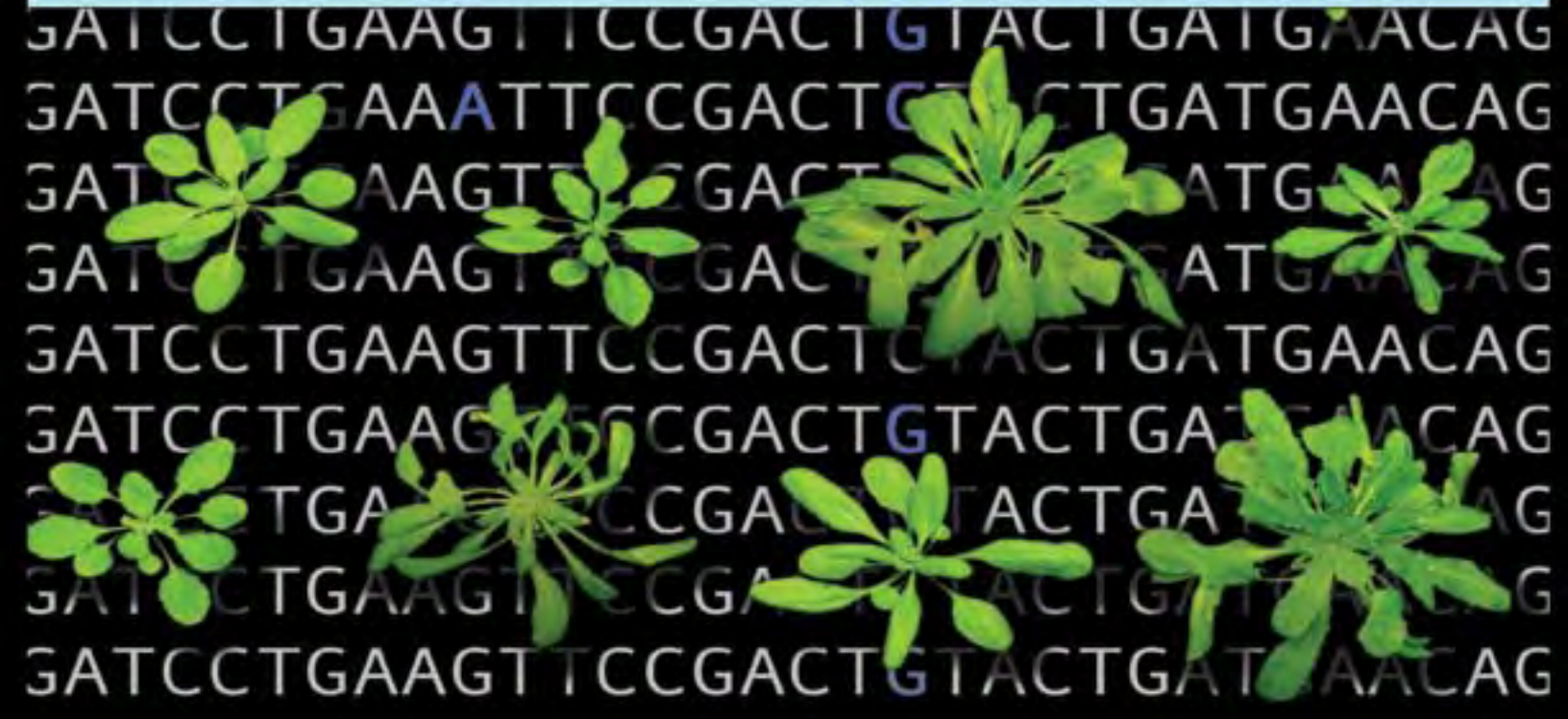
The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2008

Geographical distribution of ecotypes of *A. thaliana* *(adapted from J. Clarke)*



The Multinational *Arabidopsis* Steering Committee July 2008

The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2008

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The Multinational *Arabidopsis* Steering Committee—July 2008

Front Cover

Design

Philippe Lamesch, Curator at TAIR/Carnegie Institute for Science, and Joanna Friesner, MASC Coordinator at the University of California, Davis, USA

Images

Map of geographical distribution of ecotypes of *Arabidopsis thaliana*

Updated representation contributed by Philippe Lamesch, adapted from Jonathon Clarke, UK (1993). The distribution map of J. Clarke was re-drawn from an original by George Redei, USA (1969). World map: courtesy of Kingston University London, UK.

Arabidopsis thaliana natural accessions overlaying DNA sequences

Contributed by Korbinian Schneeberger, Kirsten Bomblies, and Detlef Weigel, Max Planck Institute for Developmental Biology, Germany. The newly-proposed 1,001 Genomes project (http://1001genomes.org) aims to discover sequence variation, such as the single-nucleotide polymorphisms (SNPs) at G/C and A/T base pairs highlighted in blue, in 1,001 natural *Arabidopsis thaliana* accessions.

Back Cover

Arabidopsis plant from the 'Vårhallarna' population collected in Skåne, Sweden (Latitude: 55.70187, Longitude: 13.51756). Image contributed by Alison Anastasio in the lab of Joy Bergelson, Department of Ecology and Evolution, University of Chicago, USA.

Table of Contents

Foreword to the Report

This is the 2007/2008 annual report of the Multinational Arabidopsis Steering Committee (MASC) on the status of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. The project was proposed as a follow-up to the Multinational Coordinated *Arabidopsis thaliana* Genome Research Project that concluded with the release of the reference genome sequence in 2000. The success of the genome sequencing effort motivated researchers to propose an even more ambitious goal: to determine the function for every Arabidopsis gene by the year 2010. The Functional Genomics Project, described by some as 'the second-phase of the far-reaching vision' by those who launched the Genome Project, was an ambitious and inspiring endeavor. Since the project was proposed in 2001, the very definition of gene function has expanded, making it clear that it is not trivial to determine the 'function' of a gene and leading researchers into new and exciting avenues of discovery. Over the last 8 years, international projects have generated vast datasets and resources and produced numerous breakthroughs in understanding the fundamental processes underlying plant growth and development. The benefits of focused efforts on Arabidopsis are increasingly being appreciated; it is widely recognized as the most suitable plant for experimentation in genetics and genomics and has gained almost universal support as the central reference and conceptual framework for much of plant biology, particularly for molecular studies. The value of Arabidopsis as a central reference is well justified by the huge strides forward in our understanding of basic plant science, efforts that are underscored by a strong publication record whose trajectory sharply increased following the release of the reference genome sequence. 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. As highlighted in this year's report, such 'knowledge transfer' is occurring at many levels by many different routes. Furthermore, there are undoubtedly many more examples of research that has benefited from Arabidopsis resources and knowledge, such as work performed in private companies that have not yet made their approaches and data publicly-known, or translational efforts that result in crop improvement where the link to 'proof-of-concept' work performed in Arabidopsis is not always clear. In addition, it is difficult to quantify the frequency by which Arabidopsis resources are used by researchers from outside Arabidopsis, or even outside plant systems. This is partly due to the collegiality of many researchers in the Arabidopsis community who make their resources freely available through data repositories such as TAIR and genetic repositories such as ABRC and NASC, and resource-sharing is often required by funding agencies. One indication of the utility of Arabidopsis resources to scientists studying other organisms was revealed in a recent survey of users of TAIR (The Arabidopsis Information Resource). It was found that only 34% of respondents focus their research exclusively on Arabidopsis, 62% focus on other species including crops and other model organisms in addition to Arabidopsis, and 3% work exclusively on other species (see page 16 for survey details.) The results from this small sample is a positive reflection on the Arabidopsis community and the investment by government agencies that focused funding on Arabidopsis, and suggests that Arabidopsis resources are informing and benefiting a wide range of basic and applied studies.

This report details progress made over the last year by the international Arabidopsis functional genomics community. It 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. Success in acquiring a fundamental understanding of plant biology, and indeed, for translating basic plant knowledge to other systems, relies on maintaining and strengthening funding streams and world-wide collaboration. Resources need to be coordinated to maximize synergy and only sustained collaborations will enable the Arabidopsis community to achieve its ambitious goals. As the Functional Genomics Project nears its conclusion, the research community and funding agencies must consider the future directions for Arabidopsis and plant research. The Multinational Arabidopsis Steering Committee has already begun facilitating the process of obtaining input from important stakeholders, including members of the global Arabidopsis and plant communities, through workshops and extended planning discussions at MASC Annual meetings.

It is clear that a thorough understanding of the basic biology and ecology of plants will be required to address many of the challenges facing the world today, including greater food requirements of a rapidly increasing human population, the need to develop renewable energy sources, loss of habitat, and global climate instability. At this critical juncture, fundamental studies using Arabidopsis are more important than ever, and efforts to strengthen links between researchers working with model and crop plants, and between basic and applied science are needed.

The Multinational Arabidopsis Steering Committee
July 2008

Executive Summary

The need for detailed understanding of the basic biology and ecology of plants has never been greater. The increasing demands on agriculture to supply food, fiber and fuel to an ever growing, and ever more prosperous, human population in a sustainable manner represents one of the greatest challenges facing humankind. 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. A thorough understanding of the basic biology and ecology of plants is needed to address the myriad challenges facing the world today and will enable improved agricultural productivity while minimizing negative impacts. It is evident that the dramatic advances achieved in plant biology over the last two decades are largely due to the concentrated focus on Arabidopsis by plant researchers worldwide. It is equally certain that there is still much to be learned. In the next 10 years we will witness more rapid translation of basic research discoveries into promising agriculture, energy, and environmental improvements. Dedicated support for basic research by government funding agencies has been, and will continue to be, crucial to successfully developing Arabidopsis and for leveraging the knowledge gained for applied studies in other plants.

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 17,800 Arabidopsis researchers in approximately 6,800 laboratories worldwide. Arabidopsis, with its early emphasis on multi-disciplinary projects, should continue to serve as an ideal training system for future generations of researchers with broadened expertise. Resources need to be coordinated to maximize synergy and only sustained collaborations and timely sharing of data, stocks, and other resources will enable the Arabidopsis community to achieve its ambitious goals. 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 current and future challenging questions. Continued and expanded funding and international collaboration is critical to future success; the increasingly globalized research community suggests that centers of excellence will emerge in non-traditional areas outside of North America, Japan and Western Europe. Maintaining and strengthening ties between researchers in all parts of the world, and between basic and applied scientists, will create the synergy needed to effectively meet the challenges of tomorrow.

Highlights in *Arabidopsis* research

The past year continued to be strong for Arabidopsis publications following a 20 year trend of increasing publication number. 2,334 Arabidopsis peer-reviewed research papers were published in 2007, nearly a 35-fold increase over 1987 in which 67 peer-reviewed papers were published (see Fig. 1, page 10).

Some highlights this year include:

- Publication of the first large-scale Arabidopsis proteomic map
- Discovery of a potentially new mode of gene regulation by microRNAs that 'mimic' their targest
- A breakthrough in the quest to develop apomixis in crops
- High-density array resequencing of 20 natural Arabidopsis strains, a natural variation resource.
- The discovery of a mechanism for blue-light as an input to the circadian clock via the ZTL protein, also established it as a photoreceptor

Examples of applications arising from *Arabidopsis* research

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 2007 there were 900 utility patents referencing Arabidopsis compared to 103 in 1997 and 0 in 1987 (See Fig. 3, page 22). In reality, the time from discovery to application takes years and the pipeline is full of Arabidopsis-fueled discoveries heading for the marketplace. We have chosen just a few examples of discoveries that demonstrate how basic research in Arabidopsis can be translated into real-world applications. Several of the examples involve resistance to environmental stresses reflecting the utility of Arabidopsis research to increasing plant productivity in rapidly changing environmental conditions. Each study vitally depended on Arabidopsis data and resources:

- Mining the Arabidopsis genome sequence to develop drought-tolerant corn
- Calcium bio-fortified carrots: human feeding trials demonstrate increased calcium absorption
- Drought tolerant oilseed rape and corn
- Development of salt-tolerant tomato, alfalfa, canola and rice
- Stress tolerant rice and wheat

Major new initiatives announced this year

- **China**-The National Science Foundation of China initiated a new program to further understanding of the mode of plant hormone action with a budget of 150 million RMB (approximately $21.8 million) over an 8 year period. Five million will be allocated to promote international collaboration in plant hormone research.
- **Japan**- A research program entitled "Plant regulatory systems that control developmental interactions between meristems and lateral organs" funded by the Ministry of Education, Science, Culture and Sports has been initiated with a budget of 1.6 billion yen (approximately $14.45 million) over a 6 year period. The program will fund at least 13 Arabidopsis projects.
- **UK**- The BBSRC-funded Systems Approaches to Biological Research Initiative (SABR) has awarded 3 Arabidopsis systems biology research projects with a budget of about £13.5 million (approximately $26.5 million) over a 5 year period. Projects topics include: temperature and signaling, signaling and plant stress, and leaf growth.
- **Canada**- The Competition in Applied Genomics Research in Bioproducts or Crops (Genome Canada) will provide significant funding over a 4 year period for projects that address two main topics: Plant Nutrition and Bioproducts. An estimate of funding allocation was not available. Both applied and basic research will be considered.

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 20-21). This year the thermometers are measured against the TAIR8 genome release. The availability of high-quality genetic resources will facilitate future studies and contribute to our expanding pool of knowledge.

- Availability of confirmed homozygous mutant plant lines: with two or more insertions = 5,192 genes; with one confirmed homozygous allele insertion = an additional 7,631 genes, giving a total of 12,823 unique genes with one or more homozygous insertion. As of May, seeds from 20,588 lines have been sent to the Arabidopsis Biological Resource Center (ABRC) for preparation and distribution. The first 8,889 lines of this collection were shipped to users in Spring, 2008.
- 26,772 of 28,523 unique Arabidopsis genes (excluding pseudogenes) contain at least one sequenced insertion element. Importantly, the proportion of genes with one homozygous mutation has more than doubled since May, 2007. Newly procured since last year are the collection of two or more homozygous insertions available for over 18% of genes.
- Availability of nearly 36,000 RNAi clones targeting at least 22,969 genes (excluding pseudogenes); RNAi clones for 3,592 genes have been transformed into Arabidopsis.
- Isolation of full-length cDNAs for 20,623 of 28,523 genes; clones of 19,639 are currently being distributed.
- Availability of fully-sequenced ORF clones for 15,907 genes and partially-sequenced clones for 1,236 more.
- 26,670 of 28,523 genes whose expression has been detected by cDNA, EST, MPSS, sage or microarray data

MASC Subcommittees

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

- Bioinformatics- Results of the final Web Services project were presented at the 2007 Arabidopsis conference. This project sparked the creation of dozens of web services as well as client tools. The Chair participated in the iPlant Collaborative (iPC) kickoff in April. The Subcommittee aims to participate in this process to ensure alignment of integration efforts between the iPC and Arabidopsis functional genomics.
- Clone-based Functional Genomics (ORFeomics)- Significant progress continues to be made towards achieving the long-term community goal of obtaining full length (FL)-cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein coding genes. Running totals from all the major projects are included in Table 3 (page 27).
- Natural Variation and Comparative Genomics- A number of notable publications in the areas of variation and comparative genomics were published in the past year including a study describing the resequencing of 20 Arabidopsis accessions. Data from that and other studies, most available at TAIR, are being used for genome-wide association mapping and to design a commercially available SNP chip for looking at genetic variation.
- Phenomics- Construction of the Australian Plant Phenomics Facilities (APPF) began this spring with full commissioning of the initial Arabidopsis screening module in Canberra expected at the end of 2008. In addition, several automated platforms for Arabidopsis phenotyping are being developed in France. Insertion and RNAi resources are listed (Fig. 2, pages 20-21; also see Table 4, page 30).
- Proteomics- A MASC proteomics webpage was established including standards for different proteomic techniques, databases, procedures, meetings, etc. The Subcommittee held a workshop at the 2007 ICAR and will hold another at the 2008 ICAR. The establishment of large protein interaction databases with links to MASC proteomics resources is the main goal of the next years.
- Systems Biology- The Systems Biology and Bioinformatics Subcommittees will co-host a workshop on "Frontiers in Plant Systems Biology" at the 2008 Arabidopsis conference. The goal is to bring together groups that produce, integrate and model data from a systems perspective and to stimulate discussion on the role of systems biology research in addressing the grand challenges in plant biology. The workshop will discuss interactions with the iPlant Collaborative (iPC) and discuss how best to use iPC to advance systems biology research in Arabidopsis.

MASC Recommendations from Arabidopsis Research Planning Workshops

1. Major and specific support to integrate molecular, cellular, organismal and ecological research on Arabidopsis should continue to facilitate understanding of how a living organism develops, functions and adapts to its environment.
2. Arabidopsis research should be viewed as an essential component of a continuum of plant science research from the fundamental to the applied. Strong investment is needed in Arabidopsis research to generate fundamental knowledge as well as novel technologies, and in crop plant research to deliver translational outputs.
3. Systems approaches that integrate levels of biological organization, with the parallel development of mathematical platforms to handle, quantify, integrate and interpret biological data should be emphasized. Collaborations between biologists, mathematicians, computer scientists, engineers, and scientists in other quantitative disciplines should be established to enable quantitative systems biology approaches.
4. Data acquisition should remain a major focus of future programs to fuel data analysis, integration, hypothesis generation and testing.
5. International collaborations have been key to the successes achieved thus far in Arabidopsis research. Arabidopsis can continue to forge scientific strength and cooperation throughout the world, including with developing countries that place a high value on agriculture-related research.
6. Publicly-accessible data are critical to the advancement of plant research. We must ensure the security of our major data and resource repositories such as TAIR and stock centers and support timely sharing of resources. Sufficient repositories for current and future datasets and resources must be available.
7. Support should be provided to develop additional and new types of large-scale experimental genomics resources.
8. The Arabidopsis community should continue to play a vital role in attracting and developing highly-trained researchers in the plant sciences that can apply their knowledge and skills in the agricultural and other areas of plant biology. Integrating advanced techniques and approaches with current and future datasets will continue to attract high-quality interdisciplinary researchers.
9. Arabidopsis should provide the 'how-to' guide for the development of other plant research systems.
10. The wealth of genomic and functional data and systems biology tools available for Arabidopsis should be leveraged for population genomic analyses and understanding phenotype-genotype relationships, species-level variation, environmental adaptation, and biological systems up to the ecological level.
11. Standardization of data collection and annotation is needed, including the development of tools for phenotype description, sample preparation and storage, metabolite profiling, proteomics, etc.

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

- As the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project nears its conclusion in 2010, continued dialog on future research directions and funding streams is needed. A second MASC planning meeting at the 2008 Arabidopsis Conference will include presentations from US and European workshops on the future of Arabidopsis research. In addition, further input from the broader community should be obtained.
- The Arabidopsis community should participate with and support the new iPlant Collaborative (iPC).
- The 1,001 Arabidopsis genomes project should be supported. The community should also look at representative transcriptomes and epigenomes of these same accessions at the level of tissues or individual cells
- Accessibility of Arabidopsis knowledge and resources should be increased by establishing materials and annotation handling standards with all major plant biology journals in addition to the first partnership established between TAIR and Plant Physiology. Also needed are ways to capture most of the primary literature in machine readable format.
- Projects to obtain detailed highly replicated expression, epigenetic, and proteomic profiling across spatial, temporal, environmental, developmental, and genotype series are highly desirable. Detection at the level of individual cell type, rather than in whole tissues/plants, is preferred.
- A common ontology and appropriate connected databases are needed to facilitate phenotype recording and store and share phenotype data.
- Techniques and efforts to address protein complexes are needed, for example, by improved fluorescent tag methods that allow real-time detection of protein complexes, or by cell sorting followed by sensitive detection of protein complexes.

Progress and Activities of Multinational *Arabidopsis* Functional Genomics Projects

Progress and activities of the MASC in 2007/2008

In 2007/2008, Xing Wang Deng (Yale University) succeeded Ian Small (University of Western Australia) to become the MASC chair and Joe Kieber (University of North Carolina, Chapel Hill) became co-chair. Dr. Kieber will become the new MASC chair when Dr. Deng steps down following the annual International Conference on Arabidopsis Research (ICAR) in July, 2008. At the 2006 annual MASC meeting, MASC members recommended that TAIR take over abstract submission for future ICARs. This was done to facilitate inclusion of Arabidopsis genes being studied by the community in order to 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. Joanna Friesner, the MASC Coordinator, worked with TAIR staff in 2006 to design an abstract submission process that included a request for voluntarily submission of gene AGI codes under study in submitted abstracts. The database was used for the 2007 ICAR: 369 of 776 submitted abstracts contributed a total of 2,077 AGI codes, of which 1,722 were distinct (ie, not shared with another abstract.) There were 535 loci from the abstracts that were not already associated to literature in TAIR at that time. Providing these links between abstracts and AGI codes will allow the community to learn of new results presented during the ICARs. In 2008, abstract submission was not facilitated by TAIR due to usage of a different database by conference staff. However, AGI codes were still collected during abstract submission and the data will be entered into the TAIR database after the conference.

Google Analytics were employed beginning June, 2007 to track the usage of webpages at TAIR, including the MASC pages which are maintained by the MASC Coordinator. Visits to the MASC pages are frequent: in the 1 year period between June 1, 2007 and May 31, 2008, 125 different MASC pages were viewed 14,720 times, or about 1225 views a month on average. The top-viewed page (www.arabidopsis.org/portals/masc/projects.jsp) contains information on the projects funded through the NSF 2010 project. Another frequently viewed page was the Coordinator's Journal (described below) which was first available on the MASC webpages in September 2007.

