive expression ORF collections from S. P. Dinesh Kumar and S. Clouse continue to be received, with over 11,000 of these currently in-house. We expect to receive 9,000 ORF clones in yeast two hybrid bait and prey vectors in the near future. Further additions to the amiRNA collection are also anticipated. We are pleased to report that 10,000 loci are now represented by clones in both a Gateway™ entry vector and the pUNI51 vector, 4,000 loci are represented only by a clone in a Gateway™ entry vector and 2000 are represented only by a clone in the pUNI51 vector.

Management and supervisory roles at ABRC are under reorganization to accommodate the retirement of Randy Scholl in August, 2009. Dr. Erich Grotewold of OSU's Department of Plant Cellular and Molecular Biology will become the new Director. The ABRC has just made a new senior hire (Dr. Jelena Brkljacic), which together with the reorganization of the existing personnel, will ensure a swift transition.

## Measuring Gene Function Knowledge

In 2003, MASC members agreed that it would be useful to establish an improved means to update gene function knowledge and quantify the number of genes with known function. Since the 2004 MASC annual report this was illustrated by thermometers to provide visual illustrations of the progress in Arabidopsis functional genomics efforts. This year, like last year, the thermometers are measured against the TAIR8 genome release and include the number of loci (1) containing sequence-indexed insertion elements, (2) targeted by RNAi constructs, (3) with full-length cDNA clones, sequencing status and availability, (4) with Open Reading Frame (ORF) clones available as stocks and (5) with gene expression detected. The thermometers are updated with data available at the end of May 2009.

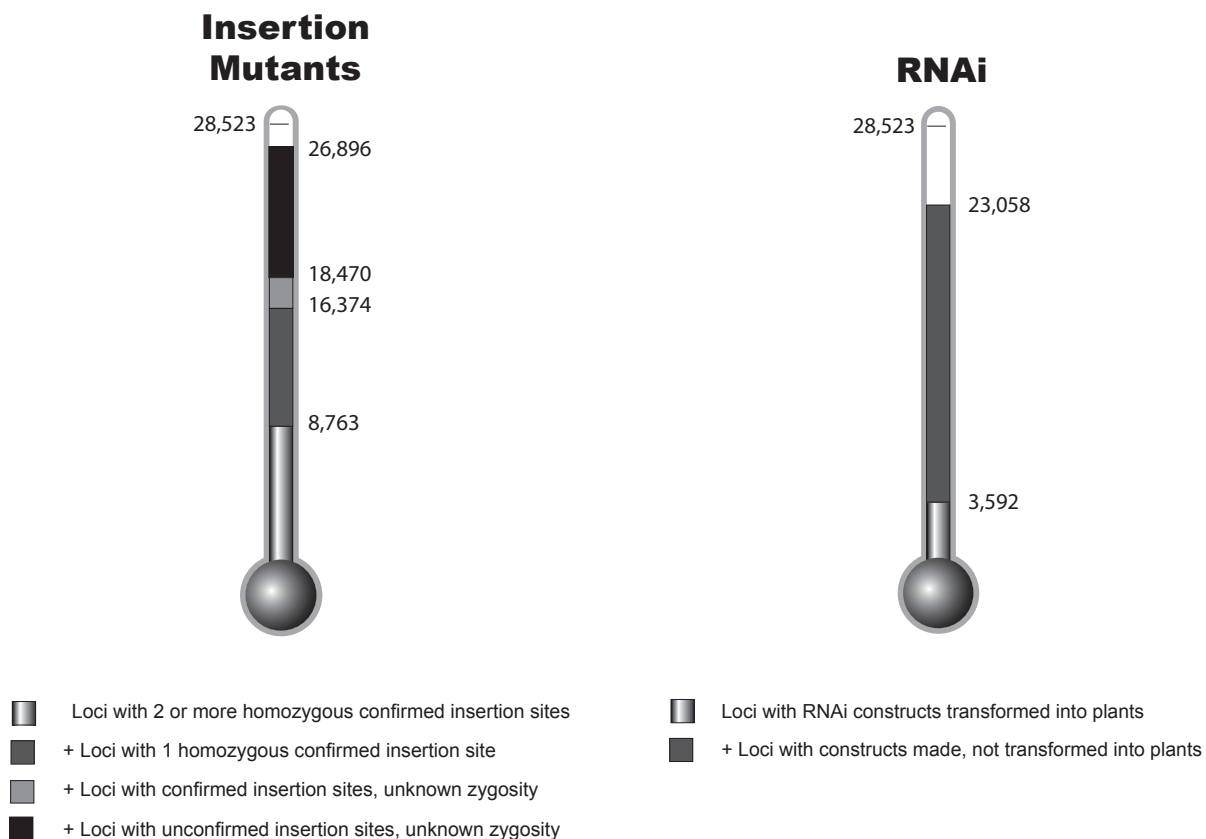
It is likely that the thermometers do not include all existing data and resources given that there are individual labs and private companies that have not publicly shared information, as well as publicly-available resources that are not easily accessible. In 2007, the MASC re-evaluated the usefulness of the tracking thermometers and the majority opinion was that in general, the thermometers are useful even if they are an underestimate of the existing resources. MASC also felt that (1) the thermometers should not track data and resources that are not freely shared as their emphasis is on readily-available resources, (2) a caveat that not all existing resources are included should be noted and the sources for the thermometers should be listed, and (3) researchers with currently inaccessible data and resources must be encouraged to submit them to major public repositories so they can be tracked. Based on this discussion we have included updated thermometers for 2009 with the sources of data and resource counts listed accompanied by the caveat that they do not represent all existing data and resources in the listed categories but do represent a large proportion of what is publicly available in large repositories and databases.

As shown in the thermometers below, slowing, but steady progress is being made on resource development and acquiring gene function knowledge. The greatest recent strides have been made in expanding resources to knockout or knockdown gene expression including the isolation of two or more confirmed homozygous insertion mutants for an additional 12.5% of genes and isolation of insertion mutants with at least one confirmed homozygous insertion for an additional 12.4% of genes, during the past year. This brings the current total to 16,374, or nearly 60% of unique genes, with one or more confirmed homozygous insertion, made up of 8,763 genes with two or more homozygous insertion sites and an additional 7,611 genes with one homozygous insertion site. To date, 26,285 of these lines have been received by ABRC; the first 8,889 lines of the collection were shipped to users in Spring, 2008 and 11,000 will be shipped in 2009. Pools of confirmed SALK lines will be available in 2009. In all, 26,896 of 28,523 unique Arabidopsis genes (94%) contain at least one sequenced insertion element. Increases in the other resource categories have been much more modest which likely reflects the conclusion of several large-scale projects, such as the AGRICOLA RNAi resource. However, there is some information about the majority of unique Arabidopsis

genes; for example, numerous gene expression studies and resources available demonstrate confirmed expression for 27,103 of 28,523 genes (95%), including new input this year from a project that is sequencing small RNAs.



# Tracking Thermometers *(continued next page)*



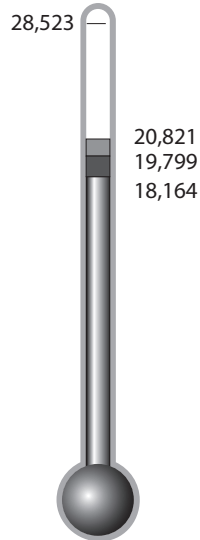
**Figure 2: Measuring Arabidopsis Genomics Resources.** All data are as of May, 2009. For consistency, all resources are measured against the TAIR8 genome release (including noncoding RNAs and organelle-encoded genes but excluding transposon genes and pseudogenes, a total of 28,523 genes). Five categories are included: (A) Loci with insertion mutants - 8,763 genes with two or more homozygous confirmed insertion sites, an additional 7,611 genes with one homozygous confirmed insertion site, an additional 2,096 genes with confirmed insertion sites and homozygous status unknown, and an additional 8,426 genes with unconfirmed insertions, homozygous status unknown (data from Huaming Chen/Joe Ecker, SIGnAL, including data from the Salk collections, the Arabidopsis community, and GABI); (B) Loci with targeted RNAi knockdowns - 3,592 genes with RNAi constructs transformed into plant lines and an additional 19,466 genes with RNAi knockdown constructs made but not transformed into plant lines, (data from Emma Knee/Randy Scholl (ABRC), the 2010 amiRNA project (CSHL), Martine Vanhoucke/Pierre Hilson (PSB/LMBP), Ian Small (AGRIKOLA), Graeme Gill/Sean May (NASC), and chromDB project); (C) Loci with full length cDNA clones - 18,164 genes with full length cDNAs fully sequenced and known to be available for ordering, an additional 1,635 genes with cDNAs not fully sequenced but known to be available and an additional 1,022 genes with fully sequenced cDNAs but stock availability unknown, (data from Huaming Chen/Joe Ecker, SIGnAL); (D) Loci with ORF clones - 16,127 genes with fully-sequenced ORF clones and an additional 1,136 with partially sequenced ORF clones (data from Huaming Chen/Joe Ecker, SIGnAL); (E) Expression detected - 21,645 loci with cDNAs (data from Huaming Chen/Joe Ecker, SIGnAL and Eva Huala, TAIR), an additional 3,272 loci with ESTs (data from Eva Huala/TAIR), an additional 1,453 loci with expression detected by MPSS or SAGE (MPSS data from Blake Meyers <http://mpss.udel.edu/at/>), SAGE data from 2006 thermometer (provided by Hank Wu, TIGR, no update available), an additional 523 loci with expression detected only by microarray analysis (data provided by Eva Huala/TAIR, GEO, and NASCArrays) and an additional 210 loci detected through small RNA (smRNA) sequencing (data from Ryan Lister/Joe Ecker, SIGnAL.)

Note: Detailed information on ORF, cDNA, and amiRNAi clone projects can be found in the ORFeomics and Phenomics Subcommittee Reports (pages 24-28).

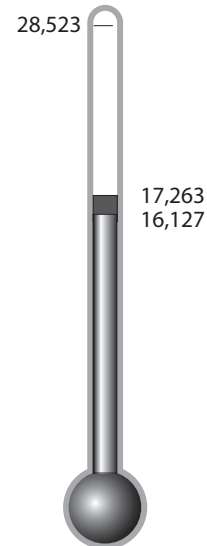


# Tracking Thermometers

## Full-length cDNA clones



## ORF



- Loci with fl-cDNA clones, fully sequenced and available
- + Loci with clones, not fully sequenced, and available
- + Loci with clones, fully sequenced, unknown availability

- Loci with fully sequenced ORF clones,
- + Loci with partially sequenced ORF clones

## Expression



- Loci with cDNAs
- + Loci with ESTs
- + Loci with mpss or sage
- + Loci with microarray expression
- + Loci with smRNA expression

# 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 labor between the public and private sector is successful due to their complementary approaches; publicly-funded basic research, frequently 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 typically more focused on applications with commercial value. In this system, where initial discovery often takes place in the public sphere and commercial development in the private sphere, 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 attempt to quantitate the usefulness of basic research to applied approaches. 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.

An example of one such public-private research endeavor is provided by Mendel Biotechnology, which over the past decade has undertaken a systematic analysis of the estimated 1500+ Arabidopsis transcription factors by leveraging data produced by the publicly-financed Arabidopsis Genome Project. A recent, comprehensive review by Mendel researchers provides insight into public and private efforts to use plant transcriptional regulators to develop agricultural products, with commercial interest particularly in those that significantly increase yield (1). Mendel regularly partners with Monsanto which pursues commercialization of promising leads. A recent press release describes that Monsanto's 'Roundup Ready 2 Yield' soybeans, including an Arabidopsis gene identified by Mendel, is now entering expanded field trials, regulatory studies, and introduction into additional soybean lines. The engineered plants were developed to produce roughly 6-7 percent more soybeans per plant and future plans include stacking the yield enhancement trait with additional technology shown to provide a 7-11 percent yield increase in field trials (2). Notably, it has

been estimated to take up to 12 years or more to navigate the commercialization pipeline from initial discoveries to agricultural products (3), a timeframe consistent with the establishment of Mendel in 1997, Arabidopsis complete public genome release in 2000, and public announcement of regulatory trials in 2009.

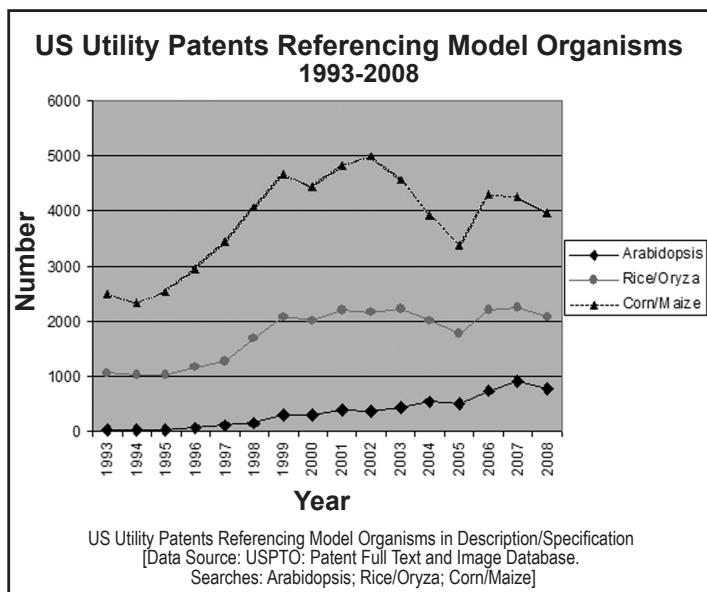
While the examples of ways that basic Arabidopsis studies impact applied plant research are mounting, it is also undoubtedly the case that Arabidopsis studies facilitate advances in medical research and lead to discoveries that have direct relevance to human health and disease (4). A recent publication describes the development of a small molecule inhibitor which targets the NEDD8-activating enzyme (NAE), part of the ubiquitin-proteasome protein degradation system, to selectively disrupt cancer cell growth (5). A comment accompanying the publication notes that the research underlying the new drug candidate, currently in clinical trials as an anticancer agent, has its roots in an Arabidopsis mutant screen performed more than 15 years ago which first uncovered NAE genes (6), reflecting the idea that discoveries in Arabidopsis can have broad implications, sometimes many years later.

When evaluating the success of Arabidopsis as a means of advancing applied research, as well as its future potential, it is important to keep the realities of public vs. private research and the 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 (7), 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 (8) 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 1993 and 2008, the number of peer-reviewed Arabidopsis publications increased by nearly 10-fold, while rice and corn publications increased roughly 4-fold and 2-fold, respectively (Fig. 1, page 10). In that same timeframe, while the number of U.S. patents referencing rice and corn increased 1.6-2 fold, the number of patents citing Arabidopsis increased nearly 45-

fold (Fig. 3). The absolute number of patents citing rice and corn currently far exceed those citing Arabidopsis; however, the current patent trend could be expected to continue based on the steady strong increases in Arabidopsis publications. Of course, this depends heavily on continued, strong, funding of basic Arabidopsis research by government agencies which have been crucial to successfully developing Arabidopsis as the reference for plant biology, and for leveraging the knowledge gained for applied studies in other plants. 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, leading scientists at Mendel to conclude “Primarily thanks to the application of functional genomics in Arabidopsis and other plants, the industry is now overwhelmed with candidate genes for transgenic intervention points (3).”

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.



**Figure 3**

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- (5) Soucy TA et al., *An inhibitor of NEDD8-activating enzyme as a new approach to treat cancer*. *Nature*, April 9 2009; 458: 732–37
- (6) Deshaies RJ, *Fresh target for cancer therapy*. *Nature*, April 9 2009; 458: 709–10
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## Translational Research Examples Using Arabidopsis

### Folate-fortified Foods: Engineering Good Health

By: Joanna Friesner, MASC Coordinator

Folates are B-vitamins that are essential for a number of metabolic activities. Humans are unable to synthesize folates and therefore rely on external supplementation, usually through a plant-based diet. In developed countries, folates are frequently consumed through vitamin supplements, fortified foods, green leafy vegetables and some legumes. However, common plant sources such as rice, wheat, and maize, contain very low amounts of folate. Folate deficiency in pregnant women can lead to birth defects of the spine, brain, and skull. Folate is needed most quite early in embryonic development, often before prenatal supplements are taken, leading the U.S. Federal Drug Agency to pass regulations requiring enriched grain products including cereals, flours, and rice to contain additional folic acid. In children, folate deficiency can lead to growth retardation; in adults, long-term deficiency can cause anemia, and is linked to cardiovascular disease (1). In developing countries, it is may not be feasible to implement a vitamin supplement program or to distribute enriched foods. An alternative approach is to develop biofortified foods containing high levels of folate.