MASC subcommittees, proposed at the 13th ICAR held in 2002, were established to help track progress towards the goals outlined in the 2002 Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. Over the last 6 years, in response to evolving needs of the community, a number of subcommittees were initiated and several discontinued. No new subcommittees were proposed over the last year, however, three subcommittees changed chairs: ORFeomics, previously chaired by Pierre Hilson, is now chaired by Joe Ecker; Metabolomics, previously co-chaired by Ian Graham and Basil Nikolau, is now chaired solely by Basil; and Natural Variation and Comparative Genomics, previously chaired by Tom Mitchell-Olds, is now co-chaired by Julin Maloof and Chris Pires. This report includes reports from 6 of 7 current MASC subcommittees: Bioinformatics, cDNAs and Clone-based Functional Proteomics (ORFeomics), Natural Variation and Comparative Genomics, Phenomics, Proteomics, and Systems Biology (a Metabolomics report was not submitted this year.) Wolfram Weckwerth and other members of the Proteomics subcommittee developed a website that includes links to existing databases of Arabidopsis proteomics. The subcommittee held a Proteomics workshop at the 18th ICAR, which included oral and poster presentations, and have another workshop planned for the 19th ICAR in 2008. Further information on these projects can be found in the Proteomics subcommittee report. Chris Town and Heiko Schoof, co-chairs of the Bioinformatics subcommittee, continued their Web Services projects that aim to improve data integration in the Arabidopsis community. A third developers' workshop was held in May 2007 at JCVI (John Craig Venter Institute), and results were presented at the 18th ICAR in June, 2007. A request to continue the project was not funded; however, members of the subcommittee will take part in a joint workshop with the Systems Biology subcommittee, entitled 'Frontiers in Plant Systems Biology, at the 19th ICAR in 2008. Further information can be found in the Bioinformatics and Systems Biology subcommittee reports.

A full-time MASC coordinator position, established in 2002, has been supported for 5 of the last 6 years by the NSF (US) and by the DFG (Germany) in 2004. The current MASC coordinator, Dr. Joanna Friesner (University of California, Davis), was awarded an NSF grant, with Charles Gasser, to provide Coordinator funding through late spring 2009. It is expected that a new MASC member country will assume funding for the Coordinator position at the conclusion of the current grant (discussions for future funding are underway.) In September 2007 the Coordinator established the 'Coordinator's Journal' webpage at the MASC pages in order to provide additional outreach and communication. The Journal chronicles conferences and workshops attended by the Coordinator, and of interest to the Arabidopsis community, and relays other relevant information (www.arabidopsis.org/portals/masc/journal.jsp). The MASC Coordinator functions to provide help and coordination to the MASC, the North American Arabidopsis Steering Committee (NAASC), 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, editing, and publishing 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

The continual increase in the number of Arabidopsis research articles published each year reflects the maturity of the field, advances made in resource development, the creativity of Arabidopsis researchers, and the collaborative nature of the community (Figure 1).

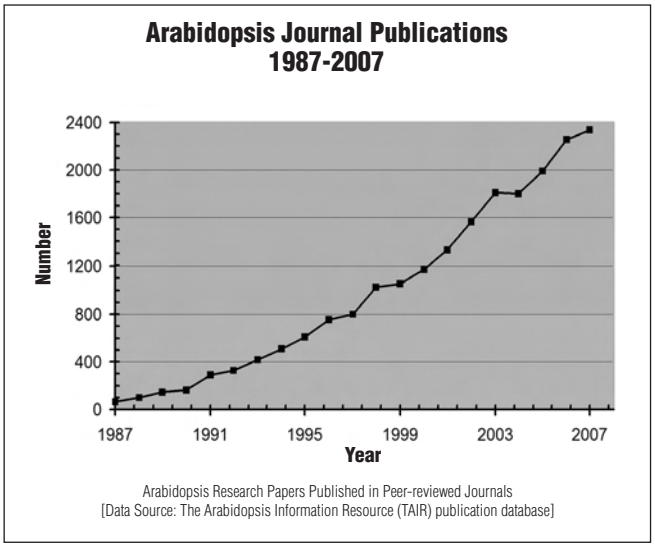


Figure 1

Initiatives that support resource development have provided useful tools that allowed many researchers to engage in Arabidopsis research and continue to facilitate the attraction of Arabidopsis as a research system across disciplines. Furthermore, studies using Arabidopsis are found not only in high-ranking plant journals; when compared to other model organisms, Arabidopsis publications are significantly represented in high-ranking general journal publications such as Science and Nature. Compared to five other model organisms including mouse, fruit fly, budding yeast, nematode, and maize, Arabidopsis journal articles rank third in number over both one year (Table 1A) and five year periods (Table 1B).

Insights from Arabidopsis inform studies in plants of economic importance including food, feed and fuel crops. 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. It is often easier and faster to study disease genes in Arabidopsis than in mammalian models, particularly because defects in some disease genes are lethal in mammals yet viable in plants. The Arabidopsis genome sequencing project revealed that the genome contained sequences similar to 48% of human disease genes (1) and 70% of genes implicated in cancer (2). A recent article in the journal Cell highlights a number of ways that studies in Arabidopsis have impacted advances in medical research and led to discoveries that have direct relevance to human health and disease (2). Given the impressive breakthroughs from Arabidopsis research thus far, especially given its relative newness as a model organism, continued research in Arabidopsis is sure to bring big dividends in crop science, human health, natural variation, and environmental response, among other areas. The following section provides summaries of just a sample of the scientific breakthroughs produced by the Arabidopsis research community in the last year. Many of these are the result of collaborative international efforts exemplifying the efficacy and importance of coordinated research.

References:

1. Arabidopsis Genome Initiative. Nature, Dec. 2000, 14: 408 (6814): 796-815

2. Jones AM, Chory J, Dangl JL, Estelle M, Jacobsen SE, Meyerowitz EM, Nordborg M, and Weigel D. Cell, Jun. 2008, 133: 939-943

Who Needs Sex?

By: Joanna Friesner, MASC Coordinator

Many important crops have undergone plant breeding methods that require the production of hybrids for propagation. A drawback to this is that hybrid plants themselves are unlikely to produce similarly robust offspring due to loss of heterozygosity of parental alleles during reproduction. The ability to produce offspring asexually, essentially giving clones, would allow hybrid vigor traits to be fixed and propagated directly. Apomixis, the process that produces asexual seeds, and thus clonal offspring, is found in numerous plant species. However, the basic molecular mechanisms of apomixis are not known. For example, the number of genes underlying apomictic ability, or the reasons why certain plants are apomictic and others, including Arabidopsis and many crop species, are not, remain unclear. A recent paper by Ravi et. al. demonstrates that partial loss of function of a single Arabidopsis gene results in the production of unreduced diploid female gametes, a critical step in the apomictic process. This breakthrough in understanding apomixis provides an important step towards developing apomixis in crops and suggests that asexually reproducing apomictic plants may evolve from sexually reproducing plants through alteration of a small number of genes.

Ravi et. al. studied plants defective in the Arabidopsis *DYAD/SWITCH1 (SWI1)* gene which is required for proper sister chromatid cohesion and centromere organization during meiosis. *swi1* plants are defective in the first meiotic phase; rather than segregate pairs of chromosomes equally, followed by another round of division to produce four haploid spores, *swi1* plants undergo a single separation to produce 2 diploid spores which typically fail to produce a female gametophyte.

Table 1A. Journal Articles Referencing Model Organisms in Title or Abstract Over 1 Year (2007)*

	Science		Nature	
Model Organism	**Journals normalized to 'mouse' value**	**Total number of Journal articles**	**Journals normalized to 'mouse' value**	**Total number of Journal articles**
	Total Science Journal articles 2007: 1,355		Total Nature Journal articles 2007: 1,105	
Mouse	1	66	1	124
Drosophila melanogaster	0.44	29	0.29	36
Arabidopsis thaliana	0.30	20	0.15	19
Caenorhabditis elegans	0.17	11	0.09	11
Saccharomyces cerevisiae	0.09	6	0.11	14
Maize/zea mays	0.03	2	0	0

*Data were retrieved using Advanced Search at PubMed (www.ncbi.nlm.nih.gov/pubmed). Searches were limited to the indicated Journal, AND (genus OR species name in abstract/title) AND indicated timeframe, AND limited to Journal articles. For mouse, searches were performed with these keywords: mouse OR mice OR mus musculus. For maize, searches were performed with these keywords: maize OR corn OR zea mays.

Table 1B. Journal Articles Referencing Model Organisms in Title or Abstract Over 5 Years (2003 - 2007)*

	Science		Nature	
Model Organism	**Journals normalized to 'mouse' value**	**Total number of Journal articles**	**Journals normalized to 'mouse' value**	**Total number of Journal articles**
	Total Science Journal articles 2003 - 2007: 6,597		Total Nature Journal articles 2003 - 2007: 6,216	
Mouse	1	360	1	488
Drosophila melanogaster	0.39	140	0.36	174
Arabidopsis thaliana	0.24	88	0.17	82
Caenorhabditis elegans	0.14	51	0.15	75
Saccharomyces cerevisiae	0.08	28	0.14	68
Maize/zea mays	0.04	14	0.04	18

*Searches performed as described in previous table.

The hypomorphic *dyad* allele of *SWI1* specifically causes female sterility with incomplete penetrance; functional female gamete formation is about 0.24%, with most *dyad* plants producing just a few seeds compared to about 2,000 in wild-type plants. The majority of plants from viable seeds via *dyad* self-pollination have larger flowers and produce heterogeneously-sized pollen suggesting abnormal ploidy of the *dyad* parent. Through analyses of chromosome counts, seed weight from *dyad* plants, and reciprocal crosses between wild-type diploid and tetraploid plants to determine the effect of maternal and paternal excess on seed weight, the authors found that the majority of seeds produced by dyad mutant plants are triploid and that the increase in ploidy arises from an excess maternal genome contribution. By outcrossing *dyad* and examining a number of polymorphic markers, they further showed that loss of heterozygosity occurred almost exclusively in diploids, but not in triploids, indicating absence of recombination in the diploid maternal gamete. These data suggest that triploid offspring from *dyad* result from fertilization of an unreduced maternal gamete by a normal haploid paternal gamete. While

there is still much to be learned, the results of this study provide an important advance in understanding apomixis in plants. *Reference: Ravi M, Marimuthu MPA, and Siddiqi I, Gamete formation without meiosis in Arabidopsis. Nature, Feb 28 2008; 451: 1121-1124.*

The First Large-scale Arabidopsis Proteome Map

By: Joanna Friesner, MASC Coordinator

The release of the *Arabidopsis thaliana* genome sequence in 2000 provided an important resource for gene function studies and both plant and non-plant communities are benefiting from the knowledge obtained through bioinformatic and experimental analysis of the Arabidopsis genome. Proteins, encoded by gene sequences, are the primary effectors of the genome; protein synthesis, modification, localization, degradation, and interactions with other cellular components transfer genetic potential into phenotypic output. Therefore, a fundamental understanding of biology requires studies that go beyond the genome and explore the proteome. A recent publication by Baerenfaller et. al. provides the first large-scale quantitative Arabidopsis proteomic map. 1354 tandem mass spectroscopy (MS/MS) runs using protein extracts of differentiated plant organs and undifferentiated cell culture produced 790,181 MS/MS spectra. From this, the authors identified 13,029 proteins with 86,456 unique peptides, representing nearly half of the TAIR7 predicted gene models. In comparison to TAIR7, the MS/MS data revealed 57 new or altered gene models with the majority (22/57) containing different 5' or 3' gene ends. There were seven gene models each in which peptides were identified in predicted intron or intergenic regions. Peptides were also found for 15 sequences annotated as pseudogenes, six of which were related to transposable element open reading frames. Alternate open reading frames were established for two gene models and four additional models combined a mixture of types. Protein abundance profile comparisons between organ type revealed that organs differed significantly in the types of proteins present. 571 proteins were identified in only one organ; these 'organ-specific biomarkers' clustered similarly in the different organs with biomarkers identified in previous transcriptional profiling studies. Transcriptional and proteomic profiling data were integrated and compared to determine the level of correlation between transcripts and protein accumulation in each organ. Overall they found positive correlations between transcription and protein levels suggesting that protein accumulation in Arabidopsis is regulated significantly at the level of transcription.

The dataset of 13,029 proteins, original MS/MS spectra, and information on protein and peptide identification, are a publicly-available online resource and are found in the PRIDE database, PRIDE BioMart (www.ebi.ac.uk/pride/)/ with an enhanced view at www.AtProteome.ethz.ch.

Reference: Baerenfaller K, Grossmann J, Grobei MA, Hull R, Hirsch-Hoffmann M, Yalovsky S, Zimmermann P, Grossniklaus U, Gruissem W, and Baginsky S, Genome-scale proteomics reveals Arabidopsis thaliana gene models and proteome dynamics. Science, May 16 2008; 320: 938-941.

The Demise of JAZ Sets Signals in Motion

By: Joanna Friesner, MASC Coordinator

Jasmonates are signaling molecules involved in modulating plant development and defense responses to both abiotic and biotic challenges. Previous studies suggested that jasmonate signaling involved degradation of repressor proteins by the COI1-dependent E3 ubiquitin ligase. However, the identity of these hypothetical repressor proteins, predicted to regulate a suite of transcription factors involved in jasmonate signaling, has remained a mystery. Two recent back-to-back publications by Thines et. al. and Chini et. al. identify the long-hypothesized repressors as members of a new family of transcription factors. Importantly, these proteins provide the link between COI1-mediated repressor degradation and transcriptional activation of effector genes in response to jasmonate perception.

Chini et. al. identified JAZ member JAI3/JAZ3 through positional cloning of the *jai3-1* jasmonate-insensitive dominant mutant. Thines et. al. identified a number of JAZ members as early-induced transcripts in the *opr3* jasmonate synthesis mutant and generated a JAZ1 dominant mutant through deletion experiments. Chini et. al. showed that JAI3/JAZ3 directly interacts with the transcriptional activator MYC2 to act as a transcriptional repressor of key jasmonate-responsive effector genes, a finding supported by microarray analysis of *jai3-1*. Through *in vitro* and *in planta* assays both groups demonstrated direct interaction of COI1 with JAI3, and COI1 with JAZ1, and that full-length, but not truncated, JAZ proteins are degraded upon jasmonate treatment. Thines et. al. further showed that jasmonoyl-isoleucine, but not other jasmonates, promoted COI1 and JAZ1 interaction. Thus, it appears that a jasmonate amino acid conjugate is the active form of the hormone for this response. The precise nature of dominant jasmonate insensitivity in the *jai3-1* and *jaz1ΔC* mutants isn't clear. Two possible explanations are that truncated JAZ proteins sequester (ie, poison) COI1 or that truncated JAZ proteins are unable to properly bind COI1 and can act as repressors themselves. Taken together these and other data suggest this simplified model for jasmonate signaling: In the absence of jasmonate, JAZ proteins bind MYC2 to prevent transcriptional activation of jasmonate effector genes. Jasmonate perception, likely via jasmonoyl-isoleucine (JA-Ile), results in COI1-dependent proteasomal degradation of JAZ proteins. Loss of JAZ repressors allows MYC2-mediated transcriptional activation of jasmonate effector genes. The current studies also find evidence for a negative feedback loop whereby effector genes activated by MYC2 include JAZ proteins which, in turn, act to re-establish repression of MYC2.

References:

1. *Thines B, Katsir L, Melotto M, Niu Y, Mandaokar A, Liu G, Nomura K, He SY, Howe GA, and Browse J, JAZ repressor proteins are targets of the SCF(COI1) complex during jasmonate signaling. Nature, Aug 9 2007; 448 (7154): 661-665.*
2. *Chini A, Fonseca S, Fernandez G, Adie B, Chico JM, Lorenzo O, Garcia-Casado G, Lopez-Vidriero I, Lozano FM, Ponce MR, Micol JL, and Solano R, The JAZ family of repressors is the missing link in jasmonate signaling. Nature, Aug 9 2007; 448 (7154): 666-671.*

MicroRNAs That Mimic- a New Approach to Gene Regulation?

By: Joanna Friesner, MASC Coordinator

Although plant microRNAs (miRNAs) were discovered fairly recently, their ability to regulate essential processes including growth and development is becoming increasingly appreciated. Several hundred miRNA genes have been identified in the Arabidopsis genome, many of which are conserved in other plants. In plants, miRNAs act primarily at the post-transcriptional level as negative regulators by degrading target RNAs, many of which encode regulatory proteins. In what appears to be a new type of miRNA regulation a recent study by Franco-Zorrilla et al. describes the gene *IPS1* which shares a region of complementarity with miR-399, a phosphate (P_i) starvation-induced miRNA that can effect cleavage of *PHO2* mRNA to regulate shoot P_i content. However, the presence of a critical mismatch at the miR-399 predicted cleavage site of *IPS1* renders this non-coding RNA resistant to degradation. Instead, *IPS1* transcripts physically sequester miR-399, reducing the free miR-399 pool and inhibiting miR-399's negative effect on *PHO2* transcription. The authors define 'target mimicry' as the non-productive interaction between an apparent (non-cleavable) target site and a miRNA resulting in inhibition of miRNA activity.

Overexpression of *IPS1* was found to inhibit miR-399's effect on *PHO2* transcription suggesting that *IPS1* antagonizes miR-399. Transient assays in tobacco using complementary and compensatory mutant forms of miR-399, *PHO2*, and *IPS1*, confirmed direct interactions between miR-399 and *PHO2*, and *IPS1* and miR-399. The authors also generated a mutant form of *IPS1* that perfectly matched miR-399 in the *IPS1* complementary region by removal of the critical mismatch. Perfect-match $ips1^{PM}$, unlike wild-type *IPS1*, was effectively cleaved by miR-399. Concomitantly, $ips1^{PM}$ failed to inhibit miR-399-mediated *PHO2*-cleavage. These results demonstrate that the *IPS1* mismatch is critical for resisting miR-399 cleavage and for suppressing miR-399 activity. Finally, the authors showed that target mimicry can extend to other miRNAs by artificially engineering *IPS1* in the miR-399 complementarity region to mimic target sites for miR-156 and miR-319. Overexpression of the target mimic constructs produced plants with marked phenotypes that were the reverse of those reported for plants with increased expression of wild-type miR-156 and miR-319. Furthermore, a number of miR-156 and miR-319 targets were found to be more highly expressed in the target mimic plants suggesting that the target mimics were effectively inhibiting their corresponding miRNAs. This study indicates that target mimicry may be a new way to regulate miRNA activity naturally during plant growth and development and that the principle can be exploited to inhibit miRNA activity by engineering artificial target mimics.

Reference: Franco-Zorrilla JM, Valli A, Todesco M, Mateos I, Puga MI, Rubio-Somoza I, Leyva A, Weigel D, Garcia JA, and Paz-Ares J, Target mimicry provides a new mechanism for regulation of microRNA activity. Nature Genetics, Aug 2007; 39 (8): 1033-1037.

Plants that SLAC Off Are Sensitive to the Environment

By: Joanna Friesner, MASC Coordinator

Stomata, pores formed by two adjacent guard cells which regulate the opening or closing of the central pore, are found in the epidermis of plant leaves. Stomata control gas exchange by regulating the influx of carbon dioxide (CO_2) and the efflux of water vapor from plant cells. These activities are important for basic plant processes including controlling water loss, providing needed components for photosynthesis and respiration, and excluding pollutants such as ozone. Stomata also respond to stimuli such as abscisic acid (ABA), calcium ions (Ca^{2+}), light/dark transitions, and humidity changes. While previous research suggests that anion channels within guard cells are important mechanisms that regulate stomatal aperture, the genes encoding the membrane proteins involved in the process had not yet been identified. Two recent back-to-back publications provide the first molecular identification of a component essential to anion efflux in plants.

SLAC1 (SLOW ANION CHANNEL-ASSOCIATED 1) was identified through independent screens for Arabidopsis mutants with ozone or carbon dioxide sensitivity. Vahisalu et. al. discovered that ozone treatment of the *slac1-1* mutant caused leaf cholorosis and failed to trigger normal decreased stomatal conductance and closure. They found that the mutant plants had constitutively higher stomatal conductance, increased water loss and a reduced sensitivity to abscisic acid when compared to wild-type plants whose stomata closed properly. Negi et. al. performed a thermal imaging screen measuring leaf temperature fluctuation and uncovered a mutant, *slac1-2*, which was inhibited in CO_2-induced stomatal closure which results in increased leaf temperature in response to high CO_2. *SLAC1* encodes a distant homolog of fungal and bacterial dicarboxylate/malic acid transport proteins and both groups demonstrated that it is highly and specifically expressed in guard cells. Both groups examined deletion mutants; Negi et. al. found altered organic anion guard cell homeostasis in *slac1-2* plants and Vahisalu et. al. found that stomata of *slac1-1* plants failed to close properly in response to ABA, Ca^{2+}, CO_2, hydrogen peroxide and light/dark transitions. Electrophysiology experiments using whole cell patch clamping by Vahisalu et. al. demonstrated that S-type anion currents are specifically disrupted in *slac1-1* plants while R-type anion channels and calcium channels remain unaffected. Negi et. al. examined 3 Arabidopsis genes closely related to *SLAC1* and found that none are expressed in guard cells; however, 2 of the related genes complemented the *slac1-2* mutant phenotype when expressed under the *SLAC1* guard cell-specific promoter. These combined data strongly support an important role for *SLAC1* in the function of S-type anion channels and provide genetic evidence for the model that these anion channels are key components in regulating stomatal closure in response to multiple physiological stimuli.

References:

1. Negi J, Matsuda O, Nagasawa T, Oba Y, Takahashi H, Kawai-Yamada M, Uchimiya H, Hashimoto M, and Iba K, CO_2 regulator SLAC1 and its homologues are essential for anion homeostasis in plant cells. Nature, Mar 27 2008; 452: 483-486.

2. Vahisalu T, Kollist H, Wang, YF, Nishimura N, Chan WY, Valerio G,

Lamminmaki A, Brosche M, Moldau H, Desikan R, Schroeder JI, and Kangasjarvi J, SLAC1 is required for plant guard cell S-type anion channel function in stomatal signaling. Nature, Mar 27 2008; 452: 487-491.

A Wealth of Sequence Data Reveals Diversity in Arabidopsis Accessions

By: Joanna Friesner, MASC Coordinator

Arabidopsis thaliana was selected as the first plant for genome sequencing in part due to its relatively compact genome. Since the release of the reference *Col-0* sequence in 2000 it has become increasingly clear that significant genotypic variation exists in even this 'small-genome' plant. The extent of variation hasn't fully been explored due to lack of full-coverage sequences derived from multiple diverse accessions. A recent publication by Clark et. al. provides an in-depth look at Arabidopsis sequence variation and includes some surprising findings. High-density array resequencing was performed on 20 diverse, natural *A. thaliana* strains including the reference *Col-0*. The hybridization technique allowed for identification of 'polymorphic region predictions' (PRPs) which include deletions and longer sequences that are dissimilar to *Col-0*, and for more than 1 million non-redundant single-nucleotide polymorphisms (SNPs). Surprisingly, more than 4% of the reference genome is included in PRPs and roughly 110,000 SNPs cause amino acid changes, demonstrating flexibility in protein sequence. Perhaps more striking was the finding that some 2,000 SNPs are predicted to cause major changes in gene structure including the introduction of premature stop codons, removal of annotated stop codons, and alteration of initiation residues and splice donor and acceptor sites. Called 'major-effect changes', these 'large-effect SNPs' and PRPs affected 2,495, or 9.4%, of protein-coding genes.

Most strikingly affected were genes encoding the NB-LRR class of pathogen-resistance proteins, of which nearly 60% had at least one major-effect change. The authors suggest, based on previous studies by others, that balancing selection to maintain relatively ancient, highly diverged alleles may underlie the high level of polymorphism in this and other gene families involved in pathogen resistance. In contrast, the study also identified several regions of low genotypic diversity indicating potential selective sweeps. One of the most impressive sweeps found in any species is a large 500 kilobase region on Chromosome 1, for which 18 of 20 strains were nearly identical. While the SNP data set generated in this study provides much-needed information on genetic variation in Arabidopsis and has applications for linkage disequilibrium mapping and for comparative genomic studies, it underscores that it is risky to think about "the" genome of a species, and that much deeper sequencing efforts are required to appreciate and understand the full complement of Arabidopsis genes.

Reference: Clark RM, Schweikert G, Toomajian C, Ossowski S, Zeller G, Shinn P, Warthmann N, Hu TT, Fu G, Hinds DA, Chen H, Frazer KA, Huson DH, Scholkopf B, Nordborg M, Ratsch G, Ecker JR, and Weigel D, Common sequence polymorphisms shaping genetic diversity in Arabidopsis thaliana. Science, Jul 20 2007; 317 (5836): 338-342.

ZTL is a Blue-light Photoreceptor That Links to the Circadian Clock

By: Joanna Friesner, MASC Coordinator

Circadian rhythms are controlled by cycling circadian clock elements whose coordination relies on inter-dependent transcriptional and translational feedback loops. Zeitlupe (ZTL), an F-box containing protein component of an SCF-type ubiquitin ligase, is rhythmically expressed and targets the TOC1 protein for degradation as part of normal oscillation. ZTL is one of only a few F-box proteins to contain a LOV (Light Oxygen and Voltage) domain which implicates it in blue-light signaling and potentially links ZTL with the light inputs predicted to be important for circadian processes. Interestingly, *ZTL* mRNA is constitutively expressed but ZTL protein levels are low at dawn and increase during the day to peak around dusk. The mechanism of ZTL's post-translational regulation and interaction with light were unknown until a recent publication by Kim et al. The authors performed *in vitro* and *in planta* interaction assays to demonstrate that ZTL protein is stabilized through direct interaction with oscillating GIGANTEA (GI), resulting in the observed oscillating ZTL pattern. Mutant analysis revealed that a specific mutation in a LOV domain residue implicated in flavin biochemistry eliminated the blue light-enhanced ZTL:GI interactions. This blue light-enhanced cooperative stabilization allows ZTL protein levels to accumulate, effectively targeting TOC1 protein for periodic degradation, and maintaining the TOC1 cycling that is necessary for normal circadian period. These new results link GI, part of the flowering and circadian clock pathways with a previously undefined function, with ZTL, a component of the ubiquitin pathway. They also reveal a mechanism for blue light as an input to the circadian clock, and importantly, establish ZTL as a photoreceptor.

Reference: Kim W-Y, Fujiwara S, Suh S-S, Kim J, Kim Y, Han L, David K, Putterill J, Nam HG, and Somers DE, ZEITLUPE is a circadian photoreceptor stabilized by GIGANTEA in blue light. Nature, Sep 20 2007; 449 (7160): 356-360.

Community Arabidopsis Projects and Resources

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

By: Eva Huala, TAIR Director

Highlights for TAIR in the past year include addition of several new tools and datasets and the start of a unique collaboration with the journal Plant Physiology to collect data at the time of publication. In addition to the highlights below, TAIR has curated 648 research articles and many community data submissions in the past year (3/1/07-2/29/08), adding 3404 Gene Ontology and 2066 Plant Ontology annotations from the literature to 2007 genes and also updating gene summaries, aliases, phenotypes, alleles and germplasm information. Data submissions from 68 2010 projects have been incorporated into TAIR or are currently in progress.

Metabolic pathway data: Two AraCyc metabolic pathway

Table 2

A) How necessary is TAIR and the data it contains for your research or teaching?						
ICAR	**Web**	**AW**	**NAW**	**C**	**All**	
83%	81%	85%	56%	79%	82%	1 (essential)
15%	12%	11%	25%	12%	12%	2
0%	6%	4%	11%	6%	4%	3
1%	1%	0%	6%	0%	1%	4
1%	0%	0%	3%	3%	1%	5 (not needed at all for my work)

B) How satisfied are you with the following aspects of TAIR? (percent who chose very satisfied or satisfied)						
ICAR	**Web**	**AW**	**NAW**	**C**	**All**	
88%	86%	86%	89%	91%	87%	Availability of website (is it always accessible)?
78%	83%	82%	75%	79%	83%	Correctness of data?
78%	75%	76%	72%	76%	77%	Completeness of data?
77%	75%	75%	78%	68%	76%	Performance (speed)?
74%	65%	68%	64%	65%	67%	Organization of web pages (easy to find information)?

C) How often do you use TAIR on average?						
ICAR	**Web**	**AW**	**NAW**	**C**	**All**	
35%	47%	48%	14%	59%	44%	Most workdays
44%	41%	43%	44%	32%	42%	Once a week or more
15%	11%	7%	33%	6%	12%	Once a month or more
5%	1%	1%	6%	3%	2%	Once a year or more
0%	0%	0%	3%	0%	0%	Less than once a year

D) Which of the following types of data would you most like to have available in TAIR?						
ICAR	**Web**	**AW**	**NAW**	**C**	**All**	
57%	57%	59%	54%	56%	57%	Promoters/cis elements, regulation of transcription
45%	56%	50%	77%	56%	53%	Orthologs from other plants and model organisms
46%	39%	46%	17%	21%	40%	Complete ecotype sequences
40%	37%	38%	31%	38%	38%	Regulatory interactions
40%	35%	38%	34%	24%	37%	Genetic interactions (e.g. epistatic, additive)
32%	36%	38%	20%	35%	35%	Protein modification data
43%	33%	37%	34%	21%	35%	Small RNAs
23%	26%	19%	60%	35%	25%	Other Brassicaceae genes/genomes
25%	24%	25%	20%	32%	24%	A. lyrata and Capsella rubella genes/genomes
30%	21%	24%	17%	21%	23%	DNA methylation patterns
14%	15%	14%	17%	24%	15%	QTL data
3%	4%	4%	3%	0%	4%	Other (please specify)

E) Which of the following tools would you most like to have available in TAIR?						
ICAR	**Web**	**AW**	**NAW**	**C**	**All**	
63%	55%	61%	41%	41%	57%	Protein interaction viewer
57%	55%	59%	35%	47%	56%	Protein domain and modification site viewer
61%	51%	57%	53%	31%	54%	Protein alignment viewer
33%	47%	42%	44%	63%	43%	Customizable bulk data retrieval and download tool
36%	25%	30%	24%	16%	27%	SNP viewer
20%	20%	17%	53%	19%	20%	Synteny viewer
18%	13%	15%	12%	16%	14%	QTL viewer
1%	3%	3%	3%	3%	3%	Other (please specify)

Table 2. Responses to five TAIR survey questions with the following respondent categories shown: ICAR, random sample of 300 abstract submitters to the 2007 ICAR conference (95 replies); Web, self selected respondents (292 replies); AW, wet lab researchers working primarily or solely on Arabidopsis (283 replies); NAW, wet lab researchers working primarily or solely on other species (36 replies); C, computational or bioinformatics researchers (34 replies); All, all respondents (387).

releases were produced by the AraCyc team in the past year (Aracyc 4.0 in July 07 and Aracyc 4.1 in November 07). The Aracyc 4.1 release contains a total of 283 metabolic pathways with 1901 genes assigned to the pathways, and 90% of these pathways have been experimentally confirmed. A new project affiliated to TAIR, the Plant Metabolic Network, will launch a website in April 2008 with the goal of generating a general metabolic pathway database for all plants as well as several new species-specific databases.

SNP data: 249,052 high-quality SNPs discovered with Perlegen resequencing arrays (Clark et al., 2007) were added to the TAIR polymorphism search and genome browsers in July 2007. More than 1 million SNPs discovered at various false discovery rates were deposited in the TAIR FTP site (Sequences directory), along with 13,470 predictions of highly polymorphic or deleted regions.

New tools: TAIR added GBrowse to its suite of genome browsers in August 2007 and has added several new sets of tracks since then. The new tracks include VISTA sequence similarity plots for several plants (including poplar, Medicago, rice, Selaginella and Physcomitrella) provided by JGI, native transposable elements annotated by Hadi Quesneville's group, EuGENE and Gnomon annotations, and Brassica sequences, MPSS expression data and methylation plots provided by AtiDB. We have also collaborated with Wormbase staff to set up an Arabidopsis version of their full-text mining tool, Textpresso, which provides powerful search and display capabilities for the TAIR publication collection (http://textpresso.org/arabidopsis/).

TAIR/Plant Physiology Collaboration: A unique partnership has been formed between the journal Plant Physiology and TAIR to ensure that Arabidopsis gene function data published in the Journal are reliably captured in TAIR's database. This collaboration provides a mechanism for authors to submit Arabidopsis gene function information to TAIR as part of the publication process.

TAIR8 genome release: The latest TAIR genome release which came out in April 2008 contains 1291 novel genes and updates to 7380 gene structures. In addition, transposon-related genes now appear as a separate gene type and are associated to specific transposable element families. TE families are now browsable in TAIR and lists of specific instances along with their coordinates are provided along with general family information.

TAIR Survey Report

TAIR recently conducted a survey of Arabidopsis researchers aimed at measuring the level of satisfaction with various aspects of TAIR's performance and learning what new data and tools the community is interested in having TAIR provide. The survey was administered in two ways: by email to a random sample of 300 abstract submitters to the 18th ICAR, and by posting a link to the survey within the header for all TAIR pages. The random sample was chosen as a representative set of Arabidopsis researchers including both frequent and infrequent visitors to the TAIR website, whereas the self-selected sample of respondents accessing the survey from the TAIR pages is biased toward frequent visitors. Questions on the respondent's characteristics, including type of institution, research focus (wet lab vs. computational biology, research organisms) and geographic location allowed us to analyze subsets of the respondents to investigate whether responses varied according to these characteristics. Other questions pertained to satisfaction with various aspects of TAIR, relative importance of data types already in TAIR and level of interest in new data and tools not currently available in TAIR.

The 387 respondents are mostly professors, postdoctoral fellows and graduate students from academic institutions and the majority (87%) use Arabidopsis as their primary research organism. However, only 34% of respondents focus their research exclusively on Arabidopsis, 62% focus on other species including crops and other model organisms in addition to Arabidopsis, and 3% work exclusively on other species. About 42% of survey respondents are located in the Americas (35% in the United States), with the remainder primarily from Europe (38.5%) and Asia (14.5%). In contrast, our usage statistics over the past year show 34% of TAIR visits originating from the Americas (including 28% from the United States), 31% from Europe and 32% from Asia (1,362,030 total visits over the last 12 months). Nine percent (34) respondents were primarily computational biologists and 82 percent (319) were primarily wet lab researchers.

The survey showed that the great majority overall (82%) consider TAIR to be essential for their research or teaching (Table 2A). Satisfaction with TAIR is also high (Table 2B) and 86% of respondents use TAIR once a week or more (Table 2C). Most respondents find TAIR's gene structures to be the most important type of data within TAIR, followed by seed and DNA stock information and experimentally verified gene function data (not shown). Of data types not currently in TAIR, most respondents consider data on promoters and transcription regulation as the highest priority for future integration into TAIR, followed by orthologous genes from other plants and model organisms and complete ecotype sequences (Table 2D). The tools that respondents would most like to see within TAIR in the future included a protein interaction viewer, a protein domain and modification site viewer and a protein alignment viewer (Table 2E).

The survey results were broken down in several ways to search for possible differences between subgroups. In one analysis, 95 responses from the random sample of 300 abstract submitters to the 18th ICAR conference (Table 2A-E, ICAR column) were compared with those from the 293 self-selected respondents who accessed the survey from the TAIR pages (Web column). While the two response sets differed somewhat in their geographic distribution and type of institution, no significant differences were found in their satisfaction with TAIR, importance of TAIR to their work or frequency of TAIR use, and the minor differences found in their rankings of data types or tools appear to be due to a higher proportion of computational biologists in the web sample (11%) than in the ICAR sample (3%). The most informative analysis, with clear differences among the subgroups, was a comparison of Arabidopsis wet lab researchers, non-Arabidopsis wet lab researchers and computational biology/bioinformatics researchers (Table 2A-E, columns AW, NAW and

C). A full analysis of the survey results will be available from the TAIR homepage (http://arabidopsis.org).

NASC, The European Arabidopsis Stock Centre (http://arabidopsis.info)

By: Sean May, NASC Director

NASC distributes, collects and preserves seed, DNA and data resources for *Arabidopsis* and related species (but also embraces a limited set of resources for transgenic tomato and other *Solanaceae*). We also specialize in the collection, generation and distribution of transcriptomics data (especially Affymetrix). Our primary array repository (NASCarrays) cross-references our mature integrated genome browser AtEnsEMBL (http://atensembl.arabidopsis.info/). which incorporates both TAIR and MIPS genome annotations and further links through to all of our other databases and resources (as well as external data such as Brassica gene information). We have an ongoing mutual interchange of *Arabidopsis* and related species stocks with our sister center in the United States (ABRC). This greatly facilitates user-led distribution to the research community worldwide.

NASCArray Statistics:

We currently hold 3,727 publicly available chip hybridizations (May 08). Of these, most have been directly processed at NASC for users from 4 continents and external groups have donated 586 chip datasets. This is increasing such that in 2007-8 the ratio is 45% donated, 55% processed at NASC where the USA, Japan, Germany, UK and Canada account for 96% of these donations. We also have approximately 1,000 in-house hybridizations at various stages of (short) confidentiality periods, most to be released within 2008.

Seed Statistics:

In 2007-8 most of the seeds received as donations at NASC were from Germany (55,446) and the USA (17,209), with the majority of the remainder coming from the Netherlands (423) and Hong Kong (199). The largest users [~Kp/a]* of NASC in 2007/8 were Germany [9], Netherlands [2], Belgium [1], UK [8], France [3], Spain [2], Switzerland [2], Sweden [1], China [1] and Japan [1]. Please remember that non-European users can also use ABRC so their statistics are an underestimate in this section. Additionally, American users are obliged to order stocks from ABRC if the stocks are contained there. Romania, Hong Kong, Germany and the USA all have the distinction of donating more seed than they ordered from NASC in 2007/8.

* *thousands of stocks per year*

Please note that most of our data is openly available through SOAP and BioMOBY web services and may be actively mined by third party tools such as Taverna (http://taverna.sourceforge.net/). Please visit our website (http://arabidopsis.info/) for more information.

The Arabidopsis Biological Resource Center (ABRC, 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. In 2008, ABRC continues to focus on serving various aspects of post-genomics research. 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, 20,588 of these lines have been received. The stocks being utilized for this project include the J. Ecker (SALK) population plus lines from Syngenta (SAIL), B. Weisshaar (GABI-Kat) and P. Krysan/R. Amasino/M. Sussman (Wisconsin Ds-Lox). Sets of the confirmed SALK T-DNA lines are being prepared at ABRC for forward screening for distribution to labs which have expressed interest in the resource. The first 8,889 lines of this collection were shipped to users in Spring, 2008. In addition, pools of confirmed SALK lines will be available, and it should be possible to order the first sets of these pools at the end of 2008. Receipt and distribution of Entry and Expression ORFeome clones has been a priority. Entry clones were received from the J. Ecker, (SSP and SALK) and the C. Town projects, as well as several individuals in the research community. The extensive expression ORF collections from S. P. Dinesh Kumar and S. Clouse are being received, with over 5,000 of these currently in-house. We are pleased to report that the majority of the SSP ORFs are now available in a Gateway™ entry vector in addition to the pUNI form in which these were originally received.

Current ABRC seed stock holdings include insertion lines covering 25,000 genes, the 10,000+ lines of the Arabidopsis TILLING service, 1,346 distinct natural accessions (now being genetically fingerprinted so that this entire collection will be marker-validated), 20 recombinant inbred populations, related species and RNAi lines including the AGRIKOLA lines (www.agrikola.org). In regards to DNA resources, ABRC presently houses full-length ORF and cDNA clones for ca. 13,500 genes, BACs covering the entire genome, BACS of nine related species, the AGRIKOLA RNAi entry clones and various sets of expression clones. The present collection of vector constructs represents a rich and diverse set of resources for investigation of gene expression. It should be emphasized that donations of published mutants and clones, including purified insertion mutants and expression clones, are very welcome. The distribution of seed and DNA stocks exceeded 90,000 in 2007, with T-DNA lines, especially confirmed lines, leading the seed orders and ORF entry clones and vector constructs anchoring DNA distribution.

ERA-NET Plant Genomics (ERA-PG, www.erapg.org)

By: Christine Bunthof, ERA-PG Executive Coordinator

ERA-PG is a networking and coordination activity supported by the ERA-NET scheme under the EU's 6th Framework Programme for strengthening the European Research Area. The rationale behind ERA-NET is that networking national funding organizations and coordination between national programs in Europe will facilitate a stepping up from national to multilateral coordination, thereby reducing redundancy and maximizing the returns on investment. Close collaboration and synergy of research efforts in plant sciences and joint investments in large-scale technologies will create critical mass, contribute to competitiveness and help to drive policy development in favor of plant sciences at national and European levels. Building on a strong foundation of existing collaborations, ERA-PG was among the first of ERA-NET projects to start in 2004. The Coordinator is NGI/NWO from The Netherlands and the founding members include ministries and funding agencies from Austria, Belgium, Denmark, Finland, France, Germany, Italy, Norway, Spain and UK. From the outset ERA-PG has been committed to expanding its network to new members engaged in launching national plant genomics initiatives. Portugal, Switzerland, Israel and Sweden became contractual members two years after the start. Bulgaria joined as affiliate in 2006 followed by Canada in 2007.

ERA-PG has undertaken a large information gathering exercise leading to a shared information resource on research activities and economic impact of plant genomics that has been valuable beyond the network itself. Researchers and science policy makers were brought together to build common ground for joint strategic activities at scientific and administrative levels, and to perform a study leading to development of common framework mechanisms and best practices. In 2006 ERA-PG launched its first joint call for research '*Structuring Plant Genomic Research in Europe*', which received more than 100 applications. 29 Projects were granted with a total budget of over 35 million Euros, making this one of the largest coordinated multinational research programs in the ERA-NET scheme. As a result of the success of this process, the majority of these funding organizations opted to commit to a further joint call, and they have also been joined by others. In January 2008 the second joint call *'Strengthening the European Research Area in Plant Genomics – integrating new technologies in plant science'* was launched, with a joint investment of about 15 million Euros, addressing researchers in Austria, Belgium, Canada, Finland, Germany, Israel, Netherlands, Portugal and United Kingdom. In the ERA-PG calls the proposals are evaluated by international peer review after which an international expert panel advices the funding organizations about the selection and funding. The application, evaluation and selection are centrally managed following commonly agreed procedures.