A number of studies have attempted to increase folate in edible portions of plants by engineering one or more steps in the folate biosynthetic pathway. One study expressed a version of the mammalian *GTP cyclohydrolase I (GTPCHI)* gene in tomato to increase pteridine, one of three folate components. However, while fruit pteridine content increased, another major folate component, PABA, was reduced, leading to only small increases in total folate content (2). In a second approach, the Arabidopsis *aminodeoxychorismate synthase (ADCS)* gene driven by a fruit-ripening specific promoter was expressed in tomato. AtADCS catalyzes the first step of PABA synthesis, and transgenic tomatoes contained approximately 19-fold higher PABA levels than controls, although folate levels were unchanged. Crossing the *GTPCHI* and *AtADCS*-overexpressing lines together gave transgenic fruit with up to 25-fold more folate than controls and up to 30-fold higher pteridine and PABA levels, without affecting plant and fruit growth. This increase provided the recommended daily allowance of folate for adults in just ½ cup of tomato fruit, several times more than can be found in green leafy vegetables or legumes which are considered high folate foods (3). A caveat to these results is that while PABA has been evaluated as safe in human toxicity trials, such studies have not been performed for pteridines to confirm their safety. An independent study using a similar ‘two-gene’ strategy in rice demonstrated that endosperm-specific overexpression of *AtGTPCHI* and *AtADCS* produced rice with up to 100-fold more folate than controls. Cooking experiments showed that even with 45% loss after boiling, most, or all, of an adult’s daily folate supply should be obtained in a 100 gram serving of biofortified rice. Notably, the transgenic rice had

lower levels of pteridine intermediates using the Arabidopsis *GTPCHI* gene, compared to the mammalian gene used in tomato, suggesting that the biosynthetic pathway was more efficient when both genes were from plant sources (4). In both experimental approaches, bioavailability studies have yet to be performed. However, since transgenic foods are not widely accepted in the U.S. and Europe, there is more interest in folate biofortification of crops for poorer countries, such as sweet potato. Several of the researchers involved in these studies have applied for additional funding to evaluate pteridine safety, as well as biofortification of folate in similarly-engineered crop staples, which may lead to future products.

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## The Oily Side of Producing Human Insulin

By: Joanna Friesner, MASC Coordinator

According to the World Health Organization, more than 180 million people worldwide have diabetes and the incidence is expected to double by 2030. Type 1 diabetes occurs when the pancreas fails to produce insulin which is needed to transport blood glucose into cells for use as an energy source. Type 2 diabetes, which make up about 90% of the cases worldwide, is characterized by insulin resistance and/or relative insulin deficiency. Type 2 diabetes is largely a result of excess body weight and physical inactivity, and if untreated, often leads to a requirement for insulin therapy, like Type 1 diabetes (1). Type 2 diabetes is of particular concern to industrialized nations which are experiencing increasing disease incidence linked to non-nutritious and sedentary lifestyles. Complications from the disease include heart disease, blindness, nerve damage which can lead to hand/foot amputations, and kidney problems. Therapy generally involves frequent insulin injections which can lead to non-compliance by patients who find the regimen painful and inconvenient. Alternative delivery mechanisms are under study, although they generally require much higher doses of insulin due to reduced bioavailability. Currently, the majority of the world's insulin (and all used for U.S. consumption) comes in the form of recombinant human insulin (rhIN), produced commercially from microbial sources. More efficient and cost-effective sources of rhIN are needed to meet the increasing worldwide demand. SemBioSys Genetics Inc. have developed a novel patented system to produce rhIN based on proof-of-concept studies in Arabidopsis that has the potential to help meet future global demands.

The technology to produce plant-based insulin relies on targeting rhIN expression to subcellular seed organelles, called oilbodies, which allows efficient, high-level protein expression coupled to cost-effective recovery via simplified flotation centrifugation. Arabidopsis plants were transformed

with an expression vector encoding a precursor of human insulin containing a trypsin-cleavable propeptide. Similar to current microbial processes, recovered plant-derived rhIN was enzymatically processed and matured *in vitro*, giving a product of the same molecular mass as a human insulin standard. Biological activity of Arabidopsis seed-derived rhIN was confirmed via mice insulin-tolerance tests which demonstrated the plant product was capable of lowering blood glucose equally effectively as industry standards (2). An additional advantage to this process is that seeds naturally undergo water loss during desiccation, providing a stable storage environment for oilbodies, and allowing rhIN recovery to be performed at a later date as needed. While SemBioSys performs all of its initial proof-of-concept studies in Arabidopsis, commercial rhIN production takes place in safflower, which allows recovery of larger scale quantities. In the last few years, the company has navigated the regulatory system for commercial production of safflower-based rhIN, called SBS-1000 or biosimilar, and recently successfully completed its first human clinical trial following regulatory approval in the U.S. and Europe. The trial demonstrated that SBS-1000 was bioequivalent to insulin products currently on the market and lacked any unexpected adverse reactions (3). The company is currently looking into partnering options to move the products to market (4).

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## Solving a 30-Year Old Mystery To Help Make Better Bread

By: Joanna Friesner, MASC Coordinator

Soil salinity caused by extensive crop irrigation or clearing of land overlying saline water tables can severely affect plant growth and productivity. Wheat is critically important to Australia's economy and studies involving tolerance to environmental stress have been underway for decades. The novel durum wheat line '149', derived from intergeneric crosses performed over 30 years ago, possesses a greater than normal ability to exclude sodium from leaves, although the gene(s) underlying the subsequent salt-tolerance were unknown. Excessive salt in the soil leads to sodium uptake and subsequent transport from the roots to aerial tissues where it can accumulate to toxic levels and interfere with photosynthesis. Recent studies involving sodium transporters, first in Arabidopsis and then in rice, provided the foundation for identifying the previously unknown genetic basis for salt-tolerance in wheat line 149 thereby demonstrating the usefulness of model systems to crop research.

Following previous studies of homologous transporters that transport both potassium and sodium, a cDNA of the Arabidopsis *HKT1* homolog was isolated and used in ion transport assays which determined it was selective for sodium transport (1). A study that examined null *athkt1*



insertion mutants found they exhibit lower root and higher shoot sodium levels compared to wild-type plants. The mutants displayed leaf Na<sup>+</sup> hypersensitivity in long-term growth assays suggesting that wild-type AtHKT1 acts to counteract salt stress in leaves by reducing leaf sodium accumulation (2). Two saline-sensitive Arabidopsis mutants that over-accumulated sodium in shoots were isolated in a forward genetics study; positional cloning of the mutated alleles revealed they corresponded to the *AtHKT1* coding sequence suggesting AtHKT1 is important for recirculation of sodium from shoots to roots to protect aerial tissue (3). AtHKT1 protein was found to be targeted to the plasma membrane in xylem parenchyma leaf cells where it could unload sodium from xylem vessels, thereby reducing leaf sodium concentrations to prevent toxic levels from interfering with photosynthesis (4). In parallel studies, a previously mapped rice QTL, known to be involved in potassium homeostasis in a salt-tolerant variety, was cloned and its protein sequence compared to plant genome databases. *AtHKT1* was most similar to this gene, *OsHKT1;5*, leading to expression and functional analyses which revealed that the rice and Arabidopsis proteins were similar in localization and selective-transport of sodium (5). The accumulated knowledge of *HKT1* homologs from Arabidopsis and rice studies recently contributed to the identification of the previously unknown *Nax2* locus involved in sodium exclusion in durum wheat line 149. Mapping data revealed cosegregation of the *Nax2* locus with a putative wheat homolog of the rice *HKT1;5* and the Arabidopsis *HKT1* genes. Based on sequence homology to HKTs and functional data from Arabidopsis, HKT genes were considered the best candidates for the wheat locus, which was then named *TmHKT1;5*. Similar to Arabidopsis, *Nax2* transports sodium out of the xylem and loss of the gene leads to increased sodium levels in leaves (6). *Nax2* was introgressed into several bread wheat cultivars which are currently under field trials for salt-tolerance in Australia (7); preliminary data suggest a 10-15% yield improvement in saline soil (8). Furthermore, studies suggest that two other major salt resistance QTL in wheat, *Kna1* and *Nax1*, are likely also encoded by HKT transporter genes that similarly function in removing Na<sup>+</sup> from the xylem sap (6, 9), as had been shown for the Arabidopsis and rice orthologs. Thus the leaf Na<sup>+</sup> exclusion mechanism identified in Arabidopsis (2,3) mediates salt tolerance in crop plants.

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## A HARDY Weed Leads to Better Grain

By: Joanna Friesner, MASC Coordinator

Increasing global demands for water, due in part to population expansion and decreasing arable land, put added pressure on farmers to grow water-efficient plants. Rice, the primary food source for several billion people and a water-usage intensive crop, is critical to the world's food supply. Numerous breeding and research efforts are underway to develop rice cultivars that can avoid or tolerate drought, as well as others that can withstand prolonged submergence given that some rice production occurs in low-lying areas that are subject to flooding. A recent study may contribute to increased water-use efficiency (WUE) in rice, a measurement of biomass produced in relation to transpiration. Based on initial findings in Arabidopsis, the authors demonstrate that ectopic expression of the Arabidopsis *HARDY* (*HRD*) gene in rice improves WUE by enhancing photosynthetic efficiency and reducing transpiration, with an associated increase in biomass. These results may contribute to successful engineering of higher WUE in additional economically important species, including crops and plants used for bioenergy purposes.

Karaba et al. identified the *hardy* dominant mutant by its smaller, thicker, and darker green leaves combined with stronger than normal root system while performing a phenotypic screen of an activation-tagged Arabidopsis mutant collection. Characterization of the mutant revealed that it over-expressed a locus encoding an AP2/ERF-like transcription factor, which was named *HARDY* (*HRD*). The *hrd* phenotype was confirmed through additional expression studies and mutant plants were shown to contain extra cell layers with abundant chloroplasts that contributed to the thicker and greener leaves. The strong root phenotype was attributed to increased secondary and tertiary roots which made up a dense root network. Drought and salt tolerance assays revealed that *hrd* plants survived longer periods of drought and up to 300 mM sodium chloride as compared to wild-type plants.

An *AtHRD* expression (OE) construct driven by a strong promoter was next introduced into rice to produce over-expression lines whose growth, seed yield, and germination were unaffected in standard greenhouse conditions. The *AtHRD* OE rice were darker green, contained more tillers, and had increased leaf bundle sheath cells than untransformed controls. A number of physiological analyses were performed which showed the OE rice were more drought-tolerant, had increased WUE, reduced transpiration rate, lower stomatal conductance, increased photosynthetic efficiency, increased carbon assimilation and increased biomass. The majority of biomass increase was due to increased shoot production under non-drought conditions and increased root growth under drought conditions. These data show that it is possible to increase WUE and biomass through decreases in stomatal conductance or increases in photosynthetic efficiency and suggest that this approach could be used in other



plants as well. Plant Research International, Wageningen, have patented the technology and are evaluating future commercial prospects.

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### Stress-relief: Helping Arabidopsis to Cope

By: Joanna Friesner, MASC Coordinator

Plants have evolved complex mechanisms to tolerate and respond to external stresses such as drought, cold, salt, and heat, which can lead to dramatic crop losses. A common plant response is to modulate stress perception and signaling pathways via regulatory factors that alter transcription levels of thousands of downstream genes, as well as through post-transcriptional and post-translational mechanisms. Researchers have elucidated a number of Arabidopsis genes over the last 15+ years that are useful for the improvement of stress tolerance in plants; several candidates have been transformed into other species resulting in stress-tolerant crops such as rice, tomato, canola, corn, cotton and wheat. While many of the identified genes are transcription factors, others, such as ion transporters, have also been found to be involved in stress-tolerance.

A functional genomics screen to identify Arabidopsis regulatory genes that control Arabidopsis stress responses, recently revealed the importance of RNA metabolism genes in coping with stress and may provide a new method to protect crops against the elements. Kant et al. identified two mutants defective in RNA helicase genes, designated *STRESS RESPONSE SUPPRESSOR1* (*STRS1*) and *STRS2* (1). In wild-type plants, *STRS1* and *STRS2* expression is down-regulated by multiple abiotic stresses, and compared to wild-type, *strs1* and *strs2* mutant plants display increased osmotic, heat and salt, but not cold, stress tolerance during germination and early growth. Examination of transcript profiles in the mutants revealed that stress application results in increased expression of several known stress-responsive genes. Transcript kinetics are similar to those of wild-type plants and increased transcription is not observed in unstressed mutants, suggesting that *STRS1* and *STRS2* normally act to attenuate expression of stress-responsive transcriptional regulators. The authors also found evidence that *STRS1* and *STRS2* regulate both ABA-dependent and independent signaling networks.

A recent follow-up publication described the development and validation of the functional genomics screen. A microarray analysis of early heat stress-responsive genes was presented and these data were included in a relational database along with microarray data investigating Arabidopsis responses to various abiotic stresses. Multiple Stress (MST) genes were identified employing a scoring system that ranked genes based on the number of various abiotic stresses that caused alterations in their expression (2). A subset of the MST genes that encode regulatory genes were designated as Multiple Stress Regulatory (MSTR) genes and a mutant defective in the highest-scoring gene was validated for altered stress-sensitivity. The database provides the basis for future experiments on putative stress-

responsive regulatory genes and should identify candidates for potential use in transgenic crops. Simon Barak of Ben-Gurion University of the Negev, lead author of the studies, recently entered into a research agreement with Bayer BioScience, part of Bayer CropScience. The collaboration will involve screening mutants in additional candidate genes as well as expanding the initial functional genomics screen (3).

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# Reports of the MASC Subcommittees

## Clone-based Functional Genomics Resources (ORFeomics)

Prepared by Joe Ecker (Chair, [ecker@salk.edu](mailto:ecker@salk.edu))

Activities during the last year represent a significant shift from the past. While some additional unique Open-Reading-Frame (ORF) have been produced, large scale ORF clone production has transitioned from ORFeome production to the construction of large set of 'destination' or 'functional' clone sets (Table 1). Examples of functional clone collection may include clone sets for *in planta* overexpression, yeast two-hybrid interactome mapping, tagged ORF expression, etc. that are derived from the ORFeome collection.

Regarding unique ORF clone production (gene ORF clones not currently available in any form) and deposition during the past year, Salk Institute Genomic Analysis Laboratory (SIGnAL) deposited 192 additional ORF clones with ABRC. In addition, it is anticipated Gateway ORF clones produced from the ATOME project will soon be available in a French stock center (<http://urgv.evry.inra.fr/ATOME/index.cgi>) and that ~500 of the unique ORF clones will be deposited with ABRC. Finally, the RIKEN Plant Science Center (PSC) project to collect full-length cDNAs (clone with 5' and 3' UTRs) from *Arabidopsis thaliana* is now completed and all RAFL clones produced were deposited with the RIKEN Bio Resource Center (BRC). In addition, the RIKEN group has collected full-length cDNAs from the salt-tolerant *Arabidopsis* relative, *Thellungiella halophila* (1). These cDNA clones are available from RIKEN BRC. More recently, RIKEN PSC activities have shifted to the collection of full-length cDNAs from various crops and trees.

Regarding 'functional' *Arabidopsis thaliana* ORF clone collections, several new large 'destination' vector clone sets were deposited in ABRC during the past year. Examples of large clone sets deposited in ABRC include: 588 ORF expression clones in a pLIC-C-TAP vector deposited by the Kumar/Snyder: Arabidopsis Protein Chip Project and 18,288 yeast two-hybrid expression clones (pDEST-AD: 9,152 ORFs and pDEST-DB: 9,106 ORFs) deposited by the Vidal/Hill/Ecker (CSSB/Salk) Plant Protein Interactome project.

Finally, there remain a significant number of annotated genes with no evidence of expression and/or no cDNA/ORF clone (see thermometers, page 17-18). The development of a new method called RNA-Seq (Lister et al. 2009) for deep, strand-specific transcriptome sequencing will likely allow the identification of transcripts for many of the remaining annotated genes along with novel spliced forms for other genes. For example, RNA-seq may be combined with flow sorted cell samples prepared from many distinct cell types to identify

rare/low expressed transcripts. Future ORF clone production for the remaining genes with no ORF clone will likely utilize deep paired-end RNA-Seq information for *in silico* gene model construction followed by standard RT-PCR subcloning/sequencing approaches or, more likely, with ever decreasing cost, these ORFs may simply be chemically synthesized.

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## Natural Variation and Comparative Genomics

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*Arabidopsis thaliana* serves not only as a model system for understanding the genetic, molecular and biochemical functions underlying plant life, but also for determining the mechanisms by which these functions (and variation in them) contribute to ecological and evolutionary success. The ease of genetic manipulation, abundant natural variation, and rich understanding of genetic and biochemical pathways all point to the suitability of *Arabidopsis* and its relatives for ecological, quantitative genetic, and evolutionary studies. Indeed *Arabidopsis* and its relatives represent an ideal system for understanding environmental adaptation, quantitative genetic variation, and microevolution at the mechanistic level. Natural variation and comparative genomics studies are required for true understanding of how genes function. For example, understanding how genes are used to build an *A. thaliana* plant requires knowledge not only about molecular functions in *A. thaliana*, but also an understanding of why *A. thaliana* genes don't make a plant that looks more like *Capsella*, or *Brassica*, or *Cleome*, or cotton. Thus, understanding the genetic basis of developmental, metabolic, or physiological differences between species is at the very crux of plant biology. Finally, diverse species with different structures, life histories, and environmental adaptations provide tools for exploring gene function (in the molecular sense), that complement those traditionally deployed in *A. thaliana*. More generally, *A. thaliana* is second only to humans when it comes to knowledge and ability to exploit sequence variation. *A. thaliana* surpasses humans when it comes to tools available for understanding how sequence variation affects biological processes. *A. thaliana* indeed is serving as a useful model for developing methods that will be applicable in medical genetics.

## Notable Advances and Publications

The most notable advances continue to be in the area of 'omics technology. Whole genome sequence of *Arabidopsis lyrata* has been assembled, annotated, and released (<http://genome.jgi-psf.org/Araly1/Araly1.home.html>). A draft sequence of papaya, a basal *Brassicales* is in the same order as *Arabidopsis*, has been produced [1]. The utility of these sequences can be seen in studies where comparison of the papaya, *Arabidopsis* and grape genomes led to the conclusion that gene transposition is much more frequent than commonly thought [2]. These three genomes along with poplar and rice were used to define ancient hexaploidy in the angiosperm lineage [3].