ERA-PG organizes program summits (first in 2007 in Tenerife, second in 2009) and monitors the granted projects. Also, ERA-PG organizes and participates in science policy meetings, builds contacts with new countries and with the European Technology Platform Plants for the Future and EPSO. The partners in ERA-PG aim to capitalize on the trans-national coordination of research and management established within the ERA-NET scheme and hope to receive funding for a follow-up under EU Framework Programme 7. The overarching goal of the follow-up project will be to form sustainable cooperation and anchor joint programming (smaller or larger initiatives) between national programs in Europe and beyond.

Measuring Gene Function Knowledge

During the 2003 MASC annual meeting members agreed that it would be useful to establish a better way to track gene function knowledge and quantify the number of Arabidopsis genes with known function. Since the 2004 MASC annual report this was illustrated by thermometers to provide a visual illustration of the progress in Arabidopsis functional genomics efforts. This year the thermometers are measured against the TAIR8 genome release and include the number of genes (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 2008.

One concern is that the thermometers do not accurately reflect all the data and resources that exist as, for example, there are individual labs, and also private companies, with data and resources that have not been shared publicly. It was also noted that there may be data and resources that are publicly-available but are not easily accessible and thus left out of the tracking effort. Additionally, there are a significant number of uncurated Arabidopsis publications that potentially contain gene function knowledge that are currently not tracked. Therefore, it was suggested at the 2007 MASC annual meeting that perhaps the thermometers should be discontinued until they can reflect all existing data and resources. MASC members discussed the suggestion and weighed the negatives and positives regarding a tracking mechanism that encompasses major resource projects and data repositories yet clearly has some limitations. The majority opinion from the MASC was that overall, the thermometers are a useful means to track progress even if they are an underestimate of the existing resources. Furthermore, it was felt that (1) data and resources not freely shared should not be tracked in the thermometers as their emphasis is on 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 should be strongly encouraged to submit them to major public repositories so they can be tracked in the future.

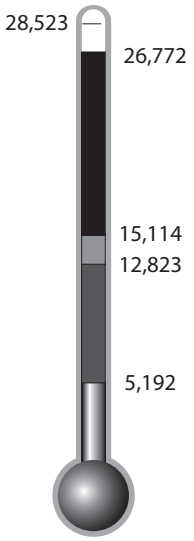
Based on this discussion, and with the caveat that not all existing data and resources are represented, we have included thermometers for 2008 with the sources of data and resources listed. Currently, the thermometers do not reflect gene function knowledge based on computational evidence; however, the field of bioinformatics has recently been able to make significant progress, especially with the increase in genome sequences available. Computational predictions are increasingly more powerful, statistically relevant, and facilitate comparative analysis across genomes. In the future, the increase in reliable

computational predictions, as well as curation efforts and methods to extract gene function data from the literature, should allow for a more in-depth cataloging of the vast knowledge accumulated by the Arabidopsis community. Furthermore, the availability of high-quality genetic resources will facilitate future studies and contribute to our expanding pool of knowledge.

As shown in the thermometers below, steady progress is being made on resource development and acquiring gene function knowledge. Great strides have been made in developing resources to knockout, or knockdown, gene expression including a doubling of the number of unique genes with at least one confirmed homozygous insertion from 6,388 to 12,823 and the isolation of two or more homozygous insertion mutants for 18% of genes just since last year. In addition, the number of RNAi plasmid constructs for gene silencing increased from approximately 26,000 to approximately 36,000. The resources will enable gene function studies for the majority of the genome.

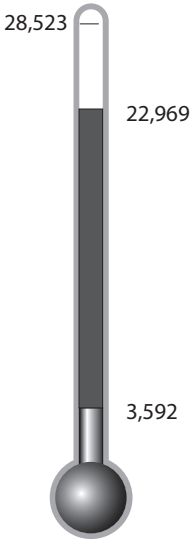
Tracking Thermometers

Insertion Mutants



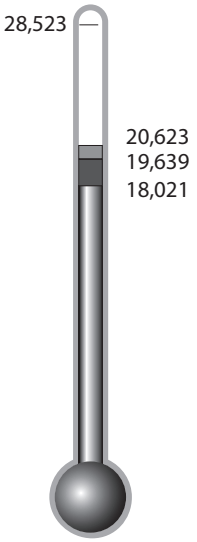
- Loci with 2 or more homozygous confirmed insertion sites
- + Loci with 1 homozygous confirmed insertion site
- + Loci with confirmed insertion sites, unknown zygosity
- + Loci with unconfirmed insertion sites, unknown zygosity

RNAi



- Loci with RNAi constructs transformed into plants
- + Loci with constructs made, not transformed into plants

Full-length cDNA clones



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

Tracking Thermometers

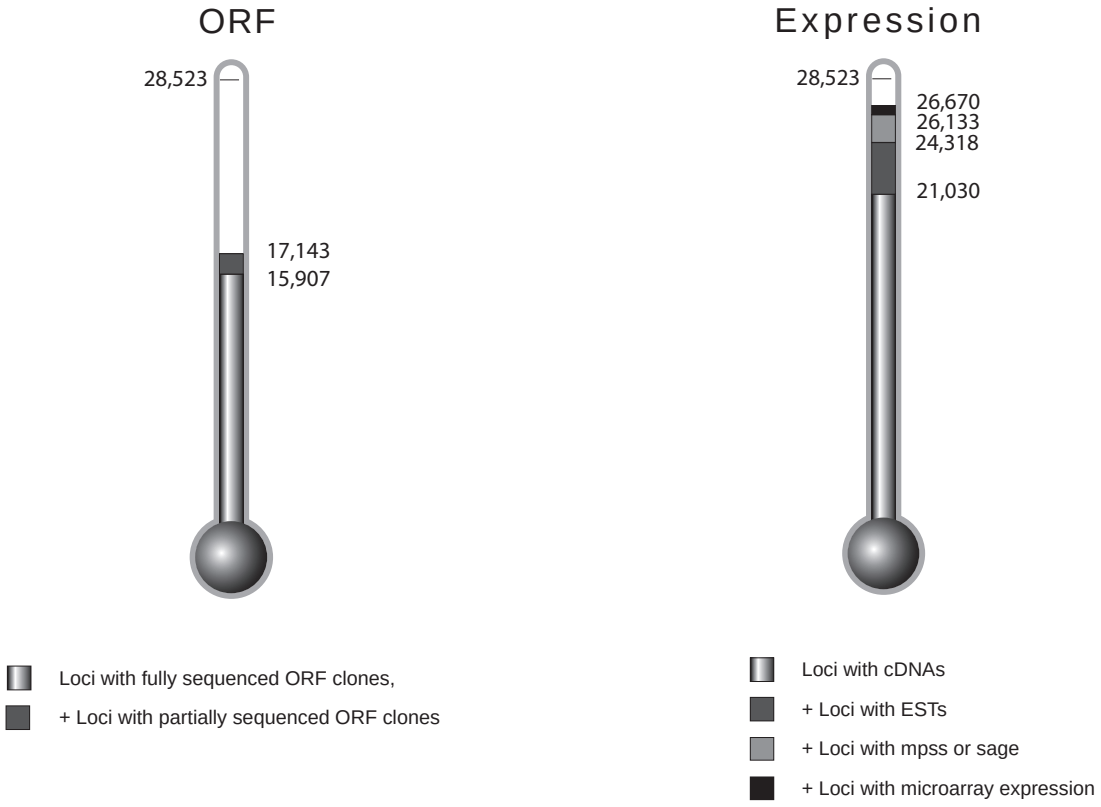


Figure 2: Measuring Arabidopsis Genomics Resources. All data are as of May, 2008. For consistency, all resources are measured against the TAIR8 genome release (including noncoding RNAs and organelle-encoded genes but excluding transposon genes and pseudogenes, a total of 28,523 genes). Five categories are included: **(A) Loci with insertion mutants** - 5,192 genes with two or more homozygous confirmed insertion sites, an additional 7,631 genes with one homozygous confirmed insertion site, an additional 2,291 with confirmed insertion sites and homozygous status unknown, and an additional 11,658 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 19,377 genes with RNAi knockdown constructs made but not transformed into plant lines, (data from Ian Small (AGRIKOLA), Randy Scholl (ABRC), Graeme Gill/Sean May (NASC), Martine Vanhoucke/Pierre Hilson (PSB/LMBP), amiRNA project website (CSHL) and chromDB project website); **(C) Loci with full length cDNA clones** - 18,021 genes with full length cDNAs fully sequenced and known to be available for ordering, an additional 1,618 genes with cDNAs not fully sequenced but known to be available and an additional 984 genes with fully sequenced cDNAs but stock availability unknown, (data from Huaming Chen/Joe Ecker, SIGnAL); **(D) Loci with ORF clones** - 15,907 genes with fully-sequenced ORF clones and an additional 1,236 with partially sequenced ORF clones (data from Huaming Chen/Joe Ecker, SIGnAL); **(E) Expression detected** – 21,030 loci with cDNAs (data from Huaming Chen/Joe Ecker, SIGnAL), an additional 3,288 loci with ESTs (data from Eva Huala/TAIR), an additional 1,815 loci with expression detected by MPSS or SAGE (MPSS data from Blake Myers, SAGE data from 2006 thermometer (provided by Hank Wu, TIGR, no update available), and an additional 537 loci with expression detected only by microarray analysis (data provided by GEO and Eva Huala/TAIR)

Note: Detailed information on ORF, cDNA, and RNAi clone projects can be found in the ORFeomics and Phenomics Subcommittee Reports (pages 26-31).

Broader Impacts of Arabidopsis Research

Impacts on Industry

A primary difference between 'basic' (or 'fundamental') and 'applied' research is that the former tends to be curiosity-driven while the latter is typically more goal-oriented. For example, an Arabidopsis researcher might be interested in the basic mechanism of opening and closing of stomatal pores located in the leaf epidermis during gas exchange. A research project might include phenotypic screens for plants with altered gas exchange dynamics which could require the development of novel experimental techniques to measure the rate of pore opening and closing. In comparison, an applied plant biologist might evaluate a specific problem, such as the need for drought-resistant corn that is productive in dry climates, and devise a breeding and experimental regimen that targets those phenotypes directly. This process may involve recurrent selection of inbred or hybrid plants and the performance of phenotypic analyses such as growth rate and seed yield for each iterative step in the process. While the applied approach to uncovering drought tolerance may be more direct, it may not always be fastest for achieving a desired result. For example, plant mutants isolated in the Arabidopsis screen may experience increased water loss through stomata that fail to close in response to stress. The genes defective in the mutants can quickly be identified using available genetic and DNA sequence resources. In addition, the availability of large sequence-indexed insertion collections and transcriptomic resources allow gene function to be confirmed. Importantly, because basic research projects often cast a fairly broad net, genes involved in other important processes may also be uncovered leading to further studies and additional unforeseen insights. A comparative genomic analysis between genes identified in Arabidopsis with crop sequences can allow the identification of candidate genes involved in drought tolerance in corn thereby directly advancing the applied research project. Ultimately, 'applied' research builds on previous basic research and most, if not all, breeding projects depend on sequence-based markers to follow known traits.

These complementary approaches are important to solving the problems that face society and one informs the other. It is critical that we do not lose sight of the vital contributions of information obtained through fundamental research to applied research. It is the basic knowledge of how plants work that allow applied research to thrive; for example, Arabidopsis development studies profoundly contribute to the body of knowledge for all plant development and insights from Arabidopsis, including vital sequence information, also inform non-plant systems. In some cases the transfer of Arabidopsis knowledge for applied use is planned, in others, it is fortuitous. It is clear that basic research provides the foundation for applied studies and that dedicated support for basic research by government funding agencies has been, and will continue to be, crucial to successfully developing Arabidopsis as the reference for plant biology, and for leveraging the knowledge gained for applied studies in other plants. Without such large-scale funding for the original Genome Project (1990-2000) or for the current Functional Genomics Project (2001-2010), the remarkable breakthroughs that are being achieved at an ever-accelerating rate would not be possible.

The filing of patents is one measure of potential commercial activity and an indicator of efforts to transfer basic knowledge into products and approaches. Many patents worldwide acknowledge research on Arabidopsis but a widely-held myth is that few of these discoveries are ever turned into useful products. The number of Arabidopsis patents continues to increase: in the US, there were 900 utility patents referencing Arabidopsis in 2007 compared to 103 in 1997 and 0 in 1987 (Figure 3). The time from discovery to application takes years and the pipeline is full of Arabidopsis-fueled discoveries heading for the marketplace. We have chosen just a few examples of discoveries that demonstrate how basic research in Arabidopsis can be translated into real-world applications. In each case the knowledge gained through basic research in Arabidopsis was critical to the success of the applied project, and commercial potential was realized after initiation of basic studies for most, if not all, projects.

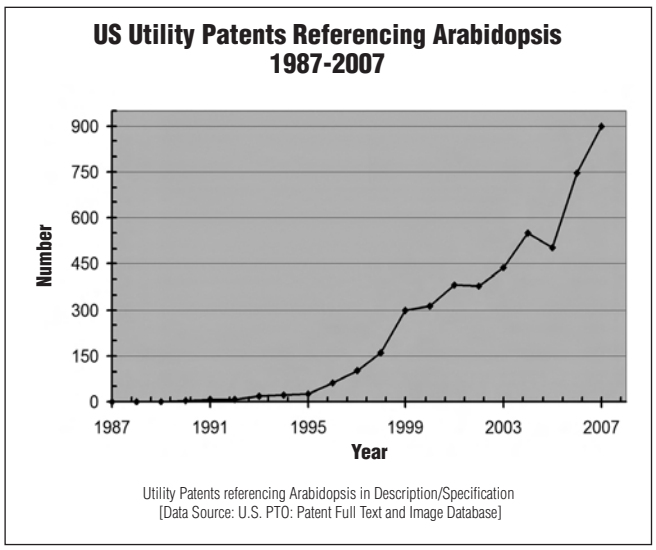


Figure 3

Translational Research Examples Using Arabidopsis

Mining the Arabidopsis Genome for Gold: Drought-tolerant Corn

By: Joanna Friesner, MASC Coordinator

Plant breeders have long been interested in improving the ability of plants to tolerate environmental stresses such as drought, freezing, high salinity and pathogens. Unmitigated stress to economically important plants can lead to reduced crop yield or even catastrophic loss, serious consequences which may translate into higher costs to consumers and food shortages. Furthermore, the increasing threat of global climate change dramatically increases the need to develop plants grown for food, fuel and fiber that are able to withstand fluctuating temperatures and climates. Plant's tolerance of drought stress, which can severely affect growth and yield, is an area that researchers and breeders are eager to improve.

In the last decade Mendel Biotechnology (1) has undertaken a systematic analysis of Arabidopsis transcription factors, leveraging the international Arabidopsis Genome Sequencing Project that concluded in 2000 with the release of the reference genome. Large-scale over-expression studies were performed to screen for candidate transcription factors involved in controlling a variety of traits. Drought tolerance assays revealed that AtNF-YB1 over-expressing transgenic plants had higher rates of photosynthesis and higher water potential under drought conditions when compared to controls (2). Expression of AtNF-YB1, a member of an expanded transcription factor gene family in Arabidopsis, increased dramatically in response to severe drought, returning to basal levels after rewatering. Microarray and expression data suggested that AtNF-YB1 does not act through either the ABA or CBF drought tolerance pathways and may represent a new pathway.

Based on these results in Arabidopsis, a bioinformatic and phylogenetic approach was taken to identify a putative *AtNF-YB1* homolog in maize, called *ZmNF-YB2*. Transgenic maize plants with constitutive *ZmNF-YB2* expression were found to recover more quickly, present less wilting, and appear significantly greener when compared to controls following drought stress. In two years of field studies, *ZmNF-YB2* transgenic plants had higher amounts of chlorophyll and higher rates of photosynthesis and stomatal conductance. Furthermore, transgenic plants showed 10-50% yield enhancement in response to drought stress with the highest enhancement achieved in the more severe drought year. Increasing drought tolerance in plants spanning a wide range of climates may be facilitated by this technology. Mendel is pursuing product development of this technology in partnership with Monsanto (3)

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Carrots That Pack a Calcium Punch

By: Kendal Hirschi
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Nutrition recommendations worldwide emphasize ingestion of plant-based diets rather than diets that rely primarily on animal products. However, this could limit the intake of essential nutrients such as calcium. Biofortification is the process where plants are developed with increased bioavailable concentrations of essential nutrients. Plant studies frequently describe changes in plant metabolism to improve nutritional content; however, this is often where the process of assessing improved nutrition ends. Ideally, these modified plants need to be used in controlled animal and human feeding studies to assess nutritional impacts. Such studies are critical if claims are to be made regarding health benefits and may be an important component in public acceptance of biofortified foods.

The Arabidopsis Ca^{2+}/H^{+} antiporters located on the vacuolar membrane are important for calcium sequestration and led to a new tool in biofortification efforts. An engineered version of the Arabidopsi*s CAX1* Ca^{2+}/H^{+} antiporter was used to increase calcium levels of edible plants, such as potatoes and carrots (1). Transgenic carrots expressing high levels of deregulated Arabidopsis *CAX1* Ca^{2+}/H^{+} antiporter accumulate almost two-fold more calcium in the edible part compared to control plants, without perturbing growth, development or fertility, under controlled lab conditions. Feeding trials using these carrots labeled with stable calcium isotopes demonstrated that calcium absorption was significantly increased in both mice and humans with diets containing the modified carrots (2). These results demonstrate a novel way of fortifying vegetables with bioavailable calcium.

Carrots are among the most popular vegetables in the United States and contain high levels of beta carotene (the precursor to Vitamin A) and other vitamins and minerals; however, like many vegetables, traditional carrots are poor sources of dietary calcium. Using the technology we have developed in Arabidopsis we can now engineer carrots and other vegetables to contain increased calcium levels to boost calcium uptake and reduce the incidence of calcium deficiencies. Commercialization of this technology currently is being considered.

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Braving the Drought by Taming PARP

By: Sandy Vanderauwera[1,2], Marc De Block[3], Michael Metzlaff[3] and Frank Van Breusegem[1,2]

[1]Department of Plant Systems Biology, Flanders Institute for Biotechnology (VIB), Ghent, Belgium

[2]Department of Molecular Genetics, Ghent University, Ghent, Belgium

[3]Bayer BioScience N.V., Ghent, Belgium

Abiotic stresses, such as drought, salinity, and heat are the major causes of yield loss in cultivated crops. Yield losses by abiotic stress are the result of a large number of mild stresses that occur throughout the growing season as well as from periodically severe stresses. The gap between the attainable and the actual yields is estimated to be 40-50% (www.isaaa.org). Therefore, breeding of crop varieties with improved responses to environmental changes is one of the important objectives in modern agriculture. Crop varieties with enhanced tolerance to abiotic stress will broaden the window of optimal growth conditions for cultivated crops, thereby increasing average yield, yield stability and productive acreage. Such traits will provide substantial benefits to farmers and processors, may reduce costs in seed production and may lead to the implementation of new strategies in plant breeding.

In poly(ADP-ribose)polymerase (PARP)-deficient transgenic Arabidopsis plants, reduced NAD^+ depletion and ATP consumption were reported to increase tolerance to a broad range of abiotic stresses, such as high light, drought and heat (1). Poly(ADP-ribosyl)ation (PAR) is a unique posttranslational protein modification mediated by the PARP enzyme that attaches long-branched poly(ADP)-ribose polymers to nuclear target proteins mainly during the cellular response to genotoxic stress. PARP uses NAD^+ as a substrate and is hence an energy-consuming process. In PARP-deficient plants NAD^+ consumption is reduced which causes higher energy-use efficiency during stress conditions. In addition, reduced NAD^+ consumption was related to abscisic acid (ABA) signaling events: a genome-wide transcript analysis of stressed PARP-deficient transgenic *Arabidopsis* revealed the specific induction of a wide set of defense-related genes that better protect the plants against abiotic stresses (2). The more moderate perturbation of ABA signal transduction in these transgenic plants seemingly keeps plant stress signaling and developmental cues in pace and leads to stress tolerant plants that do not suffer from yield penalties.

In order to determine if protection against stress extended to economically valuable plants, transgenic crops containing RNAi constructs targeting PARP transcripts were developed and found to have improved performance during environmental stress conditions. Field trials over the last 3 years (2004-2006) performed by Bayer CropScience (3) showed that transgenic experimental lines of *Brassica napus* (oilseed rape) and *Zea mays* (corn) had higher yields (~ 20-40% greater) in drought stress conditions.

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Coping With the Salt of the Earth

By: Joanna Friesner, MASC Coordinator

A consequence of crop irrigation is excess build-up of salt deposited in soil which can severely affect plant growth. In addition, predicted rising sea levels from global climate instability may encroach on coastal land used to grow crops. The combined effect may lead to saline soil that limits agricultural productivity and cause subsequent increases in world food prices and possibly food shortages. Plants monitor, compartmentalize, and secrete ions, including sodium. Therefore, it may be possible to alter a native pathway to function normally in the presence of higher sodium concentration if the excess ions can be safely sequestered, excluded or secreted. The Arabidopsis NHX1 gene encodes a plant homolog of a Na+/H+ ion antiporter involved in transporting sodium ions into the vacuole using an H+ proton-electrochemical gradient. Na+/H+ exchange rates were measured in vacuoles of wild-type plants and plants constructed to overexpress the AtNHX1 gene (1). The exchange rate in the overexpressing lines was greater than wild-type plants and found to be selective for Na+ over K+. AtNHX1-overexpressing plants watered with increasing concentrations of NaCl developed normally when treated with up to 200 mM NaCl while wild-type plants were progressively growth-inhibited. These results suggested that this approach may be feasible in other plants including crops, and led to similar studies in tomato and canola, an important oilseed crop.

Overexpression of *AtNHX1* in transgenic tomatoes and canola similarly resulted in increased Na+/H+ exchange and conferred salt-tolerance when compared to control plants. Importantly, transgenic tomato plants experienced a 20-28 fold sodium increase in leaves with only a marginal effect on fruit sodium levels (2). The sodium increase was accompanied by a 25% increase in K+ in transgenic tomatoes, and fruits were slightly smaller than controls although the number of fruits per plants was equivalent to wild-type. Sodium levels in leaves of transgenic canola plants treated with 200 mM NaCl increased 70 fold while K+ levels decreased by 75% compared to wild-type. Na+ influx under high saline conditions may compete with and displace K+. However, transgenic canola developed and set seed normally, and the oil quality and quantity did not differ significantly from wild-type plants suggesting the altered K+ status isn't of major consequence to canola oil production (3).

Arcadia Biosciences, a plant biotechnology company, has improved on these studies to develop salt-tolerant plants for field use. It has licensed the technology for use in alfalfa to Cal/West Seeds and is currently working on developing improved salt-tolerant rice, cotton, tomatoes and canola (4). The company recently announced agreements with Maharashtra Hybrid Seed Company Ltd. (MAHYCO) and the African Agricultural Technology Foundation (AATF) to expand the use of salt-

tolerant crops into India and Africa, respectively. Under the agreement with AATF, salt tolerance technology is licensed to develop African rice varieties that will be available royalty-free to smallholder farmers in Africa and Arcadia will not receive monetary compensation for research and commercial rights (5). Efforts to develop plants such as these and others that can better tolerate stresses like drought may be vital for maintaining sustainable food and feed supplies during future uncertain global climate fluctuations.

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Super Cereals: Stress-tolerant Rice and Wheat

By: Kazuo Shinozaki
RIKEN Plant Science Center, Japan

Since 2007, Kazuko Yamaguchi-Shinozaki of Japan International Research Center for Agricultural Sciences (JIRCAS) and Kazuo Shinozaki of RIKEN Plant Science Center have started a collaboration with Philippine-based International Rice Research Institute (IRRI), Mexico-based Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT) and Columbia-based Centro Internacional de Agricultura Tropical (CIAT) to apply Arabidopsis stress genes to molecular breeding of transgenic rice and wheat. This project is supported by the Ministry of Agriculture Forestry and Fisheries (MAFF) of Japan, and is so-called "the DREB project" for the contribution to the international crop production for developing countries.

Kazuko Yamaguchi-Shinozaki and Kazuo Shinozaki have identified many Arabidopsis genes that are useful for the improvement of stress tolerance to drought, freezing and high salinity stress. They have used various methods including differential screening, PCR and microarray for the discovery of drought stress-inducible genes. Among them, they used major regulatory genes in transcription, like DREB1/CBF, DREB2, AREB/ABF, and so on. They also isolated a key gene in ABA biosynthesis, 9-epoxycarotenoid dioxygenase, and a key gene involved in raffinose biosynthesis. They used these Arabidopsis genes to transform rice and wheat in collaboration with IRRI, CIAT and CIMMYT. Significant drought stress tolerance of the transgenic rice and wheat have been observed under water deficit conditions. The yields of the transgenic rice and wheat have not been analyzed, yet. The project will continue until 2011 to evaluate the usefulness of these Arabidopsis stress genes for the development of drought tolerant rice and wheat cultivars in the future.

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Reports of the MASC Subcommittees

Bioinformatics

Prepared by Heiko Schoof (Chair, schoof@mpiz-koeln.mpg.de)

The main problem limiting a transforming impact of the genomics data available for Arabidopsis is still seen as being data integration and the availability of facile tools for comprehensive analysis across data sets. The last year saw the final activities of the Web Services project that was initiated early in 2006 with funding from the DFG and NSF, details of which can be found at the project web site (http://bioinfo.mpiz-koeln.mpg.de/araws). A third developers' workshop was held in May 2007 at JCVI (John Craig Venter Institute), and results were presented at the ICAR (International Conference on Arabidopsis Research) in Beijing. This project sparked the creation of dozens of web services provided from several sites, as well as client tools for the utilization of these services. These can be web pages that include data from remote sites (MAtDB gene reports http://mips.gsf.de/proj/plant/jsf/athal/index.jsp), standalone tools like the workflow design and enactment tool Taverna (http://taverna.sf.net) or web tools such as the JABBA aggregator (http://bioinfo.mpiz-koeln.mpg.de/jabba) that automatically collects all data on an AGI locus code from all web service providers registered with BioMoby (http://biomoby.org). An important outcome of the project is that the effort to implement web services is a matter of days for most data providers. The most successful format is implementation workshops where about three days are spent to teach the basics and set up a working environment, then two days can be used to implement the first web services on the data providers' own systems. For the first production services, the workshop environment with experienced web service developers at hand is very useful to overcome initial problems arising from the heterogeneity of server and development environments as well as the initial complexity of debugging web services. Detailed project reports are available on request.

An RCN proposal to continue these efforts was not funded. However, at the next ICAR in Montreal, July 2008, a workshop will again be organized, this time under the leadership of Rodrigo Gutierrez together with the MASC Systems Biology subcommittee. Topics will be: Data Generation for Systems Biology, Data Integration, Quantitative and Qualitative Modeling, and Bioinformatics tools for Systems Biology. This workshop will also involve members of the iPlant Collaborative (www.iplantcollaborative.org). This project has received major funding from the NSF to create cyberinfrastructure that will support biologist working groups on selected grand challenge questions. Proposals for these grand challenge working groups are being collected from the community and will be discussed in workshops to take place between August and December 2008. The bioinformatics subcommittee aims to participate in this process in order to ensure alignment of integration efforts between the iPlant Collaborative and Arabidopsis functional genomics.

Clone-based Functional Genomics Resources (ORFeomics)

Prepared by Joe Ecker (Chair, ecker@salk.edu)

Significant progress continues to be made towards achieving the long-term community goal of obtaining full length (FL)-cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis thaliana protein coding genes. In addition, many other clone-based resources are being produced for gene functional analysis such as those useful for protein:protein interaction mapping. A detailed description of many of these clone resources and their utility is available (Bleys, A., Karimi, M., and Hilson, P. (2008) Cloned-based functional genomics. Methods Mol. Biol. In press). This brief update focuses on highlights from this past year in the area of ORF and FL-cDNA clone production. Running totals from all the major projects are included in Table 3.

1) Yale group (Kumar/Snyder and colleagues)

This group has produced 5,090 open-end ORF clones (ORFs containing a start but no stop codon) that have been deposited with ABRC (Table 3). Information about these ORF clones (sequence validation, vector-type, Atxgxxx name etc.) can be found at this website (http://plants.gersteinlab.org/) under 'clone status' subheading. Their goal for the coming year is to add 5,000 more open-end ORF clones into the database.

2) Salk/Invitrogen (Ecker and colleagues)

During the past year this group has produced 12,107 Gateway ORF clones (ORFs containing both native start and stop codons) that have been fully validated and deposited with ABRC (Table 3). Information about these ORF clones: sequence validation, vector-type, gene (Atxgxxx) name, etc, can be found at this website: http://methylome.salk.edu/cgi-bin/clones.cgi

3) DFCI/Salk (Vidal and colleagues)

During the past year this group has produced 9,036 activation domain (AD) yeast two-hybrid Gateway clones and corresponding transformed yeast strains and 8,916 DNA binding domain yeast two-hybrid Gateway clones and corresponding transformed yeast strains. Glycerol stocks for the ~18,000 clones/strains are being prepared and will be deposited in the ABRC by September, 2008. Information about these clones: sequence validation, vector-type, gene (Atxgxxx) name,

etc, will be available at this website: http://methylome.salk.edu/cgi-bin/clones.cgi

4) ATOME (Lurin and colleagues)

Over the past several years, this group has constructed ~5,000 ORF entry clones (with and without stop codons.) These clones can be ordered from CNRGV, a French stock center in Toulouse: (http://cnrgv.toulouse.inra.fr/en). They are currently constructing a database which will be open to the public and will present their clone information. Until this is completed, it is suggested that investigators view available information on their website (http://urgv.evry.inra.fr/orfeome/) and to order clones by sending an email to infocnrgv@toulouse.inra.fr. In the coming year, as part of the of Agron-omics project, this group plans to clone 500 ORFs (ORFs with and without stop codons) which are not currently available in other public ORF collections.

5) RIKEN (Shinozaki and colleagues)

- cDNA clone project: RIKEN PSC and BRC groups have determined full-length sequences of 7,766 RAFL cDNAs in collaboration with National Institute of Genetics (PI: Yuji Kohara), which was supported by National Bioresource Project in Japan. Contact Persons for this project: Motoaki Seki (email: mseki@psc.riken.jp), Kazuo Shinozaki (e-mail: sinozaki@rtc.riken.jp) and Masatomo Kobayashi (e-mail: kobayasi@rtc.riken.jp). Therefore, the total number of RAFL cDNA clones whose full-length sequences have been determined is 21,005 as of March 24, 2008. The number includes the results of the collaboration with the SSP groups. Some of the RAFL clones are mapped to the same AGI code according to TAIR7 gene model. The RAFL cDNA clones are available from RIKEN BRC.
- ORF clone project: RIKEN PSC groups have collected ORF clones for 443 Arabidopsis transcription factors that are not found in the RAFL cDNA collection, and determined their sequences in collaboration with National Institute of Advanced Industrial Science & Technology (PI: Masaru Ohme-Takagi). Contact Persons for this project: Kazuo Shinozaki (e-mail: sinozaki@rtc.riken.jp) and Masaru Ohme-Takagi (e-mail: m-takagi@aist.go.jp). The ORF clones will be available from RIKEN BRC.

Table 3. Arabidopsis ORF and cDNA clone repertoires*

Creator	Format	Focus	Validation	Scale	URL	Stock center†
ORF clones						
SSP consortium & Salk Institute	Univector pUNI51		Full sequence	14,214	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	1,281		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	962	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	1,527 (5,299)	plants.gersteinlab.org/	ABRC
ATOME 1	Gateway entry		5' and 3' end seq.	1,809	urgv.evry.inra.fr/orfeome/	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	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/sheenweb/category_genes.html	ABRC
cDNA clones						
RIKEN/SSP/ Salk Insitute	ZAP or PS		Full sequence	21,508	www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/Arabidopsis	CNRGV

*Modified from P. Hilson, personal communication

†Stock Center distribution list continues on next page

†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/
- Open Biosystems Inc., USA, www.openbiosystems.com/

Natural Variation and Comparative Genomics

Prepared by Julin Maloof (Co-chair, jnmaloof@ucdavis.edu) and J. Chris Pires (Co-chair,piresjc@missouri.edu)

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 only second to humans when it comes to knowledge and ability to exploit sequence variation for understanding biological processes, and indeed might serve as a useful model for developing methods that will be applicable in medical genetics.

Notable Advances and Publications

A number of publications in the last year demonstrated significant advancement in the field. We will highlight a few that represent new directions or resource development. Clark et al. [1] published results from resequencing twenty Arabidopsis accessions. These data give a genome-wide view of nucleotide variation in *Arabidopsis thaliana*, highlight genomic regions with substitution patterns suggestive of non-background selection, allow evaluation of population genetic statistics against empirical data, and provide a rich database of polymorphisms for further genetic study. Further analysis of these data by Kim et al. [2] revealed that linkage disequilibrium (LD) decays within an average of 10kb, notably faster than previous estimates. Data from these studies has been used by the Borevitz, Nordborg, and Weigel groups to design an Affymetrix™ genotyping chip that assays 250,000 SNPs. Importantly, statistical methods for association mapping in Arabidopsis have been developed to help cope with the complex population structure often present in these types of mapping populations [3,4].

Microarrays have been used to assay gene expression across accessions and in recombinant inbred line (RIL) mapping populations [5-8]. This allowed mapping of loci (eQTL) controlling variation in gene expression. Combining eQTL and traditional QTL mapping provides testable hypotheses about the mechanisms of QTL action. Further studies have used high-throughput methods to study variation in metabolites [9,10], ion content [11], and genome methylation [12,13]. In regards to comparative genomics, recent publications of the grape genome (and forthcoming publication of the papaya genome) have revised our understanding of the timing of the three nested whole genome duplication events contained within *A. thaliana*. The gamma duplication event is now thought to occur not at the origin of the angiosperms but with the origin of the eudicots or rosids, and the beta duplication event is also now considered to be much more recent.

New Resources

- The above mentioned resequencing data are integrated into the TAIR sequence viewer; the SNP genotyping chip is available from Affymetrix™. *Arabidospis lyrata* genomic sequence is in assembly at JGI; *Capsella rubella* genomic sequence is in production.
- Densely genotyped mapping populations (RILs, near isogenic lines (NILs), heterogeneous inbred families (HIFs), and panels for association mapping) are critical to the field. New RIL populations continue to become available (www.inra.fr/vast/RILs.htm) [14,15], including an interesting 19-parent advanced intercross population [16]. Genome-wide NIL introgression sets are also available for two populations [17,18]. HIFs have been helpful in fine-mapping in the Bay x Shah RIL set and could be exploited elsewhere. An expanded association mapping panel genotyped at 250,000 SNPs using the SNP chip is being developed and will be available from the stock center.

Needs and recommendations

- New resources are needed to aid the process of demonstrating functional polymorphisms for QTLs.
- Longer funding cycles (4-5 years minimum) are needed to allow QTL mapping and identification.
- Better access to mapping populations and data is needed.

We encourage the deposition of all mapping populations in the stock centers as institutional Material Transfer Agreements (MTAs) may impede resource sharing. An organized effort to collect and organize NILs and HIFs for each RIL population is needed. All genotyping data should be provided in a common and easily transformable format.

- New collections of wild genotypes with documented location information, particularly from native regions, are needed. This will enable understanding of selective influence of environment and is key for ecological evolutionary questions.
- Detailed phenotyping in lab and field environments, with multiple measurements over time and detailed environmental sensing, is needed.
- There is a need for an inexpensive "fingerprinting" method for identifying *A. thaliana* stocks. SNP chip genotyping will provide the reference data but we need a method for individual labs to fingerprint their own stocks.
- An integrated database for storing and retrieving QTL and eQTL data and results is needed; ideally data will be incorporated into TAIR. Ideally this would use a common mapping framework to facilitate comparison. This is best carried out at the community level.
- Tracing the exact origin of the ancient duplication events will require a multi-gene nuclear phylogeny of the major lineages of the *Brassicaceae* and closely related families. Characterizing these whole genome duplication events can be done in non-model organisms by molecular cytogenetics (Comparative Genome Hybridization, CGH) and increasingly by transcriptome and whole genome sequencing. A *Brassiaceae* "genome browser" needs to be developed that could serve as a plant cyberinfrastructure model that eventually extends to other rosid genomes and eventually to all eudicots and beyond. This is also critical for researchers leveraging Arabidopsis knowledge to study morphological and physiological evolution in *Brassicaceae.* The phylogenetic project will require a consortium to deploy new approaches to solve the problem.
- High-throughput sequencing enables sequencing of multiple accessions within and across species. Full genome sequence from additional *A. thaliana* accessions and *Brassicaceae* species will aid QTL mapping and cloning and facilitate understanding of diversity, innovation, and selective pressure. Creating fixed homozygous lines of an array of diverse species and varieties within species is the first step to leverage these new genomic technologies. It is worth considering a hierarchical approach to genome sequencing (multiple very high quality references, higher number of genomes surveyed at reduced quality, very high number of genomes of low quality [e.g., just SNPs]). It is important that (re)sequencing studies allow discovery of genes absent from reference genomes such as *A. thaliana* Columbia. This is particularly important because "Next Generation" methods are particularly poor in this regard. Cost-effective strategies for accessing this very interesting aspect of variation need to be discussed and implemented.

References
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2. Kim et al (2007) Nat Genet 39: 1151-1155.
3. Kang et al (2008) Genetics 178: 1709-1723.
4. Zhao et al (2007) PLoS Genet 3: e4.
5. van Leeuwen et al (2007) Plant Cell 19: 2099-2110.
6. Kliebenstein et al (2006) BMC Bioinformatics 7: 308.
7. West et al (2006) Genetics 175: 1441-1450.
8. Keurentjes et al (2007) Proc Natl Acad Sci U S A 104: 1708-1713.
9. Meyer et al (2007) Proc Natl Acad Sci U S A 104: 4759-4764.
10. Wentzell et al (2007) PLoS Genet 3: e162.
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14. Pfalz et al (2007) PLoS ONE 2: e578.
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16. Scarcelli et al (2007) Proc Natl Acad Sci U S A 104: 16986-16991.
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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

- Homozygous mutant T-DNA collection

  A set of genetically purified, confirmed T-DNA insertion lines consisting of two alleles for each Arabidopsis gene is under development by The Salk Institute Genome Analysis Laboratory (SIGnAL) and is being made available from the Arabidopsis Biological Resource Center (ABRC). 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, 19,516 of these confirmed lines have been received by ABRC. 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. First installments of 8,889 lines of a complete set and 6,868 lines of a one-allele set are presently being distributed. 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. More details can be found in the MASC thermometers (Figure 2).
- RNAi clone resources:

  The AGRIKOLA consortium has constructed a collection of approximately 29,000 Gateway entry plasmids, with a subset of about 27,000 transferred into hairpin RNA expression vectors, each capable of triggering RNAi against a defined target sequence in an Arabidopsis transcript. In addition, a small number of RNAi clones were made by the Chromatin Functional Genomics Consortium (CFGC) against chromatin remodeling transcripts, and more recently, a collection of artificial micoRNAs (amiRNAs) was developed by researchers at Cold Spring Harbor Laboratory. There are nearly 36,000 RNAi plasmids targeting 22,969 unique loci, with transformed plant

lines available for 3,592 loci. AGRIKOLA and CGFC clones are available at low cost through the main stock centers ABRC and NASC (See Table 4 below and Figure 2 in the MASC thermometers section of the report). A subset of higher-priced clones (due to cost-recovery for clone purification and sequence validation) are distributed through BCCM/LMBP. The amiRNAs are currently only being distributed at substantially higher cost through the Open Biosystems company, although they are expected to be deposited into ABRC eventually (www.openbiosystems.com/RNAi/ArabidopsisthalianaamiRNA).

Phenotype annotation tools and ontologies

Phenote, a curation tool to facilitate annotating phenotypes using ontologies, has been developed by National Center for Biomedical Ontology (NCBO) in collaboration with Berkeley Bioinformatics and Ontologies Project (BBOP) (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). The main funding for Phenote development is due to end in July 2008. Additional funding is being sought but there will be a funding gap of at least a few months with the exception of an effort to adapt Phenote for annotation of images, which will continue as part of another project.

Several ontologies useful for controlled vocabulary phenotype annotation can be accessed at the Open Biomedical Ontologies website (www.obofoundry.org/). These include the Plant Ontology (PO) Structure (for plant anatomical parts) and Growth/Developmental Stage ontologies, the GO biological process and cellular component ontologies and the PATO ontology for phenotypic qualities. In addition, the OBO website contains an ontology for units of measurement which could be used in combination with other ontologies to capture quantitative phenotypes, and ontologies of experimental conditions (OBI) and chemical entities of biological interest (CHEBI) useful for capturing conditional phenotypes that are only apparent after experimental manipulation.

High throughput phenotyping projects and data

- Barry Pogson, Plant Phenomics project:

  Funding for the $50M Australian Plant Phenomics Facility (APPF, www.plantphenomics.org.au) has now been secured. The APPF will be based across two nodes located at CSIRO/ANU in Canberra and UA in Adelaide. Construction of both APPF facilities will begin in May 2008 with full commissioning of stage one of the Arabidopsis screening module at the High Resolution Plant Phenomics Centre in Canberra (medium throughput growth and chlorophyll fluorescence screening with mathematical morphological analysis and phenomic database capability) occurring at the end of 2008. Throughput will increase with time until the

Table 4. RNAi resources for Arabidopsis.

Creator	Format	Focus	Validation	Scale	URL	Stock center
RNAi clones						
AGRIKOLA	Gateway entry		PCR sized insert	28,000	www.agrikola.org	NASC
AGRIKOLA	Constitutive hp RNA expression		PCR sized insert	26,000	www.agrikola.org	NASC
AGRIKOLA	Gateway entry		Pure, sequence validated	1,000	bccm.belspo.be/db/lmbp_gst_clones/	BCCM/LMBP
AGRIKOLA	Constitutive hp RNA expression		Pure, sequence validated	800	bccm.belspo.be/db/lmbp_gst_clones/	BCCM/LMBP
CFGC	ds RNA expression	Chromatin remodeling	Single pass seq.	200	www.chromdb.org	ABRC
amiRNA Central	Artificial miRNA		Full sequence	10,000	2010.cshl.edu	Open Bio-systems Inc.