Short-read sequencing is being used to sequence many *Arabidopsis* accessions. Three have been published already [4],

more than one hundred are in progress, and 1001 are planned in total (<http://1001genomes.org/>). Characterization of variation in 'omics traits, and determining loci responsible for that variation, is moving beyond the transcriptome analysis that we reported last year. A whole-genome tiling array is available and is being used for analysis of variation not only in transcript levels but also splicing, allele-specific expression, and methylation [5,6]. Similarly variation in metabolite, ion, and protein abundance is being characterized and mapped [7-10]. A SNP chip that queries 250,000 polymorphisms has been developed and is being used to genotype hundreds of natural accessions (<http://walnut.usc.edu/>). This data will be a tremendous resource for genome-wide association mapping. For QTL mapping, at least seven additional Recombinant Inbred Line (RIL) populations have been developed and released [11,12].

**Table 1. Arabidopsis ORF and cDNA clone repertoires**

Creator	Format	Focus	Validation	Scale	URL	Stock center†
<b>ORF clones</b>						
SSP consortium & Salk Institute	Univector pUNI51		Full sequence	14,398	<a href="http://signal.salk.edu/cdnastatus.html">signal.salk.edu/cdnastatus.html</a> <a href="http://methylo.me.salk.edu/cgi-bin/clones.cgi">http://methylo.me.salk.edu/cgi-bin/clones.cgi</a>	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	<a href="http://signal.salk.edu/cdnastatus.html">signal.salk.edu/cdnastatus.html</a> <a href="http://methylo.me.salk.edu/cgi-bin/clones.cgi">http://methylo.me.salk.edu/cgi-bin/clones.cgi</a>	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	<a href="http://interactome.dfci.harvard.edu/A_thaliana/host.php">http://interactome.dfci.harvard.edu/A_thaliana/host.php</a>	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	<a href="http://www.tigr.org/tdb/hypos/">www.tigr.org/tdb/hypos/</a>	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.	1,281		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	962	<a href="http://gabi.rzpd.de/materials/">gabi.rzpd.de/materials/</a>	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	<a href="http://plants.gersteinlab.org/">plants.gersteinlab.org/</a>	ABRC
ATOME 1	Gateway entry		5' and 3' end seq.	1,809	<a href="http://urgv.evry.inra.fr/orfeome/">urgv.evry.inra.fr/orfeome/</a>	CNRGV
ATOME 2	Gateway entry, no stop	Originates from SSP	5' and 3' end seq.	3,476	same	CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	<a href="http://plantsubq.genomics.purdue.edu">plantsubq.genomics.purdue.edu</a>	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	<a href="http://genetics.mgh.harvard.edu/sheenweb/category_genes.html">genetics.mgh.harvard.edu/sheenweb/category_genes.html</a>	ABRC
<b>cDNA clones</b>						
RIKEN/SSP/ Salk Institute	λZAP or λPS		Full sequence	22,614	<a href="http://www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml">www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml</a>	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	<a href="http://gabi.rzpd.de/materials/">gabi.rzpd.de/materials/</a>	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	<a href="http://www.genoscope.cns.fr/Arabidopsis">www.genoscope.cns.fr/Arabidopsis</a>	CNRGV

†Stock centers 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, UK), <http://arabidopsis.info/>
- BCCM/LMBP Plasmid and DNA library collection (BCCM/LMBP, Belgium), [http://bccm.belspo.be/db/lmbp\\_gst\\_clones/](http://bccm.belspo.be/db/lmbp_gst_clones/)
- Open Biosystems Inc., USA, [www.openbiosystems.com/](http://www.openbiosystems.com/)

## Needs and recommendations

- Infrastructure for archiving, organizing, analyzing, and displaying the huge amount of sequence data that will be generated in the next few years is needed.
- Longer funding cycles (4-5 years minimum) are needed to allow QTL mapping and identification.
- Better access to mapping populations and data is needed. Some have been deposited in the stock centers whereas others are available from individual researchers. We encourage the deposition of all mapping populations in the stock centers; some of us have had problems obtaining lines from individual researchers because of institutional Material Transfer Agreements (MTAs). The community would benefit from an organized effort to collect and organize NILs and HIFs for each RIL population. Finally, all genotyping data should be provided in a common and easily transformable format.
- Last year we discussed the need for a “fingerprinting” method for identifying *A. thaliana* stocks. SNP chip genotyping will provide the reference data, but we need to develop an inexpensive way for individual labs to fingerprint their own stocks.
- An integrated database for storing and retrieving QTL data and results, especially for ‘omics traits is needed. Ideally this would use a common mapping framework to facilitate comparison among experiments and populations. This is non-trivial task and is best carried out at the community level. Ideally, this could be incorporated into TAIR.

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## Phenomics

Prepared by Eva Huala (Co-chair, huala@acoma.stanford.edu) and Sean May (Co-chair, sean@arabidopsis.info)

### *Phenomics seed and DNA resources*

The Salk Institute Genome Analysis Laboratory (SIGnAL) continues its progress toward making a set of genetically purified, confirmed T-DNA insertion lines consisting of two alleles for each *Arabidopsis* gene available for ordering from the *Arabidopsis* Biological Resource Center (ABRC). When completed, this phenome-ready population will consist of 50,000 lines, the goal being to confirm and purify two insertion alleles each for approximately 25,000 loci. To date, 28,558 confirmed lines have been received by ABRC. This set of completed lines provides two homozygous insertion alleles for 8,517 genes, and a total of 16,856 genes are currently covered by at least one homozygous insertion. A complete set of the lines as well as a one-allele per locus (‘unigene’) set are being made available from ABRC at an economical price. The confirmed population is also being organized into pools of different sizes to allow efficient forward phenotypic screening for traits that can be identified within larger populations.

ABRC has also recently begun to distribute a collection of approximately 8,000 artificial microRNA (amiRNA) clones developed by Greg Hannon, Dick McCombie, Rob Martienssen, Detlef Weigel and Ravi Sachidanandam. Production of this resource was funded by an *Arabidopsis* 2010 grant, A Comprehensive Resource for Analysis of *Arabidopsis* Gene Function (<http://2010.cshl.edu/scripts/main2.pl>), the focus of which was to develop a genome wide resource for RNAi interference in *Arabidopsis* using amiRNAs with altered targeting capacity that can efficiently and specifically silence any chosen gene. The clones received by ABRC target approximately 8,000 genes, and were previously distributed exclusively by Open Biosystems. The ultimate goal of the project is to develop several clones for each gene and these will be made available through Open Biosystems and ABRC. The clones received to date can be found and ordered through the TAIR web site.

### *Tools for Association Mapping*

Detlef Weigel, Max Planck Institute:

The 1001 Genomes Project has completed Illumina sequencing of 80 accessions at 6-12x coverage and 4 additional accessions to much higher coverage (<http://1001genomes.org>). This material will soon be available through the stock centers for association mapping, to complement the collection genotyped with the 250k SNP chip by Borevitz and Nordborg. All 250k SNPs are being called in the 84 accessions mentioned above, and they can be seamlessly integrated into any association mapping project that uses the Borevitz/Nordborg collection, or they can be used on their own. With this collection, nearly complete sequence information will be available for any haplotype that comes out of any 250k SNP association mapping project.

### *Phenotype annotation tools and ontologies*

The Plant Ontology Consortium (<http://www.plantontology>).



org/) led by Pankaj Jaiswal (Oregon State University) has received renewed funding from NSF to continue developing the plant structure and growth/developmental stage ontologies for use in describing plant phenotypes. Other useful ontologies for describing plant phenotypes and related data can be found at the Open Biomedical Ontologies website (<http://www.obofoundry.org/>). These include the GO biological process and cellular component ontologies, the PATO ontology for phenotypic qualities, and ontologies for describing units of measurement (UO), experimental conditions (OBI), and chemical entities of biological interest (CHEBI).

Phenote, a curation tool to facilitate annotating phenotypes using ontologies, was developed by National Center for Biomedical Ontology (NCBO) in collaboration with Berkeley Bioinformatics and Ontologies Project (BBOP) ([www.phenote.org](http://www.phenote.org)). It's currently in use by several model organism databases including FlyBase, ZFIN, WormBase and others. Data annotated with Phenote is based on the EQ model for representing phenotypes, combining entities from any ontology (for example GO or PO) with qualities (such as those found in PATO).

### ***Phenomics community events***

The 1st International Plant Phenomics Symposium was held in Canberra on April 22-24, 2009. This symposium, the first of its type, was focused on the use of plant phenomics and functional genomics to boost crop productivity and its proceedings will be published in a special issue of the journal *Functional Plant Biology*. Symposium participants, led by Jülich Plant Phenomics Centre (JPPC) and the Australian Plant Phenomics Facility (APPF), have begun to organize an International Plant Phenomics Initiative to provide stronger vehicle for international collaboration. Members of this Initiative are currently working to develop an agenda and will organize a meeting later in 2009 to decide on priorities and actions. The agenda will likely include exchanging protocols, validating systems, exchanging staff for technical education and developing collaborative funding bids. Please contact Bob Furbank ([Robert.Furbank@csiro.au](mailto:Robert.Furbank@csiro.au)) or Frank Gilmer ([jppc@fz-juelich.de](mailto:jppc@fz-juelich.de)) for further information on the Initiative.

### ***High throughput phenotyping projects and data***

Bob Furbank, Australian Plant Phenomics project:

The Australian Plant Phenomics Facility (APPF, [www.plantphenomics.org.au](http://www.plantphenomics.org.au)) consists of two facilities, an Arabidopsis screening module in Canberra (medium throughput growth and chlorophyll fluorescence screening with mathematical morphological analysis and phenomic database capability) and the Plant Accelerator automated glasshouse facility in Adelaide. The NCRIS funded National Facility will be available to researchers at the marginal cost of running the facility and several international collaborations are being established and encouraged. The resulting phenotype data will be freely released to the international community following a quarantine period (6-12 months) to allow data to be prepared for publication. In addition, a new Australian project, Phenomics Ontology

Driven Data Management (PODD), has received funding to provide data management services to the APFF and other Australian phenomics projects as well as providing access to phenotype data for the broader community. This project plans to collaborate with TAIR, Gramene, and the Plant Ontology Consortium in the areas of data exchange, data standards and ontology development.

Minami Matsui, RIKEN:

A comprehensive new database called the RIKEN Hub Database (<https://database.riken.jp>) has been developed by Tetsuro Toyoda to provide an integrated access point for RIKEN data. The new database includes a section on activation-tagged lines (<http://activation.psc.database.riken.jp>) which contains phenotype data and insertion site information for 500 activation-tagged lines found to have visible phenotypes (Miki Nakazawa, Youichi Kondou and Eli Kaminuma). A set of Ac/Ds transposon lines including 200 visible phenotypes and flanking sequence information for 18,000 integration sites is described at <http://rapid.psc.database.riken.jp> (Takashi Kuromori and Eli Kaminuma). Another section of the new database (<http://arabifox.psc.database.riken.jp>) contains information on 1,500 visible phenotypes and 9,000 integrated full-length cDNAs for Arabidopsis FOX (Full-length cDNA over-expressor gene) lines (Takanari Ichikawa, Youichi Kondou and Eli Kaminuma). RIKEN BRC (Bioresource center; Masatomo Kobayashi) has begun to distribute 1,000 of the Arabidopsis FOX lines, see <http://www.brc.riken.go.jp/lab/epd/Eng/species/arabidopsis.shtml> for ordering information. The "Rice FOX Arabidopsis mutant database" is now freely accessible at <http://amber.gsc.riken.jp/ricefox/>. Information on 11,000 rice full-length cDNAs that have been expressed in Arabidopsis is included, along with the resulting phenotypes which have been categorized into subsets using various criteria.

Phenotype data for 140 Ac/Ds transposon insertion lines (RAPID) generated by Dr. Takashi Kuromori and having visible phenotypes (out of 4000 lines examined) are freely available at <http://rarge.gsc.riken.jp/phenome/> and their associated phenotype data will be integrated into TAIR. An additional set of 500 activation-tagged lines with phenotypes (generated by Dr. Youichi Kondou) can be found at <http://amber.gsc.riken.jp/act/top.php> (the current requirement to sign a Materials Transfer Agreement before viewing the data is expected to be lifted soon). A new project to generate Arabidopsis Full-length cDNA overexpressing (FOX) lines for 13,000 Arabidopsis full-length cDNAs generated by Dr. Takanari Ichikawa is now underway and these will be made accessible from RIKEN BRC. A similar project for overexpressing rice cDNAs in Arabidopsis can be found at <http://ricefox.psc.riken.jp/login/> but is currently only accessible to Japanese scientists (this restriction will be lifted by the end of 2008). A hub database project has been organized by Dr. Tetsuro Toyoda at RIKEN to connect Arabidopsis genome and phenome information, including Ac/Ds and Activation-tagged line projects described above. See <http://omicspace.riken.jp/> for a full description of the new database and <http://www.psc.riken.go.jp/english/database/index.html> for access to current RIKEN databases.



Pierre Hilson, Christine Granier, AGRON-OMICS project:

The AGRON-OMICS project, which stands for Arabidopsis GROwth Network integrating OMICS technologies (<http://www.agron-omics.eu/>), is conducting an in-depth study of leaf growth in the model plant species *Arabidopsis thaliana*. Started in November 2006, this European Integrated Project aims at the identification of the molecular components controlling growth and a better understanding of their interactions. A major asset of the project is PHENOPSIS, an automated platform for Arabidopsis leaf growth phenotyping developed at INRA (Granier et al., 2006 New Phytologist). Within AGRON-OMICS, the high-throughput phenotyping efforts based on PHENOPSIS focus on the measurements of an exhaustive data sets of leaf growth variables from the rosette scale down to the cellular scale in hundreds of genotypes affected in cell cycle, endoreduplication, cell wall properties, metabolism, hormonal status, circadian rhythm and flowering time. At this time, more than 160 genotypes have been grown and phenotyped in the platform for the AGRON-OMICS project. A database has been developed to organize metadata and phenotypic data associated to the PHENOPSIS platform. It includes data from AGRON-OMICS and from other projects: the ERANET-ARABRAS project, on leaf growth in response to environmental stresses in different accessions (100 lines, 2007-2010) and the GENOPLANTE-DNV project, on the identification of leaf growth QTLs in various recombinant inbred line populations grown in a range of environmental conditions (240 recombinant inbred lines, 2007-2010). Access to the database associated to the PHENOPSIS platform is available online (<http://bioweb.supagro.inra.fr/phenopsis/>) and data stored in the database are made publicly available just after publication. Software applications are also being developed by several groups in the context of AGRON-OMICS to exchange metadata and phenotypic data and to automatically measure the growth parameters defining leaf growth at the macro- and microscopic scale.

## Proteomics

Prepared by Wolfram Weckwerth (Co-chair, [weckwerth@mpimpgolm.mpg.de](mailto:weckwerth@mpimpgolm.mpg.de)), Sacha Baginsky (Co-chair, [sbaginsky@ethz.ch](mailto:sbaginsky@ethz.ch)), Klaas van Wijk ([kv35@cornell.edu](mailto:kv35@cornell.edu)) and Harvey Millar (Co-chair, [harvey.millar@uwa.edu.au](mailto:harvey.millar@uwa.edu.au))

A MASC subcommittee for *Arabidopsis thaliana* proteomics was established to consolidate databases, technique standards and experimentally validated candidate genes and functions. Since that time many new approaches and databases were developed. Altogether the resources of the MASC Proteomics (MASCP) subcommittee provide the largest collection of proteomics data for this higher model plant. This common effort of MASCP is comparable with the HUPO organization (human proteome project) and has identical potential with respect to advanced proteomic techniques (such as Mass Western and collections of thousands of proteotypic peptides) and a large collection of proteomic databases (contacts with HUPO are established by members of MASCP).

Recent activities:

- MASCP published a joint report: "The Multinational Arabidopsis Steering Subcommittee for Proteomics Assembles the Largest Proteome Database Resource for Plant Systems Biology" (Journal of Proteome Research 2008, 7 (10), pp 4209–4210) that provides a series of resources for plant proteome researchers.
- Meetings and the organization of proteomics workshops are established on a regular basis at the International Conference on Arabidopsis Research. A well attended workshop was held in 2008 in Montreal, and another is planned for Edinburgh in 2009. The 2008 workshop included research presentations by MASCP members and others, including students and postdocs who submitted proteomics-related abstracts and were selected for oral presentation, followed by group discussion.
- A common webpage "MASC proteomics" was established including standards for different proteomic techniques, databases, procedures; meetings, proteome labs, etc. (see <http://www.masc-proteomics.org/>). This webpage will also host discussion platforms and database-crosslinks in the future.
- The last couple of years have seen significant advance in our understanding of the peroxisome proteome in Arabidopsis, thanks to a number of MASCP members (Plant Cell October 2007 19:3170-93; Plant Physiology, December 2008 148(4):1809-29; Plant Physiology, March 2009 10.1104/pp.109.137703)
- The major databases associated with MASCP, AtProteome ([www.AtProteome.ethz.ch](http://www.AtProteome.ethz.ch)), Plant Proteome Database (PPDB) (<http://ppdb.tc.cornell.edu>), SUBA ([www.plantenergy.uwa.edu.au/suba2](http://www.plantenergy.uwa.edu.au/suba2)), ProMEX (<http://promex.mpimp-golm.mpg.de/home.shtml>) and PhosPhAT (see <http://phosphat.mpimp-golm.mpg.de/>) have continued to be updated and expanded in 2008-2009.
- A special issue of the Journal of Proteomics was initiated and edited by Dr Jesús Jorrín-Novo, titled "Plant Proteomics", Volume 72, Issue 3, Pages 283-574 (13 April 2009). This contained research articles and reviews by a wide range of plant proteome researchers including a number of MASCP members. This shows the increasing breadth of proteome research in both Arabidopsis and other plants. Examples of articles in the issue include: Abiotic environmental stress induced changes in the *Arabidopsis thaliana* chloroplast, mitochondria and peroxisome proteomes; Hydroponics on a chip: Analysis of the Fe-deficient Arabidopsis thylakoid membrane proteome; Phosphoproteomic analysis of nuclei-enriched fractions from *Arabidopsis thaliana*; Blue native DIGE as a tool for comparative analyses of protein complexes, and Validation of gel-free, label-free quantitative proteomics approaches: Applications for seed allergen profiling.
- The increased use of large protein interaction databases being developed by various agencies for plant protein data and their cross-linking to MASC proteomics resources is the main goal of the next years.