Table Reference: Bleys, A., Karimi, M., and Hilson, P. (2008) Cloned-based functional genomics. Methods Mol. Biol. In press.

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, United Kingdom), http://arabidopsis.info/
- BCCM/LMBP Plasmid and DNA library collection (BCCM/LMBP, Belgium), http://bccm.belspo.be/db/lmbp_gst_clones/
- Open Biosystems Inc., www.openbiosystems.com/

full HTP Arabidopsis module is completed in Canberra at the end of 2009, by which time the Plant Accelerator automated glasshouse facility in Adelaide will also be commissioned. 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.

- Minami Matsui, RIKEN:

  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 (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). Note: 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 (www.psc.riken.go.jp/english/database/index.html) for access to current RIKEN databases.

- Detlef Weigel, Max Planck Institute:

  Population-wide association mapping has the advantage that it can potentially resolve very finely the location of causal variants affecting a trait but this approach has the inherent disadvantage that population structure has a profound confounding effect. Essentially the converse is true for Quantitative Trait Locus (QTL) mapping. One way to combine the advantages of both is perform parallel QTL mapping across several populations, and to exploit both QTL interval and haplotype information across populations. This approach, dubbed nested association mapping, has recently been introduced by Ed Buckler and colleagues for maize. To evaluate the appropriateness of this approach for *A. thaliana*, the Weigel laboratory has generated 15 F2 populations of 480 individuals each. Because the parents were drawn from the 20 accessions investigated with Perlegen arrays (Clark et al., Science 2007), detailed SNP information – on average, 1 SNP per kb in each accession – is available for the parents, and moderately dense genotyping with 400 intermediate-frequency markers will allow almost complete reconstruction of haplotypes in the 7200 F2 individuals. All individuals have been phenotyped for a number of life history traits and images have been acquired at regular intervals for each individual during vegetative growth. A database that accepts both genotype and phenotype, including image data, is being developed and the data will be made freely available following publication.

- Pierre Hilson, Christine Granier, Cyril Pommier, AGRON-OMICS project

  The Agron-omics project, which stands for Arabidopsis GROwth Network integrating OMICS technologies (http://www.agron-omics.eu/), will conduct an in-depth study of leaf growth in the model plant species *Arabidopsis thaliana*. Over a five year period starting November 2006, this network of European plant biology researchers will perform experiments to identify the molecular components controlling growth and build mathematical models to explain how these components interact. A major component is PHENOPSIS, an automated platform for Arabidopsis leaf growth phenotyping developed at INRA (Granier et al., 2006 New Phytologist). Phenotyping is focused on three main areas: 1) high-throughput phenotyping of leaf growth response to environmental stresses in different collections of accessions (ERANET, ARABRAS project, 2007-2010); 2) identification of leaf growth QTLs in different populations of recombinant inbred lines grown in different environmental conditions (at this time, Ler x An-1, Ler x Cvi-0 and Bay-0 x Sha in different day-lengths, different incident light and different soil water contents) [GENOPLANTE DNV project (2007-2010)]; 3) high-throughput phenotyping of leaf growth in genotypes affected in cell cycle, endoreduplication, cell wall properties, metabolism, hormonal status, circadian rythm and flowering time (European Integrated Project, FP6, AGRON-Omics, 2006-2011). Data from PHENOPSIS will be made freely available following publication. A second phenotyping platform with higher throughput but with a less precise description of the phenotype and environment is under development by INRA at the Versailles campus (www-ijpb.versailles.inra.fr/en/sgap/equipes/crg/phenotypage/index.html). A prototype has already been created in collaboration with ISEP (Institut Supérieur d'Electronique de Paris) and CEGS-DESTEC. Currently the IJPB, with financial support from the Région Ile de France, INRA and Génoplante, is building a new facility for 300 m2 of culture chambers, which will eventually accomodate the IJPB high throughput phenotyping platform. A dedicated chamber of 60m^2, fully automated, will allow experiments with more than 10,000 individuals in parallel.

Proteomics

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

In 2006 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 subcommittee provide the largest collection of proteomics data for this higher model plant. Below we have listed the achievements of the last two years.

- 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 largest collection of proteomics data for a single study in Arabidopsis thaliana was published in Science, 2008 (Baginsky lab), and assembled as an accessible database (www.AtProteome.ethz.ch). Links to TAIR (www.arabidopsis.org/), MIPS (http://mips.gsf.de) and TIGR (http://www.tigr.org/) were established. The data were further deposited in PRIDE and PRIDE Biomart (see http://www.ebi.ac.uk/pride/). The Arabidopsis proteome map provides expression evidence for close to 50% of all predicted gene models together with a number of alternative gene models. A set of organ specific biomarkers is provided together with organ-specific proteotypic peptides for 4,105 proteins to facilitate targeted quantitative proteomics surveys. Quantitative information for the identified proteins established correlations between transcript and protein accumulation in different plant organs. Further plans are to link the AtProteome database to existing resources in the MASC proteomics committee, such as PPDB (see http://ppdb.tc.cornell.edu/) and ProMEX (see http://promex.mpimp-golm.mpg.de/home.shtml) (see below).
- The most comprehensive study on the Arabidopsis chloroplast proteome, their sorting signals and PTMs as well as protein abundance, using high accuracy mass spectrometry (Orbitrap), was published 2008 in PLOS-One (van Wijk lab). These and other data are available via the plant proteome database (PPDB – link above) for Arabidopsis and maize. PPDB provides genome-wide experimental and functional characterization of the proteomes, including PTMs and subcellular localization, with emphasis on leaf and plastid proteins. Maize and Arabidopsis proteome information are directly linked via internal BLAST alignments and each protein is linked to TAIR, SUBA, ProMEX.
- The most comprehensive database on subcellular localization of proteins–SUBA- was established by the Millar lab (www.plantenergy.uwa.edu.au/applications/suba/index.php). These data are cross-linked to TAIR protein pages (www.arabidopsis .org) and selected data are provided as web services via the BioMoby Dashboard.
- The most comprehensive database of published and predicted phosphorylation sites in Arabidopsis was established, called PhosPhAT (see http://phosphat.mpimp-golm.mpg.de/) (Heazlewood/Weckwerth/Schulze lab). This database is crosslinked to ProMEX.
- ProMEX: a central searchable database of MS/MS reference spectra derived from Arabidopsis thaliana, Chlamydomonas reinhardtii, Medicago truncatula, potato, tomato and other proteomics samples was established and cross-referenced to the UNIPROT plant genome annotation initiative in 2007 (see http://promex.mpimp-golm.mpg.de/home.shtml) (Weckwerth lab). This database also facilitates the design of proteotypic peptides for targeted accurate protein quantification in complex samples. ProMEX has also crosslinks to PhosPhAT, PPDB and the Golmer Metabolome database (see GMD http://csbdb.mpimp-golm.mpg.de/csbdb/gmd/gmd.html). Links to AtProteome are in progress.
- AnnoJ: a Web 2.0 genome browser developed by Julian Tonti-Filippini in the Millar lab, is currently being used for displaying deep sequencing DNA and RNA data (Cell, May 2, 2008, http://neomorph.salk.edu/epigenome.html) and will be established for proteogenomic mapping of MS/MS spectral data in 2008/09.
- Meetings and the organization of proteomics workshops are established at a regular basis at the International Conference on Arabidopsis research (see ICAR http://www.plantconferences.org/Arabidopsis2008/). A workshop was held in 2007 in Beijing, and another is planned for Montreal in 2008.
- The establishment of large protein interaction databases and their cross-linking to MASC proteomics resources is the main goal of the next years.

Systems Biology

Prepared by Philip Benfey (Chair, philip.benfey@duke.edu)

The field of systems biology has advanced rapidly over the past year. Although there is no universally accepted definition of systems biology, most would agree that it encompasses efforts to find the interconnections among cellular components, emergent properties and network dynamics. The MASC Systems Biology and Bioinformatics Subcommittees are planning a joint workshop on "Frontiers in Plant Systems Biology" for the upcoming Arabidopsis conference in Montreal, 2008. The goal is to bring together groups that produce, integrate and model data from a systems perspective. There will be talks that address the new frontiers in genomic data collection for systems biology and the challenges in data storage, analysis and integration. There will be contributions from biologists performing cutting-edge systems research. Contributors are requested to discuss the state-of-the-art as well as provide a vision for systems research in plants. The hope is that this workshop will stimulate discussion on the role of systems biology research in addressing the grand challenges in plant biology. The workshop will discuss interactions with the

new NSF-funded iPlant Collaborative initiative. The workshop will provide a means to communicate the goals of the iPlant initiative as well as to discuss how best to use iPlant to advance systems biology research in Arabidopsis. The workshop has invited four leaders in the field of systems biology. The draft program includes: [1] Introduction including a brief discussion of the 2020 workshop report, [2] Data generation for systems biology (Xing Wang Deng,Yale University), (3) Data integration (speaker: Chris Town, J. Craig Venter Institute), [4] Data modeling (speaker: Gloria Coruzzi, New York University), [5] The iPlant initiative (speaker: Steve Rounsley, The University of Arizona), [6] Open discussion.

1. As applied to Arabidopsis research there were several notable publications, of which a few examples are listed below. Baerenfaller K, Grossmann J, Grobei MA, Hull R, Hirsch-Hoffmann M, Yalovsky S, Zimmermann P, Grossniklaus U, Gruissem W, Baginsky S. Genome-Scale Proteomics Reveals Arabidopsis thaliana Gene Models and Proteome Dynamics. Science. 2008 Apr 24 [Epub ahead of print]
2. Lu Y, Savage LJ, Ajjawi I, Imre KM, Yoder DW, Benning C, Dellapenna D, Ohlrogge JB, Osteryoung KW, Weber AP, Wilkerson CG, Last RL. New Connections across Pathways and Cellular Processes: Industrialized Mutant Screening Reveals Novel Associations between Diverse Phenotypes in Arabidopsis. Plant Physiol. 2008 Apr;146(4):1482-500.
3. Brady SM, Orlando DA, Lee JY, Wang JY, Koch J, Dinneny JR, Mace D, Ohler U, Benfey PN. A high-resolution root spatiotemporal map reveals dominant expression patterns. Science. 2007 Nov 2;318(5851):801-6.

Analysis and Recommendations

There are myriad challenges facing the world today including loss of habitat, greater food requirements of a rapidly increasing human population, the need to develop renewable energy sources including biofuels, and global climate instability which will have repercussions on all aspects of life on this planet. To address these challenges requires a thorough understanding of the basic biology and ecology of plants, including how plants develop, interact with the environment, and respond to internal and external stimuli. An understanding of the basic processes of plants will allow us to predict and manipulate plant growth and enable improved agricultural productivity while minimizing negative impacts. It is evident that the dramatic advances achieved in plant biology over the last two decades are largely due to the concentrated focus on Arabidopsis by plant researchers worldwide. It is equally certain that there is still much to be learned. Dedicated support for basic research by government funding agencies has been, and will continue to be, crucial to successfully developing Arabidopsis as the reference for plant biology, and for leveraging the knowledge gained for applied studies in other plants. Without such large-scale funding for the original Genome Project (1990-2000) or for the current Functional Genomics Project (2001-2010), the remarkable breakthroughs that are being achieved at an ever-accelerating rate would not be possible.

We are now at a very exciting time in Arabidopsis research, and indeed, in biological research in general. The benefits from coordinated efforts of numerous researchers are now being realized: the availability of genetic, genomic, proteomic, metabolomic and natural variation datasets and tools, just to name a few, are facilitating comprehensive and systems-biology approaches in plant biology in ways not dreamed of as recently as a decade ago. Due to early-established and maintained international collaborations there is wide availability of Arabidopsis resources. There are also important database resources, exemplified by The Arabidopsis Information Resource (TAIR), that provide Arabidopsis sequence and gene function information as well as analytical and comparative tools. These resources enable researchers from other fields to rapidly gain insights by leveraging Arabidopsis knowledge in addition to facilitating experimentation by those within the Arabidopsis community itself. For example, it is becoming more common for researchers to approach biological questions using multiple organisms such as investigating developmental mechanisms in Arabidopsis and fruit fly, natural variation in Arabidopsis and wheat, or cellular signaling processes in Arabidopsis and humans. The nexus of information and tools generated by the Arabidopsis community will continue to revolutionize biology by allowing research to evolve from a descriptive to a predictive science. Arabidopsis is 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 current and future challenging questions.

Insights from Arabidopsis also inform studies in plants of economic importance including food, feed and fuel crops. However, the utility of Arabidopsis extends beyond the plant realm; researchers studying other organisms such as humans, flies, worms, fungi, and mice increasingly rely on the extensive collections of Arabidopsis resources to inform their own research. For example, sequencing the Arabidopsis genome revealed that it contained genes similar to a vast number of human disease genes, and in some cases, it is easier and faster to study processes in Arabidopsis than in mammalian models. As the Arabidopsis Functional Genomics Project nears its conclusion, future directions for Arabidopsis and plant research are under discussion. This critical juncture requires input on future directions from all the important stakeholders, including members of the global Arabidopsis community. The MASC planning meeting during the 18th Arabidopsis Conference (Beijing, June, 2007) consisted of MASC representatives from various countries, MASC subcommittee members, representatives from funding agencies, and community members. The primary meeting goal was to begin coordinated discussion about the next phase of research following 2010. Members of the North American Arabidopsis Steering Committee (NAASC) and other US researchers initiated the planning meeting in Spring, 2007 in response to discussions about the need for a comprehensive and forward-looking plan for Arabidopsis research. The Beijing meeting was the first of a series of discussions by the international community to reflect on the remarkable amount of Arabidopsis knowledge and resources developed in the last decade, to strategically determine how to leverage those resources to address current and future needs, and to ensure adequate funding for basic science research is maintained to address important biological challenges using Arabidopsis.

US 2020 Vision for Biology Workshop

A workshop was held in January of 2008 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. A report, entitled 'Plant Systems 2020: A systems understanding of development and adaptation at the level of cells, tissues, organisms and ecosystems', was produced from the workshop and is available at the MASC website (www.arabidopsis.org/portals/masc/

masc_docs/masc_wk_rep.jsp). Outcomes of the workshop will be presented at the 2008 annual MASC meeting held during the International Conference on Arabidopsis Research. The following are a number of recommendations drawn from the US 2020 report.

Recommendations from the US Workshop

1. Major and specific support to integrate molecular, cellular, organismal and ecological research on Arabidopsis should continue to facilitate understanding of how a living organism develops, functions and adapts to its environment. It is essential that dedicated support continue for studies of basic biology in Arabidopsis, the premier plant system for addressing many biological questions. This will allow further payoffs from previous investment and the breakthroughs achieved in this reference plant will undoubtedly lay the most efficient foundation to the future optimization of species of economic importance.
2. Support should be provided to develop additional and new types of large-scale experimental genomics resources that are needed to address current and future biological challenges.
3. Data acquisition should remain a major focus of future programs to fuel data analysis, integration, hypothesis generation and testing. New technologies will enable the collection of new and higher quality data, thus allowing more sophisticated analysis.
4. The development of new quantitative approaches to the study of biological systems using Arabidopsis is encouraged. Dynamic and quantitative information about genes, RNAs, proteins and metabolites (i.e. the genome, the transcriptome, the proteome and the metabolome) is needed to transform maps of genetic and protein interactions into networks of dynamic interactions within living cells.
5. Emphasis should be placed on systems approaches that integrate all levels of biological organization with the parallel development of mathematical platforms to handle, quantify, integrate and interpret biological data from diverse experimental platforms. Data obtained through quantitative systems approaches should be integrated and analyzed to build predictive models which must then be tested and refined in an iterative fashion. Such approaches will require the development of powerful genetic and genomic technologies, new analytical tools, and advances in cell imaging/visualization. Collaborations between biologists and scientists in other quantitative disciplines should be established to enable these approaches.
6. The wealth of genomic and functional data and systems biology tools available for Arabidopsis should be leveraged for population genomic analyses and understanding phenotype-genotype relationships, species-level variation, environmental adaptation, and biological systems up to the ecological level.
7. Arabidopsis should provide the 'how-to' guide for the development of other plant research systems. Expanding the toolkit in Arabidopsis will serve as the test site for possible expansions into other plant species.
8. Arabidopsis, with its early emphasis on multi-disciplinary projects, should continue to serve as an ideal training system for future generations of researchers with broadened expertise. Arabidopsis could provide a major teaching tool in graduate curricula for computational and systems biology. Arabidopsis can also serve as the conduit to help improve the scientific literacy of the general public.
9. International collaborations have been key to the successes achieved thus far in Arabidopsis research. Arabidopsis can continue to forge scientific strength and cooperation throughout the world, including with developing countries that place a high value on agriculture-related research.

EU 2020 Vision for Plant Science Workshop

A workshop for European plant biology researchers was held in June, 2008 with the same goal as the US 2020 workshop held in January. Results of the workshop will also be presented at the 2008 annual MASC meeting. A report of the workshop is in preparation and will soon be made publicly available in the future at the MASC webpages (www.arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp), and other locations. The following recommendations were summarized by Joanna Friesner, the MASC Coordinator, who participated as an observer at the workshop, with input provided by several workshop participants.

Recommendations from the EU Workshop

1. Global food security will inform strategic thinking in plant research in the next 10 years. For plant science this will require a two-pronged approach with strong investment in Arabidopsis research, to generate fundamental knowledge as well as novel technologies, and in crop plant research to deliver translational outputs.
2. During the last 10 years Arabidopsis has underpinned the development and application of genomics technologies in plant science. Many of the genes and techniques being used in the crop sector were developed first in Arabidopsis. Arabidopsis will now play a major role in developing next generation approaches. These will include quantitatively modeling plant behavior at multiple levels, systems biology approaches based on extensive data sets, analyzing how plant genomes and gene functions have evolved, accessing the full range of genetic variation available in plant populations, as well as continued intensive analysis of the roles of plant proteins, determination of protein structure and regulation in fundamental studies of the growth and development of plants.
3. Arabidopsis has a central role to play in the transition from a descriptive to a predictive science in the plant sciences. It is the major plant platform in which the development of quantitative techniques necessary to produce predictive systems models is feasible. An essential component of this will be maintaining a large and active research community

focused on the Arabidopsis model system.

4. Publicly-accessible data are critical to the advancement of plant research and data sharing is needed. We must ensure the security of our major data and resource repositories such as TAIR and stock centers and support timely sharing of resources. Sufficient repositories for current and future datasets and resources must be available.
5. The iPlant Collaborative was seen as an excellent opportunity to develop a comprehensive toolkit of software resources that will allow easy access to datasets that are currently available and to develop new standards by which future datasets are made available. The Arabidopsis community was strongly encouraged to participate in this initiative.
6. Standardization of data collection and annotation is needed, including the development of tools for phenotype description, sample preparation and storage, metabolite profiling, proteomics, etc.
7. Arabidopsis research should be viewed as an essential component of a continuum of plant science research from the fundamental to the applied. Also, other model systems will be required to study traits not accessible in Arabidopsis. The Arabidopsis community will play a vital role in attracting and developing highly-trained researchers in the plant sciences that can apply their knowledge and skills in agricultural and other areas of plant biology.

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

- As the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project nears its conclusion in 2010, continued dialog on future research directions and funding streams is needed by members of MASC, the Arabidopsis community, other plant communities, and funding agencies. A second planning meeting will be held by MASC during the International Arabidopsis Conference in Montreal (July 23-27, 2008) and will include presentations from recent US and European workshops on the future of Arabidopsis research. In addition, further input from the broader community should be obtained.
- The Arabidopsis community should participate with and support the new iPlant Collaborative (iPC) The project goal is to develop a community-driven cyberinfrastructure collaborative for the plant sciences that would enable new conceptual advances through integrative, computational thinking. Arabidopsis, with its advanced resources, datasets and extensive research community, should play an integral part in the iPC (http://iplantcollaborative.org/)
- The 1,001 Arabidopsis genomes project should be supported (www.1001genomes.org). This project aims to determine the whole-genome sequence variation of 1,001 natural Arabidopsis accessions to enable large-scale association studies in natural populations and allow the identification of alleles underlying phenotypic diversity. Previous data from 20 accessions revealed that nearly 10% of protein-coding genes had a major-effect single-nucleotide polymorphisms in at least 1 accession highlighting the need for sequences beyond the reference genome. The community should also look into the representative transcriptomes and epigenomes of those same accessions at the level of tissues or individual cells.
- Projects to obtain detailed highly replicated expression, epigenetic, and proteomic profiling across spatial, temporal, environmental, developmental, and genotype series are highly desirable. Detection at the level of individual cell type, rather than in whole tissues/plants, is preferred.
- Accessibility of Arabidopsis knowledge and resources should be increased by establishing materials and annotation handling standards with all major plant biology journals, similar to the new collaboration between TAIR and Plant Physiology Journal. Also needed are ways to capture most of the primary literature in machine readable format.
- A common ontology and appropriate connected databases are needed to facilitate phenotype recording and store and share phenotype data.
- Techniques and efforts to address protein complexes are needed, for example, by improved fluorescent tag methods that allow real-time detection of protein complexes, or by cell sorting followed by sensitive detection of protein complexes.

The International *Arabidopsis* Functional Genomics Community

Country Highlights

Argentina

- 11 new grants that support Arabidopsis research including one joint proposal with the Max Planck Institute, two Young Investigator Awards, and two from Howard Hughes Medical Institute.