## Systems Biology

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

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

A primary goal of the Systems Biology Subcommittee is to further the use of Systems Biology among Arabidopsis researchers to elucidate the structure, dynamics, and organizational principles of the regulatory and metabolic networks that support living cells. The MASC Systems Biology and Bioinformatics Subcommittees held a joint workshop on “Frontiers in Plant Systems Biology” at the Arabidopsis conference in Montreal, 2008. The goal was to bring together groups that produce, integrate and model data from a systems perspective. There were talks from biologists performing cutting-edge systems research that highlighted the new frontiers in genomic data collection for systems biology and the challenges in data storage, analysis and integration. Contributors also discussed the state-of-the art and vision for systems research in plants. There was also a presentation from the NSF-funded iPlant Collaborative initiative. The goals of the iPlant and the contribution of the iPlant initiative to advance systems biology research in Arabidopsis were communicated at the workshop.

The Systems Biology Subcommittee has a Wiki at [http://arabidopsis.info/wiki/index.php/Plant\\_Systems\\_Biology](http://arabidopsis.info/wiki/index.php/Plant_Systems_Biology). We encourage researchers to post questions, comments, suggestions, news or any other material that may stimulate discussion related to Systems Biology approaches in Arabidopsis. Several excellent publications last year illustrated the growing breadth and sophistication of Systems Biology approaches to gene network, signaling and developmental research in Arabidopsis; only a few can be highlighted here:

- Systems approach identifies an organic nitrogen-responsive gene network that is regulated by the master clock control gene CCA1. Gutiérrez RA, Stokes TL, Thum K, Xu X, Obertello M, Katari MS, Tanurdzic M, Dean A, Nero DC, McClung CR, Coruzzi GM. *Proc Natl Acad Sci U S A*. 2008. 105:4939-44.
- A systems approach reveals regulatory circuitry for Arabidopsis trichome initiation by the GL3 and GL1 selectors. Morohashi K, Grotewold E. *PLoS Genet*. 2009. 5:e1000396.
- MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays. Popescu SC, Popescu GV, Bachan S, Zhang Z, Gerstein M, Snyder M, Dinesh-Kumar SP. *Genes Dev*. 2009. 23:80-92.
- Root system architecture from coupling cell shape to auxin transport. Laskowski M, Grieneisen VA, Hoffhuis H, Hove CA, Hogeweg P, Marée AF, Scheres B. *PLoS Biol*. 2008 Dec 16;6(12):e307.

# Analysis and Recommendations

We are at a watershed moment in plant biology research. There is a dire need for a more thorough understanding of plant biology in order to meet the increasing demands on agriculture for food, fuel and fiber in a sustainable manner. The revolution in genome sciences has led to an unprecedented increase in information for a number of target plant species, much of which is based on studies in *Arabidopsis*. These advances in *Arabidopsis* research lay the foundation for the understanding of plant biology required to meet the substantial challenges faced by agriculture and will lead to a deeper understanding of fundamental biological questions.

Research in *Arabidopsis* continues at an impressive pace. This is the result of the interplay of a variety of factors including the inherent properties of this remarkable organism, the synergistic development of a powerful set of tools in *Arabidopsis*, the easy access to various stocks and other key reagents, the openness and collegiality of the *Arabidopsis* community, and the generous support from government and private sources. We have entered a new era of plant biology research, allowing questions to be addressed at an unprecedented scale including studies at the level of the genome, transcriptome, proteome, metabolome and multiple other “omic” approaches. This presents both unparalleled opportunities, as well as important challenges that need to be met to continue to promote discovery in this reference species.

As the 2010 project in the US and other affiliated programs begin to wind down, there needs to be funding vehicles in place for support of large-scale projects and tool development, in addition to high level funding of individual labs pursuing cutting edge, creative research on more focused topics. This is essential in order to maintain high level research in plants. For the optimal development and implementation of these tools, it is essential that the open spirit of collaboration and communication remains robust in the *Arabidopsis* community. MASC will continue to play a role in maintaining this open dialogue and will help enable international cooperation among researchers.

A long term goal of plant biology is to be able to predict and modify growth and developmental characteristics using mathematical models based on a set of known parameters, including plant signaling elements and transcriptional responses, both in the course of normal growth and development and in response to various environmental and genetic perturbations. The use of modeling techniques is at a nascent stage but several successes have been achieved and it is expected that the pace of this approach will accelerate as the iPlant Collaborative and other initiatives promoting bioinformatics, mathematical tools, and computational approaches hit their stride. Predictive biology will underpin the developing area of synthetic biology

and the molecular tools available from *Arabidopsis* research provide essential building blocks to generate potentially new pathways of signaling, metabolism and development. While mathematical modeling is an important tool to achieve this, it is imperative that data continue to be obtained both through large collaborative projects generating high throughput “omic” data, but also by individual research labs doing work focused on a smaller scale.

The increasing ability to obtain sequence data at decreasing costs has altered the research landscape in *Arabidopsis* and other species. This will allow comparisons among genomes to understand the genetic basis for natural selection, the evolution of genomes, and the adaptability of plants. It offers the possibility of rapid identification of genes corresponding to mutations via whole genome sequencing and provides a novel avenue for transcript profiling and other high throughput analysis such as ChIP-seq. However, the volume and variety of data being generated in these and other “omic” approaches present significant challenges for data storage, retrieval and integration. The cooperation and communication of those running large databases throughout the international *Arabidopsis* community is essential to ensure easy retrieval and integration of these data. Central portals such as TAIR need to remain strongly supported, both by funding agencies and contributors of data sets.

It is evident that the breakthroughs in *Arabidopsis* research have contributed both directly and indirectly to research in agriculturally relevant plant species. This translational research will continue as a natural extension of the basic research breakthroughs obtained in this model species. While it may seem counterintuitive to some to work on a simple weed to understand how to improve crop species, past experience clearly supports the notion that a fuller understanding of how basic processes work in model systems translates in direct and unexpected ways to practical applications. This message must continue to be impressed upon the general public, the broader plant biology community, as well as government officials.

Following initial discussion by MASC in summer, 2007, a series of “*Arabidopsis* 2020” meetings were held in the US, Europe and Japan in 2008 at which directions for the next decade of *Arabidopsis* research following the completion of the 2010 projects were discussed. These goals were further discussed at the 2008 MASC meeting during the International *Arabidopsis* Conference in Montreal and there was broad consensus regarding important areas on which the community should focus. Based on the outcomes of these meetings and additional discussions, the following are the recommendations by MASC as the most important goals for the next year of *Arabidopsis* research.

## MASC Recommendations and Short-term Goals for the Next Year

1. Work towards the completion of a reference collection of homozygous insertional lines for all *Arabidopsis* genes. Ideally, this will include two alleles for all genes. While other methods are important for helping decipher the function of genes, the characterization of loss-of-function alleles remains the gold standard for defining gene function. The development of an easily accessible, large scale collection of insertions in *Arabidopsis* has been an important resource that has made a major contribution to the rapid pace of research in plant biology. Likewise, an easily available collection of homozygous insertion mutant lines represents the next logical step to increase the utility of this tool which would enable high-throughput saturation screens, efficient and rapid assessment of gene function, and testing of novel hypotheses, as well as other studies. However, genetic redundancy continues to pose significant limitations to genetic approaches; therefore, additional facile approaches need to be developed, such as the development of artificial microRNAs and RNAi resources to reduce the function of multiple target genes.
2. Support projects that work towards obtaining detailed and dynamic patterns of gene expression and epigenetic modifications across spatial, developmental, and environmental variables.
3. Continue to expand the large scale analysis of proteins, including the interactome, the description of changes in protein modifications such as phosphorylation and the analysis of the spatial and temporal pattern of expression of the proteome. These data need to be incorporated into accessible and compatible databases to enable system biology approaches.
4. Continue to develop methods for high throughput analysis of metabolites across spatial, developmental, and environmental variables, ultimately including analysis at single cell resolutions.
5. The community should support the development of a complete, readily accessible collection of *Arabidopsis* Open Reading Frames (ORFs). The lack of a complete collection of full-length ORFs hampers some high throughput approaches, including those that are obvious now, such as defining the interactome, and others that are just being conceived.
6. Continue to address the roles of the large number of genes in *Arabidopsis* with relatively little functional information. Some hypotheses as to the functions of these genes will come from system biology approaches in which predictive models for gene function will emerge from correlative patterns of expression, interaction, etc. derived from analysis of large databases comprised of high quality information. An important avenue to the understanding of these genes will come from analysis of loss-of-function lines, including methods to address functional overlap.
7. Continue to develop large collections of transgenic lines expressing fluorescently-tagged proteins, or other methods to visualize the intracellular localization of all the proteins in *Arabidopsis*.
8. Work towards the goal of improving curation approaches and making databases compatible; facilitate the storage and integration of phenotypic data, expression data etc. This is increasingly important as the volume of data obtained grows at an ever more expanding rate.
9. The community should continue to work with the iPlant Collaborative, and other similar groups, to develop the mathematical tools and informatics infrastructure necessary to enable new conceptual advances, integrative studies, and systems biology in *Arabidopsis*. As more information becomes available, the ability to model biological processes in plants will increase in importance. These modeling tools need to be accessible to the general *Arabidopsis* community to aid in the analysis of various developmental, signaling, metabolic and other pathways. The ultimate goal is be able to predict how the various molecular parts of a plant interact to achieve a particular pattern of growth and development in a given environmental condition.
10. Expand the collection of sequenced wild accessions and species closely related to *Arabidopsis* to at least several hundred. These datasets will be important in helping understand the evolution and genome dynamics of plants and will enable large-scale association studies in natural populations and the identification of alleles contributing to phenotypic diversity.
11. Continue to expand our understanding of the multitude of signaling pathways that act in plants and how these interact to modulate plant growth and development across various environmental contexts. As more information becomes available, mathematical modeling tools can be used to help decipher how these pathways function in detail and enable predictions of how perturbations affect the output of these signaling networks.



# The International Arabidopsis Functional Genomics Community

## Country Highlights

### Argentina

There continues to be a steady increase in Argentinean Arabidopsis publications including peer-reviewed articles and reviews in international journals, with notable rate increases after 2005. See Argentina report for graph.

### Australia and New Zealand

- Construction of high throughput phenotyping facilities in Canberra and Adelaide is underway with full commissioning in 2009.
- Arabidopsis 2013 - The 24th International Conference on Arabidopsis Research will be held in Australia.
- The 1st International Plant Phenomics Symposium, focused on the use of plant phenomics and functional genomics to boost crop productivity, was held in Canberra on April 22-24, 2009.

### Austria

- Notable appointments: Magnus Nordborg has been appointed as director of the Gregor Mendel Institute. Wolfram Weckwerth has been newly appointed as Head of the Molecular Systems Biology at the University of Vienna.
- Award: Karel Riha received one of eight START prizes of the FWF for studies on telomere components in Arabidopsis, receiving €1.2 million award for research over the next 6 years.

### Belgium

Recent notable publications involving Belgian researchers: Dhonukshe et al. (2008) Generation of cell polarity in plants links endocytosis, auxin distribution and cell fate decisions. *Nature* 456, 962-966. De Smet et al. (2008) Receptor like kinase ACR4 restricts formative cell divisions in the Arabidopsis root. *Science* 322, 594-597

### Canada

Canada hosted the 19th ICAR in Montreal in July, 2008, the first time the meeting has come to Canada.

### China

- In 2008, the National Science Foundation of China (NSFC) funded over 50 projects mainly using Arabidopsis and rice model species under the "Molecular Mechanisms of Plant Hormone Initiative."

- The Institute of Plant Sciences, headed by Dr. Hong Ma who recently returned from Pennsylvania State University, USA, was inaugurated on December 3, 2008 at Fudan University, Shanghai.
- Several Chinese journals, including *Molecular Plant*, *Journal of Integrative Plant Biology*, *Journal of Genetics and Genomics*, and *Cell Research*, now are international, publishing peer-reviewed English articles.

### France

Notable publications involving French researchers: Gomez-Roldan et al. (2008) Strigolactone inhibition of shoot branching. *Nature* 455, 189-194. Blein et al. (2008) A conserved molecular framework for compound leaf development. *Science* 322, 1835-1839. Navarro et al. (2008) Suppression of the microRNA pathway by bacterial effector proteins. *Science* 321, 964-967. Brodersen et al. (2008) Widespread translational inhibition by plant miRNAs and siRNAs. *Science* 320, 1185-1190. Bikard et al. (2009) Divergent evolution of duplicate genes leads to genetic incompatibilities within *A. thaliana*. *Science* 323, 623-626.

### Germany

- The 5th Tri-National Arabidopsis Meeting (Germany-Austria-Switzerland), attended by around 200 participants, was held in Zuerich, Switzerland; September 10-13, 2008, and was organized by ETH Zuerich.
- The Young Researcher Exchange Program (by AFGN) concludes this year after supporting 7 PhD students.

### Israel

- In 2008, ~40 research articles employing Arabidopsis were published from groups in Israel.
- Last year it was reported that BARD was canceling the panel that funded the majority of Arabidopsis research. While this year's awards have yet to be announced, according to a senior BARD official: "Rumors of the death of Arabidopsis at BARD are premature."

### Italy

- Several Italian labs working on Arabidopsis are involved in two different ERA-PG projects: CISCODE (Cis-element conservation and divergence in plant reproductive development) and MULTI-STRESS.
- Felice Cervone of University La Sapienza – Rome was the recipient of a European Research Council Advanced Grant.

## Japan

- Dr. Kazuo Shinozaki received 1st place for the most cited researchers in Plant Science in 1997 - 2007. [Science Watch ISI Thomson]
- The 2010 International Conference on Arabidopsis Research (ICAR) will be held in Japan for the first time in its 45 year history.
- Noteworthy Japanese publication: Umehara et al. (2008) Inhibition of shoot branching by new terpenoid plant hormones. *Nature* 455:195-200.

## The Netherlands

- The Dutch Government approved the second phase of the CBSG project which supports Arabidopsis research, including bioinformatics and enabling technologies, with 4.5 M€.
- Ben Scheres (University of Utrecht) obtained a 2.2 M€ Advanced Investigator Grant for Arabidopsis research from the European Union, to be spent on a combination of experimental and computational approaches for the study of root development and plant architecture.

## The Nordic Arabidopsis Network

The second period of the Norwegian Plant Functional Genomics Program runs from 2008-2012 and funding will focus on support to functional genomics projects, including several involving plant systems biology.

## United Kingdom.

- New Funding: (1) There are four new BBSRC committees for funding which include area that Arabidopsis is positioned to address. (2) BBSRC and industry have established a Sustainable Bioenergy Centre to bring together world-leading scientists and industrialists to make sustainable bioenergy an economically and socially viable alternative to fossil fuels. Arabidopsis researchers are involved in a number of the programs. (3) BBSRC has launched the new national Genome Analysis Centre to analyze plant, animal and microbial genomes. (4) The second joint call of the ERA-Net for Plant Genomics funded 12 collaborative research projects in 2008. UK researchers lead 5 of these 12 projects, and all but one involve a UK research group.
- Awards: Prof. David Baulcombe, University of Cambridge, was awarded the Lasker Prize for basic medical research. Prof. Ottoline Leyser, University of York, was awarded a Commander of the British Empire in recognition of her pioneering work in plant biology.

## United States

- The current US-based MASC Coordinator has served since January, 2006 and will pass over duties to a new UK-based Coordinator in fall, 2009. The US National Science Foundation funded the MASC Coordinator position from 2002-2004, and 2005-2009.
- The two newly elected members to the North American Arabidopsis Steering Committee are Xinnian Dong (Duke University) and Blake Meyers (Deleware Biotechnology Institute).
- The iPlant Collaborative (iPC) completed its first year of funding and held 5 Grand Challenge workshops in 2008. The current focus is on development of specific cyberinfrastructure components starting with two Grand Challenge Collaborations: Plant Phylogenetics and Genotype-to-Phenotype.
- U.S. Arabidopsis researchers elected to the National Academy of Sciences in 2008 and 2009 are: James Carrington, Steve Kay, Martin Yanofsky, Johanna Schmitt, Robert Fischer, Sarah Hake, and Detlef Weigel.
- Randy Scholl, Director of the Arabidopsis Biological Resource Stock Center, will retire this fall after serving in the position since 1991.

# Argentina

<http://www.arabidopsis.org/portals/masc/countries/Argentina.jsp>  
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## New Grants from Agencia Nacional de Promoción Científica y Tecnológica (ANPCYT), Argentina, which support Arabidopsis research:

- PICT-2007-00691. Marina Clemente. Production of recombinant proteins with immunoprotective value for the development of plant-based vaccines and characterisation of 90 heat-shock proteins from *Arabidopsis thaliana* and *Nicotiana benthamiana* for their use as adjuvant. National Research Council of Argentina (CONICET).
- PICT-2007-00691 PICT-2007-01244. Lorenzo Lamattina. Biological processes and mechanisms regulated by Nitric Oxide in photosynthetic organisms. Universidad Nacional de Mar del Plata
- PICT-2007-00492. Hernán Boccacandro. Mechanisms associated to the control of water loss, transport and absorption by light quality in *Arabidopsis thaliana* and *Vitis vinifera*. Universidad Nacional de Cuyo

### Young investigator awards:

PICT-2007-00729. Ramiro Esteban Rodríguez Virasoro. Function of GRF transcription factors in *Arabidopsis thaliana*. National Research Council of Argentina (CONICET).