Australia: Database and Genome Browser

- SUBA: This database houses large scale proteomic and GFP localization sets and contains precompiled bioinformatic predictions for protein subcellular localizations. SUBA 2.2 encompasses 10 distinct subcellular locations and over 8000 non-redundant proteins representing transcripts of over 50% of Arabidopsis ESTs.
- Anno-J: Interactive web-based genome browsing in Arabidopsis for large datasets in functional genomics. Anno-J uses Web 2.0 technologies for greatly enhanced style control, data syndication, data maintenance, user-interface and flexibility. Co-visualization of complex data sets from remote sources is a key strength.

Austria: Research Consortia

Current Consortia include: (1) "Lasting effects of abiotic stress in plant genomes and their potential for breeding strategies", (2) "Chromosome dynamics - unraveling the functions of chromosomal domains", a multi-organismal project with the focus on the interaction of kinetochore –microtubules, biochemistry of sister-chromatid cohesion, chromosome pairing and recombination, and (3) "Targets of calcium-dependent protein kinases", with participants from Austria, Germany, The Netherlands, and Spain.

Belgium: Automated Phenotyping Platform

A major component the Agron-omics project (Arabidopsis GROwth Network integrating OMICS technologies), is PHENOPSIS, an automated platform for leaf growth phenotyping. Data from PHENOPSIS will be made freely available following publication. A second platform with higher throughput but with a less precise description of the phenotype and environment is under development (for more information see the Phenomics Subcommittee report).

Canada: Hosts 19th ICAR, New Plant Genomics Initiative

The 19th International Conference on Arabidopsis Research will be held in Montréal, Québec in 2008. This is the first time that ICAR will be held in Canada. Conference organization is a joint effort between NAASC and Joanna Friesner as the main organizers, and members of the Canadian Arabidopsis community: George Haughn (UBC) as a Canadian NAASC member and Tamara Western and Hugo Zheng as local organizers from McGill University. The presence of ICAR coincides with a ground-breaking multi-million dollar Genome Canada funding initiative for Applied Genomics Research in Bioproducts or Crops and represents a unique opportunity for the advancement of plant genomics in Canada. (**Note**: A Canada report was not submitted for 2008).

China: Strong Arabidopsis Funding in 2007

The National Science Foundation of China initiated a new program on understanding the mode of plant hormone action with a 150 million RMB (1USD=7RMB) budget for eight years. Five million will be allocated to promote international collaboration in plant hormone research. The Ministry of Science and Technology funded several projects such as plant reproduction and fertility, plant stem cells, and cell-cell recognition during plant pollination. A large portion of these funds will go to Arabidopsis and rice research.

France: New Research Programs Funded in 2007

- National Research Agency, Genoplante program, 4 new projects: 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.
- National Research Agency, Non-thematic program ('Blanc'), 9 new projects: The Blanc program 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.

Germany: AFGN Renewed, GABI Continues to Support Translational Work

- AFGN: The AFGN, founded in 2001 as a DFG-funded basic research program, was renewed in 2007 (3rd funding period) and currently supports 22 projects involving basic Arabidopsis research.
- BMBF: The BMBF funded plant genome research program was launched in 1999 and is now in its third major funding phase (called `GABI-FUTURE´). While only a few of the 38 current projects focus exclusively on Arabidopsis, research on this organism is an integral part of a very large fraction of projects in which basic research on A. thaliana is combined with research activities on crops.

Israel: Arabidopsis Research Takes a Big Cut in '08

Arabidopsis projects in Israel are funded via national and bi-national grants, one being The US - Israel Binational Agricultural Research and Development Fund (BARD). Rather disturbingly, BARD announced that their "Model System and Functional Biology in the Service of Agriculture" panel, the panel that funded the majority of Arabidopsis research, will be discontinued in the coming year. As BARD sponsored ~$1 million in Arabidopsis research annually, this is potentially a large loss for the Israeli Arabidopsis community. A possible positive change in the general acceptance of Arabidopsis as a model for basic science was seen in the recent Federation of Israeli Societies of Experimental Biology congress. While Arabidopsis talks at this large congress were in the past placed in plant-specific sessions, Arabidopsis and other plant talks this year were integrated within the main sessions.

Italy: Breakthroughs in Research

An important breakthrough this year was the discovery of a previously unrecognized regulatory circuit underlying plant response to canopy shade, which involves both auxin and cytokinin, suggests that crop yield could be increased by reducing the expression of cytokinin oxidase genes in leaf organs. Another breakthrough concerns the functional analysis of a transcriptional modulator of physiological responses in guard cells. These data open new possibilities to improve crop survival and productivity during drought, and relevant patents have been obtained.

Japan: New Research Program Started

In 2007, a 6-year research program on plant molecular, cellular, and developmental biology supported by a Grant-in-Aid for Scientific Research on Priority Areas from MEXT was started. The program consists of about 40 projects including 14 core projects (13 of which are mainly on Arabidopsis) from 10 research institutes. It focuses on such topics as mechanism of meristem formation and organ formation, cell proliferation and differentiation during organogenesis, regulation of meristem function by local and long-distance signaling, genetic and epigenetic regulation, and search for novel signals and their receptors.

The Netherlands- More Awards for Arabidopsis Researchers in 2007

- Marcel Dicke received the prestigious SPINOZA prize among others for his combination of a molecular genetic approach with an ecological approach in which Arabidopsis is used as a model for other brassicaceous plants. In recent work from his lab, a 70-mer Arabidopsis oligo array was successfully used to determine global transcriptional changes in Brassica oleracea in response to insect feeding.
- The Research prize of Wageningen University (best publication of the university in the past 4 years) was awarded to an Arabidopsis paper by Keurentjes et al. (Nature Genetics) describing a global analysis of QTL for metabolites using natural variation.

The Nordic Arabidopsis Network

- The Norwegian Plant Functional Genomics Program plant platform includes service activities such as transcriptional profiling, bioinformatics, genotyping and clone collection, etc. Most of the activity involves Arabidopsis and the first funding period ends this year. Systems biology is an important topic in the next program (2008-2012), and support to plant research is included.
- A plant science initiative started in Norway in 2007. The goal is to organize a joint Norwegian plant science program as a part of the Norwegian Research Council.
- The 16th Congress of the of the Federation of European Societies of Plant Biology will be held in Tampere, Finland in August 2008. Researchers studying Arabidopsis are highly represented in the program.

United Kingdom: New Initiatives Focus on Systems Biology and Translation

The SABR initiative with a budget of £25.8M aims to promote further uptake of systems biology amongst research groups in the UK. 3 of 6 funded projects involved Arabidopsis research. The joint call between the Agence Nationale de la Recherche and the BBSRC was set up to support high quality research in systems biology between France and the UK. 10 consortia were funded via this scheme including 3 that involve Arabidopsis/ Plant research. During 2007 the BBSRC put £13M into funding 18 research projects that aim to translate basic plant science in the UK into practical applications that will benefit farmers and consumers. Problems being tackled include improving willow biomass yields for bioenergy by transferring current knowledge of shoot branching in Arabidopsis to willow.

United States

- 2020 Vision for Plant Biology: A January 2008, NSF-sponsored workshop, was held to discuss 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 workshop was followed by a Germany and UK-sponsored EU2020 workshop in June.
- The new Plant Science Cyberinfrastructure Collaborative, known as the iPlant Collaborative (iPC), launched in April, 2008 with a kickoff meeting. The iPC expects to begin reviewing proposals as early as June 1, 2008.
- A unique partnership has been formed between Plant Physiology and TAIR to ensure that Arabidopsis gene function data published in the Journal are captured in TAIR's database. This provides a mechanism for authors to submit Arabidopsis gene function information to TAIR as part of the publication process.
- Members of the North American Arabidopsis Steering Committee (NAASC), have organized the annual Arabidopsis Conference in 2005, 2006, 2007, and again this year in 2008.

Argentina

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

New Grants from Agencia Nacional de Promoción Científica y Tecnológica (ANPCYT), Argentina, which support Arabidopsis research:

- PICT 614. Diego Gomez- Casati. Transcriptome analysis of male sterile plants deficient in key proteins involved in energetic metabolism in Arabidopsis thaliana. Instituto de investigaciones Biotecnológicas, IIB INTECH, Universidad Nacional de San Martin.
- PICT 1026. Marcelo Yanovsky. Molecular analysis of the interaction between Arabidopsis responses to shade and immunity. Universidad de Buenos Aires.
- PICT 1296. Carlos Luis Ballaré. Effects of the light environment perceived by phytochrome on anti-herbivore defenses. Universidad de Buenos Aires.
- PICT 1593. Pablo Diego Cerdan. The control of Arabidopsis flowering by PFT. Fundación Instituto Leloir
- PICT 1917. Javier Francisco Botto. Light control of seed germination in Arabidopsis.

Universidad de Buenos Aires

- PICT 2375. Daniel Héctor González. Functional analysis of TCP transcription factors. Universidad Nacional del Litoral.

Joint proposals with Max Planck:

- PICT 1913 Jorge José Casal and George Coupland. Molecular determinants for the quantitative relationship between flowering time and day length in Arabidopsis. Universidad de Buenos Aires and Max Planck

Young investigator awards:

- PICT 983 José Manuel Estevez. 4- Prolil hidroxylases in Arabidopsis. Universidad de Buenos Aires
- PICT 1528 Elina Welchen Functional analysis of mitochondrial proteins in Arabidopsis. Universidad Nacional del Litoral.

New grants from the Howard Hughes Medical Institute that support Arabidopsis research

- MicroRNA Networks in Plants. Javier Palatnik. IBR, Rosario.
- Signaling Circuits Controlling Circadian and Seasonal Rhythms. Marcelo Yanovsky Universidad de Buenos Aires.

Major funding sources for Arabidopsis functional genomics:

- ANPCYT (Agencia Nacional de Promoción Científica y Técnológica), 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
Contact: Barry Pogson
The Australian National University, Canberra
http://www.anu.edu.au/bambi/people/academic/pogson.php
Email: barry.pogson@anu.edu.au

Australia has a strong tradition in plant scientific research with most institutions across all states having some research involving Arabidopsis as a model system. Major areas of Arabidopsis research and functional genomics are Canberra, Melbourne and Perth. Funding for Arabidopsis in New Zealand 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, including Horticulture and Food Research Institute of New Zealand (HortResearch), and the New Zealand Institute for Crop & Food Research Limited (Crop & Food Research).

Key new developments during 2007 were:

Plant Phenomics (www.plantphenomics.org.au) Funding for the $50M Australian Plant Phenomics Facility (APPF) has now been secured. The APPF will be based across two nodes located at CSIRO / ANU in Canberra and UA at the WAITE campus in Adelaide. Construction of both APPF facilities will begin in May 2008 with full commissioning of stage one of the Arabidopsis screening module at the High Resolution Plant Phenomics Centre in Canberra (medium throughput growth and chlorophyll fluorescence screening with mathematical morphological analysis and phenomic database capability) occurring at the end of 2008. Throughput will increase with time until the full HTP Arabidopsis module is completed in Canberra at the end of 2009, by which time The Plant Accelerator automated glasshouse facility in Adelaide will also be commissioned. 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 info contact Bob Furbank (Robert.Furbank@csiro.au) or Mark Tester (mark.tester@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 localisation data in SUBA encompasses 10 distinct subcellular locations, over 8000 non-redundant proteins and represents the proteins encoded in the transcripts responsible for over 50% of Arabidopsis ESTs. The SUBA database provides a powerful means by which to assess protein subcellularlocalisation in Arabidopsis (http://www.suba.bcs.uwa.edu.au)

Anno-J: Interactive web-based genome browsing in Arabidopsis for large datasets in functional genomics by Julian Tonti-Filippini and A. Harvey Millar (hmillar@cyllene.uwa.edu.au), The University of Western Australia. 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. Tracks are discrete plugins within Anno-J, allowing each to implement *ad hoc* functionality and controls. Scrolling along the genome in each track is accomplished by dragging and dropping the viewable area and continual scrolling is achieved via caches on either side of the visible range that are updated asynchronously as the user scrolls. Zooming allows rapid and fluid visualisation of the data over a four orders of magnitude from large chromosomal sections to single base resolution. Tracks have been created and tailored for short read deep sequencing data (eg from Illumina GA), genome tiling arrays, and proteogenomic mapping of peptide mass spectra. Co-visualisation of complex data sets from remote sources is a key strength of the AnnoJ architecture.

Major Research Institutions involved in Functional Genomics of Arabidopsis

- Australian Research Council (ARC) Centre of Excellence in Plant Energy Biology (www.plantenergy.uwa.edu.au/). The focus of the Centre is Arabidopsis functional genomics as it pertains to the roles of the chloroplast, mitochondria and peroxisome in energy metabolisms and plant development.
- CSIRO Plant Industry (www.pi.csiro.au). Major Programs on Genomics, micro RNAs and Plant Development. This program investigates several aspects of plant function and, importantly, is developing major facilities for Arabidopsis functional genomics work.

Major funding sources for Arabidopsis functional genomics in Australia

Funding is mainly available through the Australian Research Council's (ARC's) Discovery and Linkage Grant Schemes and its Centre of Excellence Scheme (www.arc.gov.au).

- Linkage Grants - supporting projects between academic institutions and industry
- Discovery Grants and Fellowships - supporting fundamental research
- Linkage-International - In the context of the International Arabidopsis Research Community, the Linkage-International Scheme is particularly relevant. It provides funding for movement of researchers at both senior and junior levels between Australian research institutions and centers of research excellence overseas. Two types of awards include (1) Fellowships, under international agreements for the reciprocal exchange of postdoctoral researchers, (2) Awards, to build links between research centres of excellence in Australia and overseas by funding extended collaborations.

Other major sources of funding for Plant Science are the Research Development Councils. The funding for these organizations is based to a substantial degree on Industry levies and therefore the research is targeted to particular industries. The largest is the Grains Research and Development Corporation of Australia (GRDC). A list of the RDCs is given at www.grdc.com.au/sites/rdcorp.htm .

Major funding sources for Arabidopsis functional genomics in New Zealand

- Royal Society of New Zealand Marsden Fund: (www.rsnz.org/funding/marsden_fund/)
- New Zealand Foundation for Research, Science and Technology: (www.frst.govt.nz/)

Austria

http://www.Arabidopsis.org/info/2010_projects/Austria.jsp

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In Austria, 26 research groups at the BOKU-University of Natural Resources and Applied Life Science Vienna, the GMI-Gregor Mendel Institute of Molecular Plant Biology of the Austrian Academy of Sciences, the MFPL-Max F. Perutz Laboratories and the University of Salzburg are undertaking projects on:

Chromosome biology:

- Peter Schlögelhofer (www.mfpl.ac.at/index.php?cid=54): *meiotic recombination*
- Karel Riha (www.gmi.oeaw.ac.at/rkriha.htm): *telomeres and genome stability*
- Dieter Schweizer (www.gmi.oeaw.ac.at/dschweizer.htm): *chromosome biology, meiosis*

Development and hormones:

- Andreas Bachmair: (www.mfpl.ac.at/index.php?cid=702): *protein modifications, ubiquitination and sumoylation*
- Thomas Greb (www.gmi.oeaw.ac.at/tgreb.htm): *vascular tissue development*
- Marie-Theres Hauser (www.boku.ac.at/zag/AG_hauser.htm): *root development, cytokinesis, cytoskeleton, protein trafficking and degradation, (epigenetic) response upon UV-B stress*
- Fritz Kragler (www.mfpl.ac.at/index.php?cid=52) *proteins/ RNA movement through plasmodesmata*, *HD protein cell.to cell transport and cell cycle regulation*
- Christian Luschnig (www.dapp.boku.ac.at/5499.html): *polar auxin transport, ubiquitination and degradation, chromatin architecture*
- Brigitte Poppenberger: *brassinosteroid biosynthesis, function of the transcription factor CESTA*
- Tobias Sieberer (www.chemie.boku.ac.at/4191.html): *AMP1 in the development of the shoot apical meristem*

Epigenetics:

- Werner Aufsatz (www.gmi.oeaw.ac.at/waufsatz.htm): *histone deacetylase in RNA silencing and stress adaptation, roles of Arabidopsis Rpd3-type histone deacetylases in gene silencing and regulation, antibiotic resistance in plants*
- Antonius and Marjori Matzke (www.gmi.oeaw.ac.at/amatzke.htm): *epigenetics and interphase chromosomes*
- Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/oms.htm): *epigenetic changes in polyploids*
- Hisashi Tamaru (www.gmi.oeaw.ac.at/htamaru.htm): *asymmetric cell division and chromatin reshaping during pollen development*

Glycobiology:

- Herta Steinkellner (www.dapp.boku.ac.at/5499.html): *N-glycosylation pathway in plants*
- Richard Strasser (www.dapp.boku.ac.at/11132.html?&L=1): *galaktosyltransferases and N-acetylglukosaminidases*
- Renaud Leonard (www.chemie.boku.ac.at/4191.html): *N-glycan biosynthesis, fucosylation and defucosylation*
- Georg Seifert (https://forschung.boku.ac.at/fis/suche.person_uebersicht?sprache_in=de &person_id_in=7345): *arabinoglactan proteins and programmed cell death*
- Raimund Tenhaken (www.uni-salzburg.at/zbio/tenhaken): *biosynthesis of nucleotide sugars for cell wall polymers, UDP-glucuronic acid pyrophosphorylase,*

Plant pathogen interactions:

- Holger Bohlmann (www.dapp.boku.ac.at/2238.html): *MIOX gene in nematode induced synzytia*
- Florian Grundler (www.dapp.boku.ac.at/2238.html): *plant nematode interaction, sugar transport in syncytia*
- Gerhard Adam (www.chemie.boku.ac.at/4191.html): *role of mycotoxins in plant-pathogen interactions*

RNA metabolism:

- Andrea Barta (www.mfpl.ac.at/index.php?cid=68): *RNP complexes, spliceosome and small non-coding RNP complexes*

Stress response and signaling:

- Irute Meskiene (www.mfpl.ac.at/index.php?cid=53): *molecular mechanisms of AP2C1/2 in stress adaptation*
- Claudia Jonak (www.gmi.oeaw.ac.at/cjonak.htm): *stress signaling and physiological responses, metabolism, functional analysis of the GSK gene family,*
- Markus Teige (www.mfpl.ac.at/ index.php?cid=55): *Targets of calcium-dependent protein kinases*

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

Consortium members: Christian Luschnig (coordinator), Werner Aufsatz, Marie-Theres Hauser, Heribert Hirt, Claudia Jonak, Ortrun Mittelsten Scheid, Karel Riha

"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.

"Targets of calcium-dependent protein kinases" is a multinational research consortium with participants from Austria (Markus Teige, funded by the FWF), Germany (funded by the DFG), The Netherlands (funded by NOW), and Spain (funded by MEC).

Funding Sources

- Basic research only: FWF (Fonds zur Förderung der wissenschaftlichen Forschung) (www.fwf.ac.at)
- Vienna region: WWTF (Wiener Wisenschafts-, Forschungs- und Technologiefonds) (www.wwtf.at)
- Specific programs (GEN-AU) (Bundesministerium für Wissenschaft und Forschung) (http://www.gen-au.at/index.jsp?lang=en)
- Austrian Research Promotion Agency (FFG) (www.fff.co.at)

Public Relations - Education

Several of the research groups participate in the GEN-AU SommerSchool, an educational program for high school students. www.gen-au.at/artikel.jsp?id=68&base=vermitteln&lang=de

In addition, "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. http://www.viennaopenlab.at/index.php?lang=en

http://www.dialog-gentechnik.at/index.php?id=104908&txgroup=104908

Vienna Biocenter International PhD Program

Within this international competitive program, groups of the GMI and MFPL of the University of Vienna offer up to 4 years Arabidopsis research projects. For detailed information consult the website www.univie.ac.at/vbc/PhD/

Belgium

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

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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), modeling (R. Merckx), 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).

Major funding sources for Arabidopsis functional genomics:

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework Programmes (www.cordis.lu/)
- Belgian Federal Science Policy Office (www.belspo.be)
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; www.iwt.be)
- European ERA-Plant Genomics initiative (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).
- Large generic ongoing programs include:
  1. CATMA, a database (www.catma.org; hosted at PSB) with a repertoire of >30,000 gene-specific sequence tags for transcription profiling and RNAi, available from NASC;
  2. AGRIKOLA, a database (www.agrikola.org; hosted at PSB) presenting genome-scale resources for targeted hairpin RNA gene silencing, available from NASC; in collaboration with PSB, the Belgian Coordinated Collections of Microorganisms (BCCM/LMBP) distributes sequence validated AGRIKOLA resources (http://bccm.belspo.be/db/lmbp_gst_clones/);
  3. SAP (www.psb.ugent.be/SAP) creating and exploiting a genome-scale promoter amplicon collection for the analysis of transcriptional networks;
  4. AGRON-OMICS, a functional genomics and systems biology project funded by the 6th European Framework Programme (www.agron-omics.eu).

China

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

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Arabidopsis research community in China received strong support from funding agencies in 2007. In addition to the continued funding from the National Science Foundation of China (NSFC) for basic research, NSFC initiated a new program on understanding the mode of plant hormone action with a 150 million RMB (1USD=7RMB) budget for eight years. Five million will be allocated to promote international collaboration in plant hormone research. The program is managed by NSFC and supervised by a group of eminent Chinese scientists coordinated by Dr. Jiayang Li at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences (CAS). In 2007, NSFC funded 9 key projects and 21 smaller projects, aiming at deciphering novel mechanisms on hormonal control of plant development and environmental responses, and identifying new players in hormone signaling, as well as developing reliable and sensitive technologies for hormone detection.