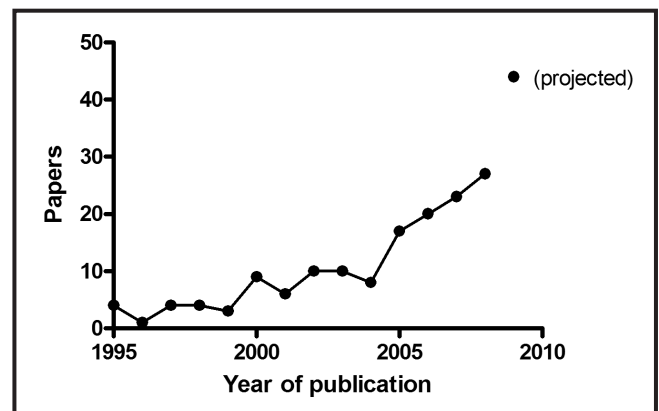
## Buenos Aires Plant Biology Lectures Series 2008

The lectures held in Buenos Aires between 27th and 29th October and attended by many students and researches from different parts of Argentina and South America had a strong Arabidopsis component.

The invited speakers included Sarah Assmann (Penn State University, PA, USA), Bonnie Bartel (Rice University, Houston, TX, USA), Justin Borevitz (University of Chicago, Chicago, IL, USA), Sarah Hake (The Plant Gene Expression Center, Albany, CA, USA).

## Argentinean Arabidopsis-related Publications

The accompanying graph shows a steady increase in Argentinean Arabidopsis publications and includes peer-reviewed articles and reviews in international journals. The papers were selected through a Scopus search using 'Arabidopsis' in the title or abstract, and the resulting list was curated to eliminate papers where the mention to Arabidopsis was only incidental to the research. (Note: The data-point for 2009 is an estimate based on publications from January through March).



## Major funding sources for Arabidopsis functional genomics:

- ANPCYT (Agencia Nacional de Promoción Científica y Tecnológica), <http://www.agencia.secyt.gov.ar/>
- CONICET (Consejo Nacional de Investigaciones Científicas y Técnicas), <http://www.conicet.gov.ar/>
- TWAS (Third World Academy of Sciences), <http://www.twas.org/>

# Australia & New Zealand

<http://www.arabidopsis.org/portals/masc/countries/Australia.jsp>  
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Australia has a strong tradition in plant scientific research with most institutions across all states of Australia having some research involved *Arabidopsis* as a model system. Major areas of *Arabidopsis* research and functional genomics are Canberra, Melbourne and Perth. Major sites of plant science with foci on crops such as grains, grapes and legumes include Queensland, Tasmania, South Australia and NSW. Centres with a strong focus on *Arabidopsis* included Australian Research Council (ARC) Centre of Excellence in Plant Energy Biology ([www.plantenergy.uwa.edu.au/](http://www.plantenergy.uwa.edu.au/)) and CSIRO Plant Industry ([www.pi.csiro.au](http://www.pi.csiro.au)), plus numerous researchers across all the Universities in New Zealand and Australia.

Increasing numbers of New Zealand plant scientists are incorporating *Arabidopsis thaliana* into their research, and several are using functional genomics approaches. Funding is principally available through the Royal Society of New Zealand's Marsden Fund and the New Zealand Foundation for Research, Science and Technology. In addition to the projects being conducted at the universities, research programs are carried out at the Government-owned Crown Research Institutes.

## Key new developments during 2008 were:

**Plant Phenomics** ([www.plantphenomics.org.au](http://www.plantphenomics.org.au)) Construction of high throughput phenotyping facilities in Canberra and Adelaide is underway with full commissioning during 2009. The NCRIS funded National Facility will be available to researchers at the marginal cost of running the facility and several international collaborations are being established and encouraged. For more information contact Bob Furbank ([Robert.Furbank@csiro.au](mailto:Robert.Furbank@csiro.au)) or Mark Tester ([mark.testers@acpfg.com.au](mailto:mark.testers@acpfg.com.au)).

**SUBA** (a SUBcellular location database for *Arabidopsis* proteins) brings together data from chimeric fluorescent fusion protein studies and mass spectrometry surveys of subcellular compartments with protein localisation information obtained from other literature references and bioinformatic prediction tools. The SUBA database provides a powerful means to assess protein subcellular localisation in *Arabidopsis* (<http://www.suba.bcs.uwa.edu.au>).

**Anno-J:** Interactive web-based genome browsing in *Arabidopsis* for large datasets in functional genomics. Julian Tonti-Filippini and A. Harvey Millar ([hmillar@cyllene.uwa.edu.au](mailto:hmillar@cyllene.uwa.edu.au)), ARC Centre of Excellence in Plant Energy Biology, The University of Western Australia, Perth. The rapid growth of new types of genome-aligned data at the DNA, RNA and protein levels requires a renaissance in web-based genome annotation browsers to provide useful data-mining tools for quickly exploring increasing complex data sets. Anno-J is a modern web-application for visualizing genome annotation data using Web 2.0 technologies for greatly enhanced style control, data syndication, data maintenance, user-interface and flexibility. Recent publications using Anno-J include: Lister et al. 2008, *Cell* 133:523-535, Ecker et al. 2008 *Developmental Biology* 319:462, Gregory et al. 2008, *Developmental Cell* 14:854-866.

## Symposium, Australia ICAR, and a New Appointment

- The 1st International Plant Phenomics Symposium was held in Canberra, April 22-24, 2009 (<http://www.plantphenomics.org.au/IPPS09/report>). This symposium, the first of its type, focused on the use of plant phenomics and functional genomics to boost crop productivity, and its proceedings will be published in a special issue of the journal *Functional Plant Biology*. Contact Bob Furbank ([Robert.Furbank@csiro.au](mailto:Robert.Furbank@csiro.au)) or Frank Gilmer ([jppc@fz-juelich.de](mailto:jppc@fz-juelich.de)) for further information on the Initiative. Also see the MASC Phenomics Subcommittee Report for more Symposium details.
- *Arabidopsis* 2013 - The 24th International Conference on *Arabidopsis* Research will be held in Australia in 2013. Tentative dates are July 8-12, and a possible venue is tropical Cairns, in far north Australia, the gateway to the Great Barrier Reef.
- Welcome to Mary Byrne, who has moved from John Innes to Sydney University during 2008/9.



# Austria

<http://www.arabidopsis.org/portals/masc/countries/Austria.jsp>  
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In Austria, Arabidopsis projects are undertaken at four institutions (BOKU-University of Natural Resources & Applied Life Science Vienna, GMI-Gregor Mendel Institute of Molecular Plant Biology, MFPL-Max F. Perutz Laboratories, University of Salzburg) on:

## **Population genetics:**

Magnus Nordborg ([www.gmi.oeaw.ac.at/en/research/magnus-nordborg/](http://www.gmi.oeaw.ac.at/en/research/magnus-nordborg/)) has been appointed as director of the GMI

## **Systems biology:**

Wolfram Weckwerth has been newly appointed as Head of the Molecular Systems Biology at the University of Vienna

## **Chromosome biology:**

Karel Riha ([www.gmi.oeaw.ac.at/rkriha.htm](http://www.gmi.oeaw.ac.at/rkriha.htm)): telomeres and genome stability

Peter Schlögelhofer ([www.mfpl.ac.at/index.php?cid=54](http://www.mfpl.ac.at/index.php?cid=54)): meiotic recombination

Dieter Schweizer ([www.gmi.oeaw.ac.at/dschweizer.htm](http://www.gmi.oeaw.ac.at/dschweizer.htm)): SMC proteins

## **Development, hormones and stress responses:**

Andreas Bachmair ([www.mfpl.ac.at/index.php?cid=702](http://www.mfpl.ac.at/index.php?cid=702)): ubiquitination and sumoylation

Thomas Greb ([www.gmi.oeaw.ac.at/tgreb.htm](http://www.gmi.oeaw.ac.at/tgreb.htm)): vascular tissue development

Marie-Theres Hauser ([www.dagz.boku.ac.at/11135.html?&L=1](http://www.dagz.boku.ac.at/11135.html?&L=1)): development, stress

Claudia Jonak ([www.gmi.oeaw.ac.at/cjonak.htm](http://www.gmi.oeaw.ac.at/cjonak.htm)): stress signalling and adaptation

Fritz Kragler ([www.mfpl.ac.at/index.php?cid=52](http://www.mfpl.ac.at/index.php?cid=52)): proteins/ RNA cell to cell transport

Christian Luschnig ([www.dagz.boku.ac.at/7968.html?&L=1](http://www.dagz.boku.ac.at/7968.html?&L=1)): auxin, chromatin

Irute Meskiene ([www.mfpl.ac.at/index.php?cid=53](http://www.mfpl.ac.at/index.php?cid=53)): AP2C1/2 in stress adaptation

Brigitte Poppenberger: brassinosteroid biosynthesis

Tobias Sieberer ([www.chemie.boku.ac.at/4191.html](http://www.chemie.boku.ac.at/4191.html)): development of the shoot apical meristem

Markus Teige ([www.mfpl.ac.at/index.php?cid=55](http://www.mfpl.ac.at/index.php?cid=55)): Targets of calcium-dependent protein kinases

## **Epigenetics:**

Werner Aufsatz ([www.gmi.oeaw.ac.at/waufsatz.htm](http://www.gmi.oeaw.ac.at/waufsatz.htm)): RNA mediated silencing, stress adaptation

Antonius and Marjori Matzke ([www.gmi.oeaw.ac.at/amatzke.htm](http://www.gmi.oeaw.ac.at/amatzke.htm)): RdDM, nuclear architecture

Ortrun Mittelsten Scheid ([www.gmi.oeaw.ac.at/oms.htm](http://www.gmi.oeaw.ac.at/oms.htm)): epigenetic changes in polyploids

Hisashi Tamaru ([www.gmi.oeaw.ac.at/htamaru.htm](http://www.gmi.oeaw.ac.at/htamaru.htm)): chromatin during pollen development

## **Glycobiology:**

Georg Seifert ([www.dapp.boku.ac.at/ips.html?&L=1](http://www.dapp.boku.ac.at/ips.html?&L=1)): arabinogalactan proteins and PCD

Herta Steinkellner ([www.dagz.boku.ac.at/11132.html?&L=1](http://www.dagz.boku.ac.at/11132.html?&L=1)): “customised” N-glycosylation

Richard Strasser ([www.dagz.boku.ac.at/12349.html?&L=1](http://www.dagz.boku.ac.at/12349.html?&L=1)): N-glycosylation

Raimund Tenhaken ([www.uni-salzburg.at/zbio/tenhaken](http://www.uni-salzburg.at/zbio/tenhaken)): biosynthesis of nucleotide sugars for cell wall polymers, PCD

## **Plant pathogen interactions:**

Gerhard Adam ([www.dagz.boku.ac.at/11137.html?&L=1](http://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](http://www.dapp.boku.ac.at/2238.html)): MIOX gene in nematode induced syncytia

Florian Grundler ([www.dapp.boku.ac.at/2238.html](http://www.dapp.boku.ac.at/2238.html)): plant nematode interaction

## **RNA metabolism:**

Andrea Barta ([www.mfpl.ac.at/index.php?cid=68](http://www.mfpl.ac.at/index.php?cid=68)): RNP complexes, spliceosome

## **Current Research Consortia**

- “Lasting effects of abiotic stress in plant genomes and their potential for breeding strategies” is funded through the Austrian Genome Research Program GEN-AU of the Austrian Federal Ministry of Science and Research and coordinated by Christian Luschnig ([www.gen-au.at/projekt.jsp?projektId=65&lang=en](http://www.gen-au.at/projekt.jsp?projektId=65&lang=en))
- “Chromosome dynamics - unravelling the functions of chromosomal domains” is a multiorganismal project (Arabidopsis represented by Peter Schlögelhofer) with the focus on the interaction of kinetochore –microtubules, biochemistry of sister-chromatid cohesion, chromosome pairing and recombination. ([www.mfpl.ac.at/index.php?cid=647](http://www.mfpl.ac.at/index.php?cid=647))
- “From regulatory complexity to biological function: Metabolic adjustment of plant development by regulatory

bZIP factor networks” ([www.zmbp.uni-tuebingen.de/PlantPhysiology/bzip/](http://www.zmbp.uni-tuebingen.de/PlantPhysiology/bzip/)) a cooperative International Project funded by the German DFG, the Austrian FWF, the Dutch NWO, and the Spanish MEC.

- “Chloroplast Signals, COSI” ([www.univie.ac.at/cosi/](http://www.univie.ac.at/cosi/)) EC-funded Marie-Curie Initial Training Network (ITN) coordinated by the University of Vienna and investigating chloroplast signals and metabolic regulation in a network of 10 European Institutions including BayerBioScience as industrial partner.
- “Signaling to plant immunity responses” (PathoNet) is an ERANet PG project coordinated by Irute Meskiene with members from Austria, Germany and United Kingdom ([www.erapg.org/everyone/16790/18613/19533/19539](http://www.erapg.org/everyone/16790/18613/19533/19539))
- “Calcium Regulation of Plant Productivity” (CROPP) is an ERANet PG project with members from Austria, Germany, Israel and United Kingdom ([www.erapg.org/everyone/16790/18613/19533/19537](http://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](http://www.erapg.org/everyone/16790/18613/19533/19538))
- “Fusarium Metabolites and Detoxification Reactions” SFB-Project coordinated by Gerhard Adam from the BOKU-University of Natural Resources & Applied Life Sciences, Vienna

## Conferences

- ‘Plant abiotic stress tolerance’ February 8-11 2009 ([www.univie.ac.at/stressplants/Home.html](http://www.univie.ac.at/stressplants/Home.html))
- ‘Adaptation potential in plants’ March 19-21 2009 ([www.gmi.ocaw.ac.at/en/other-sites/febs/home/](http://www.gmi.ocaw.ac.at/en/other-sites/febs/home/))
- 7th ISRR Symposium ‘Root Research and Applications’ (RootRAP) September 2-4, 2009 ([rootrap.boku.ac.at/](http://rootrap.boku.ac.at/))

## Public Relations- Education

- GEN-AU Summer School: an educational program for high school students ([www.gen-au.at/artikel.jsp?id=761&base=vermitteln&lang=en](http://www.gen-au.at/artikel.jsp?id=761&base=vermitteln&lang=en))
- “Dialog Gentechnik”: an independent non-profit society dedicated to provide scientific information on molecular biology and different aspects of biotechnological applications is organizing the Vienna Open Lab where hands on courses are offered to school classes and the general public. ([www.viennaopenlab.at/index.php?lang=en](http://www.viennaopenlab.at/index.php?lang=en)) ([www.dialog-gentechnik.at/index.php?id=104908&txgroup=104908](http://www.dialog-gentechnik.at/index.php?id=104908&txgroup=104908))
- “Lange Nacht der Forschung” (Long Night of Research), a common activity of scientific and technical institutions all over Austria to present their work to the general public. ([www.langenachtderforschung.at/lnf2/?cat=7](http://www.langenachtderforschung.at/lnf2/?cat=7))

## Vienna Biocenter International PhD Programmes

These international competitive programmes offer up to 4 years working on Arabidopsis research projects. For detailed information consult the website [www.univie.ac.at/vbc/PhD/](http://www.univie.ac.at/vbc/PhD/)

## Funding Sources

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

## Awards

Karel Riha received one of eight START prizes of the FWF for studies on telomere components in Arabidopsis, a €1.2 million award for research over the next 6 years. (<http://www.gmi.ocaw.ac.at/en/news/>)

# Belgium

<http://www.arabidopsis.org/portals/masc/countries/Belgium.jsp>  
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Department of Plant Systems Biology, VIB, Ghent University  
Email: pierre.hilson@psb.ugent.be

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

## Current Research Projects

- A Belgian national research project (IAP), coordinated by D. Inzé, focuses on the study of the molecular mechanisms regulating the development of plant roots and the interaction of roots with their environment. This program also involves T. Beeckman, G. Beemster, L. De Veylder, D. Van Der Straeten, J.-P. Verbelen, M. Boutry, X. Draye, N. Verbruggen and C. Périlleux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project.
- Other current Arabidopsis research topics in Belgium include cell cycle regulation (D. Inzé, L. De Veylder), root and leaf growth and development (T. Beeckman, G. Beemster, M. Van Lijsebettens), auxin (J. Friml), brassinosteroids (J. Russinova), phytohormone interactions (Eva Benkova), oxidative stress and cell death (F. Van Breusegem), genome annotation and evolution (Y. Van de Peer, P. Rouzé), functional genomics (P. Hilson), proteomics (G. De Jaegher), quantitative biology (M. Vuylsteke), tree biotechnology and bioenergy (W. Boerjan), ethylene signaling (D. Van Der Straeten), cell biology (D. Geelen), hormone biology (E. Prinsen), membrane proteins (M. Boutry), salt stress and tolerance to heavy metal (N. Verbruggen), flowering (C. Périlleux) and plant pathogen interaction (B. Cammue).

## Notable Arabidopsis publications

- Dhonukshe, P., Tanaka, H., Goh, T., Ebine, K., Mähönen, A.P., Prasad, K., Blilou, I., Geldner, N., Xu, J., Uemura, T., Chory, J., Ueda, T., Nakano, A., Scheres, B., and Friml, J. (2008). Generation of cell polarity in plants links endocytosis, auxin distribution and cell fate decisions. *Nature* 456, 962-966
- De Smet, I., Vassileva, V., De Rybel, B., Levesque, M.P., Grunewald, W., Van Damme, D., Van Noorden, G., Naudts, M., Van Isterdael, G., De Clercq, R., Wang, J.Y., Meuli, N., Vanneste, S., Friml, J., Hilson, P., Jürgens, G., Ingram, G.C., Inzé, D., Benfey, P.N., Beeckman, T. (2008). Receptor like kinase ACR4 restricts formative cell divisions in the Arabidopsis root. *Science* 322, 594-597

## Major funding sources for Arabidopsis functional genomics

- Flanders Institute for Biotechnology (VIB; [www.vib.be](http://www.vib.be))
- European Union Framework Programmes ([www.cordis.lu/](http://www.cordis.lu/))
- Belgian Federal Science Policy Office ([www.belspo.be](http://www.belspo.be))
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; [www.iwt.be](http://www.iwt.be))
- Research Foundation – Flanders (FWO; <http://www.fwo.be/en/index.aspx>)
- European ERA-Plant Genomics initiative ([www.erapg.org](http://www.erapg.org))

## Arabidopsis genomics tools and resources

- The Department of Plant Systems Biology (PSB) continuously develops and disseminates an exhaustive collection of destination vectors, designed for the functional analysis of genes in plant cells and compatible with the recombinational cloning Gateway technology ([www.psb.ugent.be/gateway](http://www.psb.ugent.be/gateway)).
- PSB also coordinates AGRON-OMICS, a functional genomics and systems biology project funded by the 6th European Framework Programme ([www.agron-omics.be](http://www.agron-omics.be)).

# Canada

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

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In late 2008, 59 laboratory groups known to be conducting research with Arabidopsis were polled by Email for contributions to the MASC report. Of these, approximately 10 groups responded with updates to their contributions.

## Reports

- François Belzile- l'Université Laval ([fbelzile@rsvs.ulaval.ca](mailto:fbelzile@rsvs.ulaval.ca)) The Belzile lab studies Arabidopsis DNA mismatch repair in regards to microsatellite instability and homoeologous recombination.
- Thomas Berleth – University of Toronto ([thomas.berleth@utoronto.ca](mailto:thomas.berleth@utoronto.ca)) The Berleth lab developed approximately 4,000 indirect enhancer trap lines, together with ~ 70,000 indirect activation tags for use in the study of very early vascular genes. In addition, they are conducting a study to map QTLs defining Arabidopsis fibre properties.
- Malcolm Campbell – University of Toronto ([campbell@botany.utoronto.ca](mailto:campbell@botany.utoronto.ca)) The Campbell lab investigates (1) the perception of sugars, amino acids and water, and how this affects the allocation of resources to key facets of metabolism and development, (2) comparative genomic analyses with the model woody perennial genus *Populus*.
- Jin-Gui Chen – University of British Columbia ([jingui@interchange.ubc.ca](mailto:jingui@interchange.ubc.ca)) The Chen lab investigates signal transduction networks using forward- and reverse-genetic, molecular and cellular, and biochemical approaches.
- William Crosby – University of Windsor ([bcrosby@uwindsor.ca](mailto:bcrosby@uwindsor.ca)) The Crosby lab investigates the role of E3 ubiquitin ligase (E3) complexes in the regulation of patterning and development in Arabidopsis.
- Raju Datla – NRC Plant Biotechnology Institute ([raju.datla@nrc-cnrc.gc.ca](mailto:raju.datla@nrc-cnrc.gc.ca)) The Datla lab investigates embryonic gene expression, currently focusing on genes in Arabidopsis as well as the closely related *Brassica napus*.
- Michael Deyholos – University of Alberta ([deyholos@ualberta.ca](mailto:deyholos@ualberta.ca)) The Deyholos lab applies genetic analysis and functional genomics of Arabidopsis to two areas of research: vascular development, and abiotic stress responses.
- Brian Ellis – University of British Columbia, Vancouver ([bee@msl.ubc.ca](mailto:bee@msl.ubc.ca)) The Ellis lab studies regulation of secondary wall deposition and lignification (Collaborators: C. Douglas, L. Samuels, S. Mansfield (UBC)). A second project concerns the functional analysis of the Arabidopsis MAPK phosphatase gene family (Collaborators: G. Wasteneys (UBC), D. Bergmann (Stanford)). The group is undertaking the functional analysis of the Arabidopsis MAPKK gene family via characterization of the MAPK cascades (Collaborators: J. Chen (UBC); I. Kovalchuk (Lethbridge); D. Bergmann (Stanford))
- Sonia Gazzarrini – University of Toronto, Scarborough, ([gazzarrini@utsc.utoronto.ca](mailto:gazzarrini@utsc.utoronto.ca)) The Gazzarrini group uses functional genomic, molecular and chemical genetic approaches to study the molecular mechanisms that regulate early developmental phase transitions and plant resistance to abiotic stresses in Arabidopsis.
- Vojislava Grbic – University of Western Ontario ([vgrbic@uwo.ca](mailto:vgrbic@uwo.ca)) The Grbic lab investigates the diversification of plant forms by studying a set of late-flowering Arabidopsis accessions with naturally occurring variant morphology.
- George Haughn – University of British Columbia ([haughn@interchange.ubc.ca](mailto:haughn@interchange.ubc.ca)) The Haughn laboratory studies seed coat epidermal differentiation in Arabidopsis as a model system for pectin biosynthesis, modification and secretion. They are completing a microarray analysis of the Arabidopsis seed coat. Dr. Haughn also oversees the Canadian reverse genetic TILLING facility, CAN-TILL (<http://www.botany.ubc.ca/can-till/>).
- Shelley Hepworth – Carleton University ([shelley\\_hepworth@carleton.ca](mailto:shelley_hepworth@carleton.ca)) The Hepworth lab focuses on determining how positional information is translated into morphological asymmetry in plant developmental patterning.
- Ljerka Kunst – University of British Columbia ([kunst@interchange.ubc.ca](mailto:kunst@interchange.ubc.ca)) The Kunst laboratory studies lipid metabolic pathways in higher plants, focusing on two specific areas: biosynthesis of cuticular wax and seed oil.
- Xin Li – University of British Columbia ([xinli@interchange.ubc.ca](mailto:xinli@interchange.ubc.ca)) The Li group is studying R-protein signaling pathways that play central roles in recognizing pathogens and initiating downstream defense cascades.
- Jim Mattsson – Simon Fraser University ([jmattso@sfu.ca](mailto:jmattso@sfu.ca)) The Mattsson lab is interested in the molecular basis of leaf formation, leaf vein initiation and patterning, primarily in the context of auxin transport and signalling. They have identified a large set of genes that are expressed in vascular tissues and are focusing on vascular differentiation.
- Jaideep Mathur – University of Guelph ([jmathur@uoguelph.ca](mailto:jmathur@uoguelph.ca)) The Mathur lab studies sub-cellular dynamics



and organelle interactions in order to understand the early responses of plants to various abiotic / biotic stimuli.

- Doug Muench – University of Calgary (dmuench@ucalgary.ca) The Muench laboratory studies the role of the plant cytoskeleton, specifically microtubules, in mRNA localization, protein sorting, and low temperature stress signaling.
- Roger Lew – York University, Toronto (planters@yorku.ca) The Lew lab is interested in the electrical properties of Arabidopsis root hairs. Current studies involve ion transport in cellular expansion and plant cell stress response.
- Nicholas Provart – University of Toronto (nicholas.provart@utoronto.ca) The Provart lab oversees the Botany Array Resource. In addition, the wider Arabidopsis research group at the University of Toronto has generated 10,000 DEX inducible random insertion lines which will be deposited to the stock center in the future.
- Przemyslaw Prusinkiewicz – University of Calgary (pwp@cpsc.ucalgary.ca) The Prusinkiewicz group focuses on simulation modeling of Arabidopsis, including the multiple roles of auxin in plant morphogenesis, general methods of modeling plants across multiple scales of organization, and further development of simulation software.
- Dan Riggs – University of Toronto at Scarborough (riggs@utsc.utoronto.ca) The Riggs group focuses on two distinct but interrelated processes: factors which affect plant architecture and that regulate chromatin condensation.
- Owen Roland – Carleton University (owen\_roland@carleton.ca) The Roland lab studies the synthesis of cuticular waxes and their deposition onto plant surfaces via map-based cloning and reverse genetic and biochemical approaches.
- Kevin Rozwadowski – Agriculture and Agri-Food Canada, Saskatoon (rozwadowskik@agr.gc.ca) The Rozwadowski group is interested in DNA double-strand break repair in vegetative and meiotic cells. The lab uses Arabidopsis as a model to characterize the details of the repair process and evaluate plant responses to genotoxic stress.
- Lacey Samuels – University of British Columbia (lsamuels@interchange.ubc.ca) The Samuels lab is conducting a multi-disciplinary research project to study the plant cuticle involving characterizing biosynthetic mutants (Kunst Lab), studying wax export and cell structure (Samuels Lab) and analyzing the chemical composition and biosynthetic pathways of cuticular lipids (Jetter Lab).
- Dana Schroeder – University of Manitoba (shroed3@cc.umanitoba.ca) The Schroeder group is examining the role of DDB1 complexes in Arabidopsis visible and UV light response.
- Geoffrey Wasteneys – University of British Columbia (geoffwa@interchange.ubc.ca) The Wasteneys team integrates high-end microscopy with molecular genetic strategies to investigate (1) the molecular mechanisms and signaling cascades that control polymer dynamics and the spatial organization of microtubule arrays and (2) the role microtubules play in cellulose synthesis, cell shape, organ growth and chirality.
- Randall Weselake – University of Alberta (randall.weselake@afhe.ualberta.ca) The Weselake group is (1) assessing the functionality (in this case the ability to impart tolerance to abiotic stress) of a number of oilseed rape genes using Arabidopsis, and (2) researching novel methods for modifying the fatty acid composition of seed oils.
- Tamara Western – McGill University (tamara.western@mcgill.ca) The Western lab uses a combination of forward and reverse genetics to the regulation of cell wall synthesis, secretion and modification using the pectic mucilage secretory cells of the Arabidopsis seed coat as a model system.
- Stephen Wright – York University (stephenw@yorku.ca) The Wright lab is interested in understanding the forces driving Arabidopsis gene and genome evolution; testing for the accumulation and increased activity of transposable elements in the allopolyploid genome of *A. suecica*, and (3) sequencing the genomes of *A. lyrata* and *Capsella rubella*.
- Hugo Zheng – McGill University (hugo.zheng@mcgill.ca) The Zheng lab is studying how intracellular membrane trafficking is regulated as cell morphology changes during plant development and in response to environmental stresses. The approach exploits the regulatory role of Rab-A and Rab-E GTPases and strives to identify novel genes that are involved in plant-specific membrane trafficking.
- Jitao Zou – NRC Plant Biotechnology Institute (jitao.zou@nrc-cnrc.gc.ca) The Zou lab is primarily interested in lipid and carbon metabolism. They study enzymatic components of the lipid metabolic network and are also interested in exploring natural variation in wild type accessions to dissect regulatory components of seed oil deposition.

### Arabidopsis genomics tools and resources:

- Canadian reverse genetic TILLING facility, CAN-TILL (<http://www.botany.ubc.ca/can-till/>).
- Botany Array Resource (<http://bbc.botany.utoronto.ca>)

# China

<http://www.arabidopsis.org/portals/masc/countries/China.jsp>  
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In 2008, the National Science Foundation of China (NSFC) funded over 50 projects mainly using Arabidopsis and rice model species under the “Molecular Mechanisms of Plant Hormone Initiative”. These projects cover quite diverse aspects of plant hormone researches. To meet the increasing demand for hormone analysis, NSFC also supported a project to set up a core facility for quantitative analysis of plant hormones at the National Center for Plant Gene Research (Beijing) hosted by the Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences. The core facility currently provides services for quantitative analysis of IAA and ABA. Expertise on other plant hormones is being developed. In addition, NSFC also launched a new five-year initiative on epigenetics and stem cell research in 2008 in which two plant projects were funded.

“Genetic and epigenetic regulation on organ formation in higher plants”, a team project coordinated by Dr. Xiaofeng Cao of IGDB, CAS was launched by the “Development and Reproduction Program”, under the National Basic Research Initiative of China. This project includes more than 10 principal investigators from IGDB, Peking University, Shanghai Jiaotong University, Institute of Botany, CAS, etc. They mainly focus on: 1) genetic and epigenetic network governing the transition from vegetative growth to reproductive growth, 2) molecular mechanism and modeling in plant organ formation, 3) molecular basis of organ size control in higher plants.

The Institute of Plant Sciences, headed by Dr. Hong Ma recently returned from Pennsylvania State University, USA, was inaugurated in December 3, 2008 in Fudan University, Shanghai. Over 150 plant biologists from all over China attended the opening ceremony. In support of such new development, the annual symposium on Arabidopsis research was held in Shanghai Institute of Plant Physiology and Ecology, where over 300 Arabidopsis researchers and students exchanged ideas and initiated new collaborations. It is also worth mentioning that Cold Spring Harbor Laboratory recently set up an office in Suzhou to bring the Banbury Meeting to China. In addition, several Chinese journals, including Molecular Plant, Journal of Integrative Plant Biology, Journal of Genetics and Genomics, and Cell Research, now are international, publishing peer-reviewed English articles. These new developments will undoubtedly have a great impact on Chinese biological research as a whole.

## **Major funding sources for Arabidopsis functional genomics:**

National Science Foundation of China  
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Website: <http://www.nsf.gov.cn/>

Ministry of Science and Technology  
15B, Fuxing Road, Beijing, 100862, China

# France

<http://www.arabidopsis.org/portals/masc/countries/France.jsp>  
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## National Research Agency (ANR) - newly funded Arabidopsis research projects (2008)

### Plant Genomics Programme:

The plant genomics research theme is expected to provide new knowledge concerning the diversity of genes that are important targets related to a) various productivity challenges and opportunities - (plants for food and feed, plants for agro-fuels), b) environmental concerns and c) improved and safer food ingredients and products. Most of the newly-funded projects are devoted to crop plants. This year, those devoted to Arabidopsis deal mainly with pathogens.

- MOVIE: Molecular basis of virus resistance mediated by host factors required for the infectious cycle. PI : Carole CARANTA, Avignon
- NEMATARGETS: Identification of new genes as targets for development of specific strategies aimed against plant-parasitic nematodes. PI : Pierre ABAD, Sofia-Antipolis
- PhosphoStim: Phosphorylation responses of the Arabidopsis root to biotic, abiotic and nutritional stimuli. PI : Christophe MAUREL, Montpellier
- SCRIPS: Signaling Peptides and Cytoskeleton Regulators Involved in Plant Disease Susceptibility. PI : Bruno FAVERY, Sofia-Antipolis
- ViroMouv: Identification of host factors involved in plant virus long distance movement. PI : Frédéric REVERS, Bordeaux

### Non-thematic programme ('Blanc'):

The Blanc programme is a bottom-up, blue-sky call for proposal in all research fields. Its aim is to give significant impetus to ambitious projects, internationally competitive, focusing on pioneer objectives, and in breach of traditional research paths.

- AGO hook: The Argonaute hook motif: its function in RNA silencing in Arabidopsis and viral/bacterial mechanisms of evasion in plants. PI : Thierry LAGRANGE, Perpignan
- AMUCCAS: ABP1 Modulation of Ubiquitin mediated protein degradation in Cell Cycle and Auxin Signalling. Catherine PERROT-RECHENMANN, Gif
- AMUSE: Natural Variation in Arabidopsis Mucilage from Seeds: Structure, Composition and Role. PI : Helen

NORTH, Versailles

- CENTROPLANT: Centrosomal components in acentrosomal plant cells. PI : David BOUCHEZ, Versailles
- GLUTAPHOTO: Roles of glutathionylation and glutaredoxins in photosynthetic organisms. PI : Stéphane LEMAIRE, Orsay
- LTR-STRESS: Retroviral-type LTRs as intermediate of the stress response in plants. PI : Marie-Angèle GRANDBASTIEN, Versailles
- NITRAPOOL: Components controlling the status of nitrate pools in a plant cell. PI : Françoise VEDELE, Versailles.
- POLYCOMBARA: Mechanism of gene silencing mediated by a variant of Polycomb Repressive Complex 1 in Arabidopsis thaliana. PI : Valérie GAUDIN, Versailles
- PUMPKin: Energizing the plant plasma membrane: Towards a molecular framework on the integrated roles of proton pumps, Shaker K<sup>+</sup> in channels and associated protein networks. PI : Jeffrey LEUNG, Gif
- RETROMER: Role of the retromer complex in Arabidopsis development. PI : Thierry GAUDE, Lyon
- RNA Transport: RNA Transport in Plants. PI : Manfred HEINLEIN, Strasbourg
- RNAPATHS: Integrating RNA quality control and RNA silencing pathways. PI : Allison MALLORY, Versailles
- WALL INTEGRITY: Integrity surveillance of the plant cell wall. PI : Herman HÖFTE, Versailles

### Noteworthy breakthroughs published by French researchers:

- Gomez-Roldan et al. (2008). Strigolactone inhibition of shoot branching. *Nature* 455, 189-194
- Blein et al. (2008) A conserved molecular framework for compound leaf development. *Science* 322, 1835-1839
- Hamant et al. (2008). Developmental patterning by mechanical signals in Arabidopsis. *Science* 322, 1650-1655.
- Navarro et al. (2008). Suppression of the microRNA pathway by bacterial effector proteins. *Science* 321, 964-967.
- Brodersen et al. (2008). Widespread translational inhibition by plant miRNAs and siRNAs. *Science* 320, 1185-1190.
- Bikard et al. (2009). Divergent Evolution of Duplicate Genes Leads to Genetic Incompatibilities within *A. thaliana*. *Science* 323, 623-626.
- Teixeira et al. (2009). A Role for RNAi in the Selective Correction of DNA Methylation Defects. *Science*, in press.

# Germany

<http://www.arabidopsis.org/portals/masc/countries/Germany.jsp>  
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## **AFGN (Arabidopsis Functional Genomics Network; DFG funded)**

### **Aim and activities of AFGN**

AFGN was founded by a bottom-up approach of the German Arabidopsis research community in 2001 as a basic research program. AFGN currently funds 25 projects in Germany and has, almost from the start, been organized in close coordination with the 2010 Project of the United States National Science Foundation (NSF). Together with many other research programs throughout the world, these programs aim to elucidate the function of all Arabidopsis genes by the year 2010. The AFGN program was renewed in 2007 (3rd funding period). In addition, the AFGN and the 2010 Project implemented the collaborative AFGN-2010 Young Researcher Exchange Program (AFGN-2010-YREP). The program provides funding for 1 to 3 month research visits of young scientists to the US and vice versa. Since the program's inception, seven German scientists have been supported by YREP funds to visit the U.S. There were three scientists supported in the past year, which concludes the program funding period: (1) Christiane Katja Kleindt, PhD student at the University of Bielefeld advised by Bernd Weisshaar, visited Mary Wildermuth of the University of California at Berkeley to work on ATH1 GeneChip-based analysis of powdery mildew infection stages in Arabidopsis. (2) Nora Peine, PhD student at the University of Bonn, advised by Dorothea Bartels, visited Andrew Wood of Southern Illinois University to work on bioinformatics and biochemical analysis of group 3 ALDHs from Arabidopsis. (3) Christos Noutsos, PhD student at the University of Munich, advised by Dario Leister, visited Georgiana May of the University of Minnesota, St. Paul to work on bioinformatics analyses of the chloroplast proteome and its phosphorylation.

The AFGN program will continue to support basic functional genomics research in Arabidopsis, thereby contributing to the accelerated acquisition and utilization of new knowledge and innovative approaches to elucidate fundamental biological processes in higher plants. Current support concentrates on two areas of research:

- Functional Genomics of Biological Processes

Research in the AFGN has shown that different members of a given Arabidopsis multiprotein family may be multifunctional and, thus, may play a role in different biological processes and pathways. As a consequence, the focus of AFGN will move from a sole multiprotein family-based genomic approach towards the genomic analysis of multigene networks whose members functionally interact with each other in accomplishing a given biological process.

- Tools and Resources for Plant Functional Genomic Research  
There is still demand for the development of novel and genome-wide tools and technologies and additional resources in plant functional genomics to address unmet needs. It is expected that these methods and tools will complement the already existing tools and research resources, will provide quantitative readouts, will be cost effective and comprehensive, and, thus, will be readily adopted by the scientific community.

### **Tri-National Arabidopsis Meeting**

Together with colleagues from Austria and Switzerland the AFGN organizes a yearly, rotating, international conference on Arabidopsis functional genomics. Funding comes primarily from DFG which allows young scientists including PhD students and postdocs to attend.

- The 5th Tri-National Arabidopsis Meeting, attended by around 200 participants, was held in Zuerich, Switzerland; September 10-13, 2008, and was organized by the ETH Zuerich.
- The 6th Tri-National Arabidopsis Meeting will be held in Cologne, Germany from September 16-19, 2009. Around 200 participants are expected and the meeting will be organized by the MPI for Plant Breeding Research, Cologne (<http://www.tnam.org>).

### **AFGN-related Arabidopsis tools and resources:**

- AFGN:  
<http://www.uni-tuebingen.de/plantphys/AFGN/>
- AFGN-2010-YREP:  
<http://www.uni-tuebingen.de/plantphys/AFGN/yrep.htm>



# Israel

<http://www.arabidopsis.org/portals/masc/countries/Israel.jsp>  
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- In 2008, ~40 research articles employing Arabidopsis were published from groups in Israel. These included such diverse subjects, as biophysics and protein crystallography, bioinformatics, metabolic engineering and molecular development. The major centers of Arabidopsis research are in The Hebrew University of Jerusalem, Tel Aviv University, the Weizmann Institute of Science, and the Ben Gurion University of the Negev.
- Funding - “Rumors of the death of Arabidopsis at BARD are premature”: Last year we reported that BARD (The United States - Israel Binational Agricultural Research and Development Fund) was canceling their “Model System and Functional Biology in the Service of Agriculture” panel, the panel that funded the majority of Arabidopsis research (~\$1,000,000 in Arabidopsis research annually). While this year’s awards have yet to be announced, according to a senior BARD official: “Rumors of the death of Arabidopsis at BARD are premature.” If so, this is a tentative positive sign that funding of Arabidopsis research is now intimately intertwined with agricultural research and that no specific programs are needed to ensure its continuation.
- New hirings – returning postdocs: Three young Arabidopsis researchers returned to Israel from postdoctoral training in the US – Sigal Savaldi-Goldstein from the Chory lab to the Faculty of Biology at the Technion, Leor Eshed-Williams from the Fletcher lab to the Hebrew University Faculty of Agriculture, and Aaron Fait returned from the Max Planck Institute, Golm to take a position at Ben-Gurion University’s Jacob Blaustein Institutes for Desert Research.
- New collaborations between industry and academia: The laboratory of Simon Barak at the Jacob Blaustein Institutes for Desert Research of Ben-Gurion University established a research collaboration with Bayer BioScience N.V., a subsidiary of Bayer CropScience, to identify genes that allow plants to tolerate the harsh environmental stresses characteristic of arid regions. For more information, see the ‘Broader Impacts’ section of this report.
- Translational research – From Arabidopsis to Tomato: Tomato is a traditional Israeli crop and model plant. In recent years, several groups that traditionally worked with tomatoes have incorporated the advantages of Arabidopsis for functional analyses studies, conversely; several groups working on Arabidopsis have expanded their interest into tomato as a traditional crop plant system. For example, tissue-specific promoters discovered in Arabidopsis were tested and found functional in tomato, and the transactivation system and the fluorescence complementation in vivo protein interaction system, both developed in Arabidopsis, have been introduced into tomato. In these aspects, research in Arabidopsis has fulfilled its promise as a model system that can greatly promote understanding of other plant species.

# Italy

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

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## Arabidopsis projects

- Several Italian labs working on Arabidopsis are involved in two different ERA-PG projects: CISCODE (Cis-element conservation and divergence in plant reproductive development), Italian partners G. Morelli (INRAN, Rome) and L. Colombo and C. Tonelli (University of Milan); MULTI-STRESS, Italian partners P. Costantino (La Sapienza University, Rome) and I. Ruberti (CNR, Rome).
- Several National Research grants (PRIN) have been awarded to Italian Arabidopsis scientists by the Italian Ministry of University and Scientific Research (MIUR) as part of its institutional activities (<http://www.miur.it>).

## Relevant Arabidopsis meetings

A meeting for the launch of the Italian Technological Platform Plants for the Future was held in Rome on June 17 2008. The final meeting of the Marie Curie Research Training Network "Wallnet: functional genomics for the biogenesis of the plant cell wall" was held in Rome on June 19-20 2008. The mid-term meeting of the ERA-PG MULTI-STRESS project was held in Rome on October 24 2008. Food and Water for Life, 4th Conference Future of Science was held in Venice on 25-27 September 2008.

## Relevant tool and resource development

Several useful engineered Arabidopsis lines have been created, including lines overexpressing the AtMRP3 gene (by M. Cardarelli, CNR, Rome) and plants overexpressing active and inactive polygalacturonases from *A. niger*, as well as plants overexpressing the MEI genes (by the groups of F. Cervone and G. de Lorenzo). Ida Ruberti's lab has generated: new computational tools for the analysis of genome-wide expression data, new GFP-tagged lines for HD-Zip II transcription factor genes and new single and double mutants for HD-Zip II transcription factor genes. Novel Arabidopsis Guard Cell specific promoters and mutations have been generated by C. Tonelli and M. Galbiati (University of Milan)

## Highlights of groundbreaking Italian Arabidopsis journal articles from 2008-2009

- Among the most groundbreaking research carried out in the last year, two papers, published respectively in *Science* and in *Plant Cell*, have focused on plant hormones' function and interactions in Arabidopsis development: the group of S.

Sabatini/P. Costantino (La Sapienza, Rome) has discovered that the balance between cell differentiation and division necessary for determining root meristem size is the result of the interaction between cytokinin and auxin through a regulatory circuit converging on the SHY2 gene, a repressor of auxin signaling - the cytokinin-responsive transcription factor ARR1 activates transcription of the gene SHY2. SHY2 mediates cell differentiation, controlling auxin distribution as is required for the negative transcriptional control of the auxin transport facilitators PIN genes; the group of M. Cardarelli/P. Costantino (La Sapienza, Rome) has shown that auxin, synthesized in the anthers by YUC genes before the inception of late processes and perceived by the TIR/AFB receptors when late processes begin, coordinates anther dehiscence and pollen maturation and independently triggers filaments elongation.

- The group of F. Cervone/G. de Lorenzo (La Sapienza, Rome) established a new model system based on the use of *A. thaliana* and *B. cinerea* to study plant interactions with necrotrophic fungi. They demonstrated that the oxidative burst induced by OGs is not required for early gene induction or for resistance to fungal infection, and that OGs- and Flg22-mediated responses largely overlap, suggesting host- and pathogen-associated molecular patterns activate the plant innate immune system through the activation of a common signaling pathway. They conducted experiments with plants expressing a fungal polygalacturonase and revealed that pectin alterations increase resistance to pathogens and reduce sensitivity to auxin, suggesting a link between cell wall damage, activation of defense responses and hormones. This research was published in the journals *Plant Physiology*, *Proteomics* and *Molecular Plant*.
- The group of I. Ruberti (CNR, Rome) recently performed a genome-wide analysis of the Arabidopsis HD-Zip II family of transcription factors. Their results, published in several journals (*Plant signaling behavior*, *PLOS computational biology*, *Plant Molecular biology*) provide evidence for a complex pattern of expression and regulation of this gene family, and strongly suggest that HD-Zip II genes act as members of highly integrated networks in controlling organ development and plant responses to light quality changes.
- The group of C. Tonelli (University of Milan) has identified novel transcription factors involved in cuticle development (AtMYB41, *Plant Journal*) and growth rate (AtMYB 11, *J. Exp. Bot*)

## Awards to Arabidopsis researchers

Felice Cervone of University La Sapienza – Rome was the recipient of a European Research Council Advanced Grant: FUEL-PATH "Exploiting the saccharification potential of pathogenic microorganisms to improve biofuel production from plants."

# Japan

<http://www.arabidopsis.org/portals/masc/countries/Japan.jsp>  
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In Japan, Arabidopsis functional genomics is mainly carried out at RIKEN, Kazusa DNA Research Institute and National Institute of Advanced Industrial Science and Technology (AIST). RIKEN groups include the Plant Science Center (PSC), the BioResource Center (BRC) and Bioinformatics and Systems Engineering division (BASE). Funding conditions for plant research are rather getting worse in Japan even though the level of plant science becomes much better than before based on ISI Thomson. Plant science is one of the three highly cited research areas in Japan (the other two research areas are immunology and post-genomics).

1. The RIKEN PSC (<http://www.psc.riken.jp/english/index.html>) (Director: K. Shinozaki) is carrying out these projects; (1) Metabolome analysis of tagged mutants and FOX lines via GC-MS, LC-MS, CE-MS and NMR (K. Saito), (2) Hormonomics (systematic analysis of plant hormones) of Arabidopsis and rice FOX lines (H. Sakakibara, M. Matsui), (3) Transcriptomics via tiling array and Illumina-Solexa sequencer (M. Seki), (4) Phenotype analysis of Ds-tagged lines, and Arabidopsis and rice Full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (M. Matsui), (5) Phenotype analysis of 5,000 homozygous Ds-insertion lines in gene-coding regions (T. Kuromori), (6) Collection and phenome analysis of Ds- or T-DNA tagged mutants for nuclear-encoded chloroplast protein genes (F. Myouga), (7) Collection of *Thellungiella halophila* full-length cDNAs in collaboration with Tokyo University of Agriculture (Published: BMC Plant Biology 8: 115, 2008) (T. Sakurai, T. Taji), (8) Rice FOX Arabidopsis Mutant Database (<http://ricefox.psc.riken.jp/>) (Published: Plant J 57: 883-94, 2008) (M. Matsui), (9) Large-scale data of transcriptome in hormone response (Y. Shimada, [www.arabidopsis.org/info/expression/ATGenExpress.jsp](http://www.arabidopsis.org/info/expression/ATGenExpress.jsp))
2. RIKEN BRC Experimental Plant Division (PI: M. Kobayashi, [kobayasi@rtc.riken.jp](mailto:kobayasi@rtc.riken.jp)) preserves and distributes various plant materials including Arabidopsis full-length cDNA clones and transposon-tagged mutant seeds via National BioResource Project. Now, Arabidopsis FOX lines developed by RIKEN PSC are distributed. Also, Arabidopsis T87 cells are being distributed overseas. More than 1,150 laboratories and groups in the world have already received materials from RIKEN BRC (<http://www.brc.riken.go.jp/lab/epd/Eng/>).
3. The RIKEN BASE (PI: T. Toyoda) (<http://www.base.riken.jp/english/index.html>) has been carrying out (1) Bioinformatics tools and data mining, (2) Arabidopsis transcriptome informatics (CAGE, tiling-array), (3) Informatics platform

towards genome design and metabolic engineering in Arabidopsis, (4) Japan's national integrated database project covering Arabidopsis 'omics information resources, (5) PosMed (Positional Medline) for Arabidopsis genes is an intelligent search engine integrating genome information and literature (<http://omicspace.riken.jp/PosMed/search?objectSet=gene&species=At>)

4. Kazusa DNA Research Institute Metabolome analysis of transgenic Arabidopsis plant over-expressing transcription factor cDNAs via FT-MS, GC-MS, LC-MS and CE-MS. (PI: D. Shibata, (<http://www.kazusa.or.jp/e/laboratories/laboplantbiotec.html>))
5. National Institute of Advanced Industrial Science and Technology (AIST) M. Ohme-Takagi (<http://unit.aist.go.jp/rigb/gf-gre/en.html>) developed novel gene silencing system using dominant repressors (CRES-T system) and is systematically analyzing function of transcription factors in Arabidopsis and rice.

## Other new activities

- A new project on peptides hormones CLEs was funded for H. Fukuda (University of Tokyo) by BRAIN. A project on plant peptide hormones and their receptors was funded for K. Okada (NIBB) by JSPS from 2007.
- **Noteworthy breakthroughs by Japanese researchers in 2008:** Publication: Inhibition of shoot branching by new terpenoid plant hormones (Umehara M, Hanada A, Yoshida S, Akiyama K, Arite T, Takeda-Kamiya N, Magome H, Kamiya Y, Shirasu K, Yoneyama K, Kyoizuka J, Yamaguchi S, Nature 2008 Sep 455:195-200.)
- **Relevant Meetings 2008:** The Arabidopsis Workshop Japan 2008 "Frontiers of Plant Science in the 21st Century" was held at the National Institute for Basic Biology on September 13-15, 2008. The aim of the annual meeting was to promote and inspire researchers and students through intensive discussion on their research achievements and results as well as their ideas and future prospects for plant science (<http://www.nibb.ac.jp/conf55/>).
- **Awards for Arabidopsis research:** Dr. Kazuo Shinozaki received 1st place of the most cited researchers in Plant Science in 1997 - 2007. [Science Watch ISI Thomson] ([http://sciencewatch.com/dr/sci/08/jun22-08\\_4/](http://sciencewatch.com/dr/sci/08/jun22-08_4/))
- **Upcoming International Arabidopsis Conference in Japan:** The 2010 International Conference on Arabidopsis Research (ICAR) will be held in Japan for the first time. This is the 21st ICAR and the second to be held in Asia. The conference date is June 6-10, 2010 at the Pacifico Yokohama Conference Center, and is co-chaired by: Kazuo Shinozaki (RIKEN Plant Science Center) and Kiyotaka Okada (National Institute for Basic Biology). <http://arabidopsis2010.psc.riken.jp/>

# The Netherlands

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## 2009 Highlights for The Netherlands

Several Dutch Arabidopsis groups are now effectively exploiting systems biology approaches; examples are:

- The construction of transcriptional networks for the transition between vegetative and floral development (Kaufman et al., PLoS Biology 7, 2009)
- Studies on phenotypic buffering using genetical metabolomics/genomics (Fu et al Nature Genetics 41, 2009).
- Emerging insight into how auxin generates specificity (Lokerse and Weijers, Curr.Opin. Plant Biol, in press, 2009).
- The combination of computational modeling and experimental analysis to analyze lateral root formation (Laskowski et al., PLoS Biology 6, 2008)

The Dutch Government approved the second phase of the CBSG project which supports Arabidopsis research, including bioinformatics and enabling technologies, with 4.5 M€. This program involves collaborative projects between Universities and research institutes of Groningen, Wageningen and Utrecht.

Ben Scheres (University of Utrecht) obtained a 2.2 M€ Advanced Investigator Grant for Arabidopsis research from the European Union, to be spent on a combination of experimental and computational approaches for the study of root development and plant architecture.

## Major funding sources for Arabidopsis functional genomics:

- Netherlands Organization for Scientific Research ([www.nwo.nl](http://www.nwo.nl))
- The Netherlands Genomics Initiative ([www.genomics.nl](http://www.genomics.nl))
- The Netherlands Plant Genomics Network ([www.cbsg.nl](http://www.cbsg.nl))
- Foundation for Technology funded by Ministries of Economic Affairs and Education ([www.stw.nl](http://www.stw.nl))
- ERA-PG: [www.erapg.org/](http://www.erapg.org/)
- Human Frontiers Science Program (<http://www.hfsp.org/>)
- EC Framework 7 RTN
- EMBO fellowships (<http://www.embo.org/fellowships/index.html>)



# Nordic Arabidopsis Network

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## Norway

The Norwegian Plant Functional Genomics Program has entered period 2 (2008-2012). While the first period focused on building up the needed infrastructure and technology platforms for functional genomics, focus in the second period of the FUGE program is more on support to functional genomics research projects. Some of the new granted projects can be classified as systems biology and it is believed that this field will get more attention in the coming years. A plant based company named Plastid (<http://www.plastid.no/>) has been started in Stavanger. A Plant Network has been established which aim to develop a new national plant biology research program (including all photosynthesizing organisms). The 7th Norwegian Arabidopsis meeting was arranged by Professor Karsten Fischer and his colleagues (at the northernmost university of the world, University of Tromsø) in November 2008.

## Denmark

Several notable publications from Danish Arabidopsis researchers:

- Hofius D et al. (2009) Autophagic components contribute to hypersensitive cell death in Arabidopsis. *Cell*, 137 (4) 773:83.
- Qiu J et al. (2008) Arabidopsis MAP kinase 4 regulates gene expression through transcription factor release in the nucleus. *EMBO J.* 27, 2214-21.

## Arabidopsis Resources

### Norway

- Norwegian Arabidopsis Research Centre (NARC): The Norwegian service facilities are open for all scientists at equal conditions. The program is coordinated by Atle M. Bones (NTNU) and information about the services can be found at [www.narc.no](http://www.narc.no) or by request to [narc@bio.ntnu.no](mailto:narc@bio.ntnu.no).
- University of Oslo: in situ hybridization and yeast-two-hybrid analyses ([www.imbv.uio.no/gen/groups/narc/](http://www.imbv.uio.no/gen/groups/narc/))
- UMB: Arabidopsis transformation, T-DNA genotyping, seed collection: ([www.umb.no/?viewID=2552](http://www.umb.no/?viewID=2552))

## Arabidopsis Funding Sources

- Norway: Research Council of Norway ([www.forskningsradet.no](http://www.forskningsradet.no)): Functional Genomics in Norway (FUGE)
- Sweden: Wallenberg Consortium North (WCN)-Funding ([www.wcn.se/](http://www.wcn.se/))
- Finland: Finnish Project Program on Plant Genomics-Funding ([www.mm.helsinki.fi/esgemo/pg/eng\\_index.htm](http://www.mm.helsinki.fi/esgemo/pg/eng_index.htm))

# United Kingdom

[http://www.arabidopsis.org/portals/masc/countries/United\\_Kingdom.jsp](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. Theoretical approaches are receiving increased support, as illustrated by over £30 million investment in major Plant Systems Biology awards since 2005.

## New Funding Programmes in the UK

### BBSRC

In 2008, the Biotechnology and Biological Science Research Council (BBSRC), the major funder of *Arabidopsis* research, restructured its process for allocating grants in order to deliver its mission of 'excellence with impact'. There are four new BBSRC committees for UK researchers to apply for funding- A: Animal Systems, Health and Wellbeing; B: Plants, Microbes, Food and Sustainability; C: Technological and Methodological Development; D: Molecules, Cells and Industrial Biotechnology. All four committees will have the same remit of BBSRC research and policy priorities; including several areas that *Arabidopsis* research is well positioned to address: Bioenergy, Crop Science, Living with Environmental Change, Synthetic Biology and Systems Approaches to Biological Research.

The UK has established a Sustainable Bioenergy Centre; £27 million has been invested by the BBSRC and industry to bring together world-leading scientists and industrialists to make sustainable bioenergy an economically and socially viable alternative to fossil fuels. The Centre aims to address the key barriers to sustainable bioenergy by focusing on six research programmes; perennial bioenergy crops; cell wall sugars; cell wall lignin; lignocellulosic conversion to bioethanol; second generation, sustainable, bacterial biofuels and marine wood borer enzyme discovery. *Arabidopsis* researchers are involved in a number of these programmes. BBSRC has also launched

a new national centre to analyse plant, animal and microbial genomes. The new Genome Analysis Centre (TGAC) will be based in Norwich. <http://www.tgac.bbsrc.ac.uk>

## European Research Area for Plant Genomics (ERA—PG)

The second joint call of the ERA-Net for Plant Genomics (with an approximate budget of 16 Million €) funded 12 collaborative research projects in 2008 from 54 submitted proposals. UK researchers lead 5 of these 12 projects, and all but one involve a UK research group. <http://www.erapg.org/everyone>

## Relevant UK 2008 meetings

- Genetics Society 2008 *Arabidopsis* Meeting
- GARNet – SEB 2008 Plant Symposium

## Awards for Arabidopsis UK researchers in 2008

- Prof. David Baulcombe, University of Cambridge, was awarded the Lasker Prize for basic medical research.
- Prof. Ottoline Leyser, University of York, was awarded a CBE (Commander of the British Empire) in recognition of her pioneering work in plant biology.

## Noteworthy breakthroughs published by UK researchers

- Specific targeting of a plasmodesmal protein affecting cell-to-cell communication. Thomas CL, Bayer EM, Ritzenthaler C, Fernandez-Calvino L, Maule AJ. *PLoS Biol.* 2008 Jan;6(1):e7. Unlike animals plants have to deal with a rigid cell wall, which prevents transport of molecules and communication between cells. To overcome this problem plants create tunnels through the cell wall known as plasmodesmata (PD). The complex nature of PD have made them historically difficult to isolate and characterise. In this paper, UK researchers describe the isolation of a novel class of PD-located proteins (PDLPs) that show class I membrane receptor-like properties. One of these proteins, PDL1a, is shown to target PD via the secretory pathway and is able to alter cell-to-cell trafficking in GFP diffusion assays. Deletion analysis of PDL1a shows that the transmembrane domain of PDL1 is necessary and sufficient for PD targeting. This work represents a huge breakthrough in the search for PD constituents and describes the first identification of a PD localization signal.
- A developmental framework for dissected leaf formation in the *Arabidopsis* relative *Cardamine hirsuta*. Barkoulas M, Hay A, Kougioumoutzi E, Tsiantis M. *Nat Genet.* 2008 Sep; 40(9): 1136-41. This interesting study by a team of scientists at the University of Oxford reveals the power of

comparative analysis. By building on tools and resources regularly exploited in *Arabidopsis*, UK researchers have helped to develop its relative *Cardamine hirsuta* into a powerful model. By utilising forward genetics and transgenic analysis to dissect the differences between the simple leaf shape of *Arabidopsis* and the compound shape of *Cardamine*, researchers have revealed that compound leaflet initiation is associated with auxin maxima along the margin of the leaf primordial similar to the process that result in leaf initiation from the shoot apical meristem. This work clearly illustrates how species-specific deployment of fundamental growth pathways can sculpt diverse plant forms.

- The circadian clock in *Arabidopsis* roots is a simplified slave version of the clock in shoots. James AB, Monreal JA, Nimmo GA, Kelly CL, Herzyk P, Jenkins GI, Nimmo HG. 2008 Dec 19; 322(5909): 1832-5. Researchers at the University of Glasgow have discovered that only a subset of circadian clock genes are rhythmically expressed in roots grown in the dark. Studies in light-grown shoots previously suggested that the properties of the plant circadian clock were cell-autonomous, and the TOC1 protein was considered a „core“ clock component. However, TOC1 appears to have no role in the ‚dark root clock‘. The researchers also noted that a shoot-root signal was central to the correct timing of the ‚dark root clock‘ when light dark cycles were applied to the shoot. The shoot-root signal depended on photosynthesis and was affected by exogenous sucrose. This paper illustrates the importance of long-distance metabolic signalling in coordinating plant organ functions.
- DELLAs control plant immune responses by modulating the balance of jasmonic acid and salicylic acid signaling. Navarro L, Bari R, Achard P, Lison P, Nemri A, Harberd NP, Jones JD, Curr Biol 2008 May 18(9): 650-5. Navarro and colleagues have discovered that DELLA proteins control plant immune responses by regulating salicylic acid (SA) and jasmonic acid (JA) dependent defence responses. The *Arabidopsis* quadruple-della mutant (*gai-t6, rga-t2, rgl1-1, rgl2-1*) is susceptible to the necrotrophic fungi *Alternaria brassicicola* and *Botrytis cinerea*, but more resistant to biotrophic pathogens such as *Pseudomonas syringae* DC3000 and *Hyaloperonospora arabidopsidis*. Corresponding activation of marker genes for SA and repression of a marker for the JA pathway, as well as opposite effects on the defence responses for DELLA overexpressors were observed in this paper. The likelihood that GA exerts these responses is reinforced in this work by the investigation of the effects of its exogenous application. This research contributes to understanding the complex mechanisms through which hormone cross-talk is modulated in plant defence and development.

# United States

[http://www.arabidopsis.org/portals/masc/countries/United\\_States.jsp](http://www.arabidopsis.org/portals/masc/countries/United_States.jsp)

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## North American Arabidopsis Steering Committee (NAASC)

The eight member NAASC ([www.arabidopsis.org/portals/masc/countries/NAASC\\_Info.jsp](http://www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp)) is composed primarily of U.S. researchers and represents Arabidopsis researchers in the United States, Canada and Mexico. Annual elections by North American researchers registered at TAIR provide new members to replace two that rotate off the committee each year. Xinnian Dong (Duke University) and Blake Meyers (Deleware Biotechnology Institute) were recently elected to serve a four year term starting this July. Xuemei Chen and Joe Kieber conclude their term at the 2009 International Conference on Arabidopsis Research (ICAR). Additional continuing committee members include Julian Schroeder, Caren Chang, George Haughn, Scott Poethig, Mark Estelle, and Jane Glazebrook. NAASC provides North American representation to the MASC and serves as the main organizing and fundraising body for the ICAR when it is held in North America and raises funds to support young North American scientists to participate in foreign ICARs. For the

2008 ICAR, Caren Chang and Julian Schroeder spearheaded the fund-raising effort while Scott Poethig submitted funding proposals for the 2009 ICAR.

## The International Conference on Arabidopsis Research

NAASC organizes the ICAR when it is held in North America and supports young North American scientists to participate in foreign ICARs. Since 1995 the meeting had been in the U.S. 2 of every 3 years. In 2005 the NAASC changed the format of North American meetings to alternate sites with the usual location in Madison, Wisconsin. During the annual MASC meeting at the 2007 ICAR, a 3 year conference site rotation was adopted: North America, Europe, and Asia/Pacific Rim.

The 19th ICAR, held July 2009 in Montreal, marked the first time the meeting took place in Canada and over 800 attendees participated. The conference organizing committee was chaired by NAASC members Joe Kieber and Xuemei Chen, and included Tamara Western and Hugo Zheng from local McGill University. NAASC developed a meeting survey to gauge the opinions of attendees about the ICAR to help in planning future meetings. A subset of the results from the 322 responses received are presented in the accompanying Table. Joanna Friesner, U.S.-based MASC Coordinator, provided overall organization of the three conferences held from 2006-2008. The ICAR plans to return to the U.S. in 2011 following the 2010 meeting in Japan, with current plans to return to Madison, Wisconsin.

## Post-ICAR 2008 Survey

Of 322 respondents	31% Graduate Student	29% Postdoctoral Scholar	29% Faculty	5% Industry	5% Industry
First Arabidopsis Conference?	55% No	45% Yes			
Home Country	39% U.S.	28% Europe	15% Canada	15% Asia/Pacific Rim	5% Other
Opinion on length of meeting (5 days)	84% Just Right	9% Too Long	3% Too Short	4% No Opinion	
Preference on speaker type	79% Mix of Plenary/Abstract	18% Plenary Only	3% No Opinion		
Preference on speaker mix	50% Equal Mix	32% More Invited	10% More Abstract	6% Invited Only	2% No Opinion
Were 3 poster sessions enough?	68% Yes	32% No			
Quality of talks	50% Good	35% Excellent	14% Average	0.6% Poor	0.4% No Opinion
Liked community workshops?	72% Yes	4% No	24% No Opinion		
Liked 'free afternoon'?	92% Yes	8% No			



## **Follow-up to the 2020 Vision for Biology workshop: The role of plants in addressing grand challenges**

The NSF's 2010 Project, designed to elucidate gene function in *Arabidopsis*, will have its last competition for proposals in 2010. Researchers in the US began discussions in 2007 to develop a new vision to propel forward the next decade of *Arabidopsis* research in the US. In January, 2008, an NSF-sponsored workshop was held which included participants invited from different areas within the *Arabidopsis* research community as well as from other plant and animal model system communities. The goal of the workshop was to be forward-looking about the direction of biology research in the next decade and to discuss where plant biology, *Arabidopsis*, and model organisms fit into this larger vision.

The outcomes of the workshops were discussed during the 2008 MASC meeting and were made publicly available in reports posted at TAIR and described in the 2008 MASC annual report distributed to each attendee of the 2008 ICAR. A summary report can be found at: [www.arabidopsis.org/portals/masc/masc\\_docs/masc\\_wk\\_rep.jsp](http://www.arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp). NAASC members also contributed to an editorial describing the workshop outcomes that was published in the journal *Molecular Plant* (ref: *Molecular Plant* 1 (4): 561-3, July 2008). During the 2008 ICAR, NAASC also facilitated a special seminar by Dr. Jim Collins (NSF) which included a presentation to discuss future NSF funding strategies and research interests followed by an interactive discussion session.

## **Arabidopsis Researchers Elected to the National Academy of Sciences**

The National Academy of Sciences (NAS) was established in 1863. It is an honorific society of distinguished scholars engaged in scientific and engineering research, dedicated to the furtherance of science and technology and to their use for the general welfare. The Academy membership is composed of approximately 2,100 members and 380 foreign associates, of whom nearly 200 have won Nobel Prizes. Members and foreign associates of the Academy are elected in recognition of their distinguished and continuing achievements in original research; election to the Academy is considered one of the highest honors that can be accorded a scientist or engineer.

- Arabidopsis researchers elected April 28, 2008: James Carrington (Oregon State University, Corvallis), Steve Kay and Martin Yanofsky (University of California, San Diego), and Johanna Schmitt (Brown University).
- Arabidopsis researchers elected April 28, 2009: Robert Fischer (University of California, Berkeley), Sarah Hake (USDA Plant Gene Expression Center), and Detlef Weigel (now at the Max Planck Institute for Developmental Biology).

## **ABRC: Randy Scholl, Director, to retire**

Management and supervisory roles at ABRC are under reorganization to accommodate the retirement of Randy Scholl in August, 2009. Dr. Erich Grotewold of OSU's Department of Plant Cellular and Molecular Biology will become the new Director. The ABRC has just made a new senior hire (Dr. Jelena Brkljacic), which together with the reorganization of the existing personnel, will ensure a swift transition.

## **The iPlant Collaborative- One year update**

NSF funding for the iPlant Collaborative (iPC), at the level of 50 million USD for 5 years with the possibility of a second 5 year funding period, began February, 2008. The overarching goal is to develop a fluid, community-driven cyberinfrastructure collaborative for the plant sciences that would enable new conceptual advances through integrative, computational thinking. The iPC will bring together plant biologists, computer and information scientists and engineers, as well as other experts, to address 'Grand Challenges' in the plant sciences. *Arabidopsis*, with its advanced resources, datasets and extensive research community, is expected to play an integral part.

The first year goals were primarily to stimulate community participation in the project, bring together groups to propose Grand Challenges, and begin creating specific cyberinfrastructure components. In the second year, iPC will begin supporting cyberinfrastructure for selected projects. In 2008, 5 of 9 submitted Grand Challenge workshops were held which included over 300 participants from 12 countries. In January, 2009, iPC held a brainstorming workshop on what cyberinfrastructure is required for addressing challenges in plant sciences. In March, 2009, 6 Grand Challenge Collaboration requests to develop cyberinfrastructure were reviewed. The iPC will begin by supporting two efforts; the first, Plant Phylogenetics, will create cyberinfrastructure to identify and display evolutionary relationships between ½ million green plant species by creating phylogenetic trees which eventually will include linkages to species data, thereby serving as a foundation for broadly applicable specific trait and ecological information. The second Grand Challenge project, the Genotype-to-Phenotype group, will examine the Phenology of Flowering, and will focus on the needs to integrate large datasets as one of its primary objectives. The project outcomes are expected to be broadly applicable to a wide range of plant biologists. Also underway is the development of iPlant Action Teams (iPATs), two-person teams consisting of one computational and one plant biology faculty member to solve a mini-project in plant computational biology in order to develop models for successful collaborations. Other activities include the iPlant Summer Teacher Research Fellowship, now in its second year, and several workshops including 'Computational Biology for Biology Educators'. In summer and fall, 2009, iPC expects to consider additional Grand Challenge workshop proposals and collaborations.

## **US Young Researcher Exchange Program**

In 2005 a program was established to allow graduate students and post-doctoral fellows from NSF-supported US labs to engage in short-term research visits to German labs. This NSF-funded program is a collaboration with the German *Arabidopsis* Functional Genomics program, AFGN, which similarly allows German students to work in US labs. Since its inception, the US program has funded research visits to Germany by 2 post-doctoral fellows and 11 PhD students. AFGN has supported 7 PhD students. Both programs end this year.

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