Under the National Basic Research Initiative (973), the Ministry of Science and Technology (MOST) funded a five-year project on Molecular Mechanism of Sexual Plant Reproduction and Fertility Control and Its Application in Agriculture (30 million RMB) coordinated by Dr. Mengxiang Sun at Wuhan University. In addition, under the Reproduction & Development Program of the National Mid- and Long-term Science and Technology Initiative (2005-2020), the MOST funded two major projects in plant research: Molecular Mechanism of Stem Cell and Cell Differentiation in Plants (25 million RMB) coordinated by Dr. Yuxin Hu at the Institute of Botany, CAS, and Molecular Mechanism of Cell-Cell Recognition during Pollination in Plants (25 million RMB) coordinated by Dr. Xiansheng Zhang at Shandong Agricultural University. A large portion of these funds will go to Arabidopsis and rice research. Undoubtedly, with such strong financial support, Arabidopsis research in China will continue to flourish in coming years.

In June, 2007, the 18th International Conference on Arabidopsis Research (ICAR) was successfully held in Beijing, China. It was the first time that ICAR was held in an Asian country. Over 800 Chinese participants (out of about 1500 total) attended the conference; this demonstrated the growing interest of Chinese scientists in the Arabidopsis model system.

Major funding sources for Arabidopsis functional genomics:

- National Science Foundation of China
  83 Shuangqing Road, Haidian distrct, Beijijng 100080, China
  Website: www.nsfc.gov/cn/nsfc2008/index.htm

- 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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Newly funded Arabidopsis research projects (2007)

National Research Agency (ANR), Genoplante 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."

http://www.genoplante.com/doc/File/pdf/Projet GNP Ed. 2007.pdf

- FROG: Stabilizing yield under abiotic constraints: Functional characterisation of orphan genes in A. thaliana and application to rice. PI: Mylène DURAND-TARDIF, Versailles.
- REGENEOME: Genomic and epigenomic bases of plant cell totipotency: A laser-assisted microdissection approach. PI: Jean-Denis FAURE, Versailles
- RIL-KIT: Tools to optimize the use of RIL populations, for natural diversity studies and QTL cloning. PI: Christine CAMILLERI, Versailles.
- WALLTALK: Plant cell walls: where microbes meet plants. PI: Deborah GOFFNER, Toulouse.

National Research Agency (ANR), 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."

http://www.agence-nationale-recherche.fr/documents/aap/2007/selection/Blanc-2007.pdf

- COPATH: Unraveling crossover pathways with *Arabidopsis thaliana* and crop relatives. PI: Christine MEZARD, Versailles.
- DDB1 complex: Role of the DDB1 complex in integrating chromatin remodeling and DNA repair during plant development. PI: Chris BOWLER, Paris.
- DISTRIMET: Molecular mechanisms of metal compartmentation in plant cells. PI : Sébastien THOMINE, Gif.
- EIN3-REG: Regulation of plant ethylene responses by EBF1/2-dependent turnover of EIN3 protein. PI: Thomas POTUSCHAK, Strasbourg.
- LeafFlux: Flux management of water and carbon dioxide in inner leaf tissues. Role of aquaporins and consequences for whole plant hydraulics. PI: Christophe MAUREL, Montpellier.
- MITARD: Mitochondrial DNA recombination and transmission in *Arabidopsis thaliana*. PI: José GUALBERTO, Strasbourg.
- PIANO: Analysis of nitric oxide-based signals in plants challenged by biotic and abiotic stresses. PI: David WENDEHENNE, Dijon.
- Plant-TFcode: Cracking the code of transcriptional regulation: the key to the past and future evolution of plants. PI: François PARCY, Grenoble.
- SphingopolaR: Role Of Sphingolipids In Plant Cell Polarity And Development. PI: Jean-Denis FAURE, Versailles.

Major funding sources for Arabidopsis functional genomics

- Genoplante Programme : http://www.genoplante.com/?lg=en
- French National Research Agency (ANR) : http://www.agence-nationale-recherche.fr:80/Intl
- ERA-PG : http://www.erapg.org

Germany

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

Contacts
GABI Scientific Coordination Committee Representative:
Thomas Altmann; IPK-Gatersleben;
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AFGN (Arabidopsis Functional Genomics Network, DFG funded): Coordinator: Klaus Harter; University of Tuebingen;
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1. AFGN

Aim and activities of AFGN

The AFGN was founded in 2001 as a DFG-funded basic research program. The AFGN program was renewed in 2007 (3rd funding period) and currently supports 22 projects. From its beginning AFGN has been organized in close coordination with the NSF 2010 Project, including joint reviewing processes. 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*. Together with colleagues from Austria and Switzerland the AFGN has initiated a yearly international conference on Arabidopsis functional genomics. In 2008, the 5th meeting will be held in Zürich, Switzerland.

AFGN continues to support basic functional genomics research in *Arabidopsis thaliana*. Two areas of research were identified which support concentrates on:

Functional Genomics of Biological Processes: The focus of the AFGN moved towards the genomic analysis of multigene networks whose members functionally interact with each other to accomplish a given biological process.

Tools and Resources for Plant Functional Genomic Research: The development of novel and, especially, quantitative genome-wide tools and technologies and additional resources in plant functional genomics to address unmet needs.

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

2. GABI

The BMBF funded German plant genome research program has been launched in 1999 and is in its third major funding phase (called `GABI-FUTURE´) now. With the associated funding of ERA-Net PG projects of subcall B and a project towards sequencing the barley genome, total funding of plant genomics by the German Ministry of Education and Research (BMBF) has increased to an annual budget of approximately 15-17 million Euro plus additional 20% from industrial partners. GABI-FUTURE, structured as a public-private partnership thus is the biggest research activity in plant genomics in Germany. Research topics that are addressed in the program include further establishment of the plant genomics infrastructure, energy production under low input conditions, health promoting ingredients and improved nutritional quality, nutrient and water efficiency, biotic and abiotic stress tolerance, metabolic and developmental improvement of harvest organs and plant architecture. The total of 38 projects are assigned to five funding modules, Resources, Basics, Bridge Projects, Products, and Start, with the latter supporting junior research groups. While only few projects focus exclusively on Arabidopsis, research on this organism is an integral part of a very large fraction of projects in which basic research on *A. thaliana* is combined with research activities on crops. The bridging concept of research (translational research) introduced in the previous funding phase is thus further reinforced. This is also true for the further enhanced international cooperation, which through ERA-Net PG has been expanded from the initial bilateral as well as trilateral research programs between France (Génoplante), Spain, and Germany and opened to further partners. Under the acronym of `PLANT-KBBE´ (Transnational Plant Alliance for Novel Technologies – towards implementing the Knowledge-Based Bio-Economy in Europe) a new call for proposals has been launched for international co-operation on `bio-energy´, `biomaterials´, and `safer and healthier food´, based on the trilateral partnership and additional partners.

Within GABI, important resources such as the GABI-KAT lines, the world second largest T-DNA insertion line population, were generated and are available for the global research community. In 2005 the transfer of the confirmed insertion lines from Cologne to the Notthingham Stock Center (U.K.) started and is still continuing ensuring high-quality of seed stocks and related data. Other resource developments deal with an improved understanding of natural variation between different A. thaliana accessions. The generation of plant resources for analysis of natural diversity (natural accessions and experimental populations such as F1's, F2's, RIL's, IL's) as

well as their geno- and phenotyping to provide characterized biological material for researchers has been coordinated between colleagues from Génoplante (France) and GABI and is further progressing including deep genotyping and re-sequencing. Data warehousing, management and visualisation are points of main focus for bioinformatics activities in GABI-FUTURE such as the GABI-Primary Database, MAPMEN, and ARAMEMNON in addition to many decentralized bioinformatics groups within the research institutions. Experimental resources are developed in close international co-ordination through projects such as RyeExpress, TILLING, and DUPLO, which address Arabidopsis, barley, oilseed rape, sugar beet, rye, wheat, and potato.

GABI-related Arabidopsis tools and resources:

- GABI-KAT: http://www.gabi-kat.de/
- GABI-Matrix: http://mips.gsf.de/projects/plants/
- GABI-PD: http://gabi.rzpd.de/
- GABI-ARAMEMNON:http://www.uni-koeln.de/math-nat-fak/botanik/bot2/agflue/HOME/projects/GABI_rkunze/index.html
- GABI-TILLING: http://www.gabi-till.de/

Funding source:

GABI: German Federal Ministry of Education and Research http://www.bmbf.de

Additional information:

GABI: www.gabi.de

Israel

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

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Arabidopsis projects in Israel are funded via national and bi-national grants, particularly through the *The United States - Israel Binational Agricultural Research and Development Fund (BARD)*, *Israel Science Foundation (ISF)*, *German – Israeli Foundation for Scientific Research and Development (GIF)*, *U.S.-Israel Binational Science Foundation (BSF)*, and the *Deutsch-Israelische Projektkooperation (DIP)*. Rather disturbingly, *BARD* announced that their "Model System and Functional Biology in the Service of Agriculture" panel, the panel that funded the majority of Arabidopsis research, will be discontinued in the coming year. As *BARD* sponsored ~$1,000,000 in Arabidopsis research annually, this is potentially a large loss for the Israeli Arabidopsis community. There are as yet still no national funding initiatives specifically targeting Arabidopsis functional genomics.

A possible positive change in the general acceptance of Arabidopsis as a model for basic science was seen in the recent FISEB (Federation of Israeli Societies of Experimental Biology) congress. While Arabidopsis talks at this large congress (>1000 participants) were in the past placed in plant-specific sessions, Arabidopsis and other plant talks this year were integrated within the main sessions.

In 2007, ~40 research articles employing Arabidopsis were published from groups in Israel. The major centers of Arabidopsis research are in The Hebrew University of Jerusalem, Tel Aviv University and the Weizmann Institute of Science.

At least two recent papers are worth highlighting. Both deal with modulation of metabolic networks - one using Arabidopsis as a model for basic science, and one using an Arabidopsis gene for biotechnological purposes in petunia flowers.

The laboratory of Asaph Aharoni at the Weizmann Institute reported the discovery of a post-transcriptional mechanism in plants that uses a riboswitch to control a metabolic feedback loop. that results in differential RNA processing (Bocobza et al., 2007, G A possible positive change in the general acceptance of Arabidopsis as a model for basic science was seen in the recent FISEB (Federation of Israeli Societies of Experimental Biology) congress. While Arabidopsis talks at this large congress (>1000 participants) were in the past placed in plant-specific sessions, Arabidopsis and other plant talks this year were integrated within the main sessions.

- Genes Dev 21: 2874-9). In this loop, the riboswitch, located in the metabolite biosynthesis genes, directly senses the metabolite itself, which thus leads to the formation of an unstable splicing product, down-regulating the levels of the metabolite. This study paves the way for future engineering of plant riboswitches in metabolic engineering, as riboswitches transformed in plants can act autonomously to modulate gene expression.
- The laboratory of Sasha Veinshtein at the Hebrew University recently published a report where they showed that expression of a specific Arabidopsis Myb transcription factor, *Pap1*, in petunia flowers led to a large increase in volatile compounds (Zvi et al., 2008, Plant Biotechnol J). The volatile profile could then be modified by applying phenylalanine to the flowers. This opens up new options for the biotechnological modulation of scent production.

Major funding sources

- Israel Science Foundation (ISF), Jerusalem, israkeren@isf.org.il, www.isf.org.il/ Total *Arabidopsis* funding 2006 - $842,750
- The United States - Israel Binational Agricultural Research and Development Fund (BARD), Bet Dagon, bard@bard-isus.com, www.bard-isus.com/ Total *Arabidopsis* funding 2006 - $910,666
- German – Israeli Foundation for Scientific Research and Development (GIF), Jerusalem, gif-info@gif.org.il, www.gifres.org.il/ Total *Arabidopsis* funding 2006 - $257,833
- U.S.-Israel Binational Science Foundation (BSF), Jerusalem, bsf@bsf.org.il, http://www.bsf.org.il Total *Arabidopsis* funding 2006 - $74,000
- Deutsch-Israelische Projektkooperation (DIP), Bonn, nadia.meyer@dlr.de, www.internationales-buero.de/de/819.php

Italy

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

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In the last few years, Italian research on Arabidopsis has widely spread over several new labs. As a consequence, new projects have been developed and new collaborations among different laboratories have been established.

Among the most relevant developing projects a study has been initiated on the effects of auxin in processes occurring late in stamen development, which contribute to a successful pollination at anthesis (Dr. M. Cardarelli- Institute of Molecular Biology and Pathology, National Research Council, Rome). Another project stems from Dr. Serino's previous research in Dr. Xing-Wang Deng's lab at Yale University and deals with the characterization of novel pathways regulated by CSN, an evolutionarily conserved multi-protein complex which has been shown to regulate specific proteasome-mediated protein degradation events. In particular, Dr. Serino and collaborators (University of Rome- La Sapienza) are interested in CSN-mediated regulation of AtPIC2, an F-box protein which is a putative component of an SCF (Skp1, Cullin, F-box)-type ubiquitin ligase complex.

Many ongoing projects have been carried out with the financial support of Italian and European fundings and benefit from the formation of new European networks and collaborations. A very important breakthrough came from one of these projects on shade avoidance response. Specifically, Dr. Ruberti and coworkers (Institute of Molecular Biology and Pathology, National Research Council, Rome) uncovered the existence of a previously unrecognized regulatory circuit underlying plant response to canopy shade, which involves both auxin and cytokinin. The rapid changes in auxin signalling induced by low R/FR which are crucial for the plant to enhance elongation growth are also essential to arrest leaf development. Strikingly, the role of auxin in leaf primordia is to induce cytokinin degradation through the action of AtCKX6, and therefore to inhibit leaf growth. The discovery of this novel regulatory circuit suggests the possibility that crop yield could be increased by reducing the expression of cytokinin oxidase genes in leaf organs. In fact, shade avoidance is second only to disease as a cause of crop-yield losses. (Carabelli M, Possenti M, Sessa G, Ciolfi A, Sassi M, Morelli G and Ruberti I (2007). Canopy shade causes a rapid and transient arrest in leaf development through auxin-induced cytokinin oxidase activity. Genes Dev 21 1863-1868).

Another relevant breakthrough came from Chiara Tonelli's lab (University of Milan) and concerns the functional analysis of *AtMYB60*, a transcriptional modulator of physiological responses in guard cells. This gene is specifically expressed in stomata, and its expression is negatively modulated during drought. A null mutation in *AtMYB60* results in the constitutive reduction of stomatal opening and in decreased wilting under water stress conditions. These data open new possibilities to improve crop survival and productivity during drought, and they have been patented by C.Tonelli and M.Galbiati ("Stomatal guard cell-specific* promoter;" patent n. MI 2004 A000363-PTC/EP2005/001883 (ID: n. 53)*; "Promoters for constituve expression of nucleic acids in stomata", patent n. MI 2007 A2418).

Major funding sources for Arabidopsis functional genomics

- Three ERA-NET Plant Genomics projects have been funded with the support of The Italian Ministery of University and Scientific Research (MIUR) as part of its institutional activities (http://www.miur.it): CISCODE (Cis-element conservation and divergence in plant reproductive development), Italian partners Dr. G.Morelli (INRAN, Rome) and L. Colombo (University of Milan); MULTI-STRESS, Italian partners Prof. P. Costantino (University of Rome, La Sapienza) and Dr. I. Ruberti (CNR, Rome); PROTEOSTRESS, Italian partner Prof. De Lorenzo (University of Rome, La Sapienza).
- The Ministry has also funded many national projects (PRIN 2006-2008).
- The UE Marie Curie Training Network is funding the projects: "Functional Genomics for Biogenesis of the Plant Cell Wall" (2005-2009), and "Transistor" (Trans-cis Regulatory Element regulating key switches in plant development).
- The Ministry of Agriculture, The Italian Space Agency (www.asi.it), The European Space Agency (www.esa.int/esaCP/index.html), The Institute Pasteur- Cenci Bolognetti (www.pasteur.fr/pasteur/international/Dai_en/lines.html)

Japan

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

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RIKEN Plant Science Center
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In Japan, ongoing programs for *Arabidopsis* functional genomics are mainly found at RIKEN (www.riken.go.jp/engn/index.html), Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html) and **National Institute of Advanced Industrial Science and Technology (AIST)** (http://unit.aist.go.jp/rigb/gf-gre/index.html).

1. Metabolomics study on Arabidopsis is carried out in several laboratories, being RIKEN Plant Science Center (Kazuki Saito) and Kazusa DNA Research Institute (Daisuke Shibata) as the major contributors. The projects supported by Japan Science and Technology, JST, are conducted to investigate metabolic regulation of plants. Several databases for Arabidopsis metabolomics research are available.

- PRIMe; The Metabolomics database at the PSC (http://prime.psc.riken.jp/)
- KNApSacK (http://kanaya.aist-nara.ac.jp/KNApSAcK/)
- KaPPA-View (http://kpv.kazusa.or.jp/kappa-view/)
- MassBank (http://www.massbank.jp/index.html?lang=en)

2. **Integrated Database Project:** By the support of the Integrated Database Project (2006-2010) by the Ministry of Education, Culture, Sports, Science and Technology: A RIKEN and Kazusa collaborative effort to integrate with databases for Arabidopsis 'omics research information and comparative genome DB among plants (with Lotus japonicus, Eucalyptus, Tomato etc.) has been established.

3. **RIKEN** groups include the Plant Science Center (PSC), the BioResource Center (BRC) and Bioinformatics And Systems Engineering division (BASE). The RIKEN PSC (http://pfgweb.gsc.riken.go.jp/index.html) have been carrying out the following projects;

(1) A collection of full-length cDNAs (RAFL clones, Motoaki Seki), (2) Phenotype analysis of *Ds*-tagged lines (Takashi Kuromori), and Arabidopsis and rice Full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (Minami Matsui), (3) Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori), (4) Collection of Ds- or T-DNA tagged mutants for nuclear–encoded chloroplast protein genes, (5) Collection of *Thellungiella halophila* full-length cDNAs in collaboration with a group at Tokyo University of Agriculture (Teruaki Taji), (6) Rice FOX Arabidopsis Mutant Database (http://ricefox.psc.riken.jp/) (Minami Matsui, Tetsuya Sakurai). PSC is now collecting a large-scale data of transcriptome and metabolome (Yukihisa Shimada and Kazuki Saito), to develop the integrated database (www.arabidopsis.org/info/expression/ATGenExpress.jsp)..

The RIKEN BRC is supported by the National Bioresource Project and distributes plant materials developed in Japan. More than 27,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines have been provided to approximately 1,080 laboratories located in 36 countries. Homozygous seeds of Ds-tagged mutants are prepared and publicly available for approximately 1,800 lines now. Masatomo Kobayashi (kobayasi@rtc.riken.jp) is in charge of distributing *Arabidopsis* resources at the BRC (www.brc.riken.jp/lab/epd/Eng/).

RIKEN Bioinformatics And Systems Engineering division (BASE) (PI: Tetsuro Toyoda) (http://www.base.riken.jp/)

(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 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**

(1) *Arabidopsis* T87 cultured cells have been transformed with RAFL cDNAs and other cDNAs for metabolic profiling of primary and secondary metabolites (Daisuke Shibata).

(2) An open genome annotation system "KazusaAnnotation" (http://a.kazusa.or.jp/) is being constructed, with the aim of improving genome annotation for plants and plant-related microorganisms.

5. **National Institute of Advanced Industrial Science and Technology (AIST)**

The Gene Regulation Research Group in AIST (Masaru Ohme-Takagi; http://unit.aist.go.jp/rigb/gf-gre/

index.html) developed a novel gene silencing system using dominant repressors (CRES-T system) and is systematically analyzing function of transcription factors in *Arabidopsis* and identifying factors that would be useful for improvement of plant traits by preparing a chimeric repressor transgenic plants library.

6. Other *Arabidopsis* functional genomics activities

Several groups at other centers and universities are also involved in *Arabidopsis* functional genomics.

- A database on metabolites, KNApSacK, is available from NAIST (Shigehiko Kanaya).
- A database on plant promoters, ppdb (http://ppdb.gene.nagoya-u.ac.jp) is available from Nagoya University (Yoshiharu Y Yamamoto and Junichi Obokata)

In 2007, a new 6-year research program on plant molecular, cellular, and developmental biology supported by a Grant-in-Aid for Scientific Research on Priority Areas from MEXT (program leader: Yasunori Machida, Nagoya University) was started. The program consists of about 40 projects including 14 core projects (13 of which are mainly on Arabidopsis) from 10 research institutes. It focuses on such topics as mechanism of meristem formation and organ formation, cell proliferation and differentiation during organogenesis, regulation of meristem function by local and long-distance signaling, genetic and epigenetic regulation, and search for novel signals and their receptors.

Arabidopsis genomics tools and resources being developed, where they are deposited, and how the community can access them:

- RIKEN Plant Science Center (www.psc.riken.go.jp/indexE.html)
- Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html)
- RIKEN BioResource Center (www.brc.riken.jp/lab/epd/Eng/)
- RIKEN Bioinformatics And Systems Engineering division (BASE) (http://www.base.riken.jp/)
- KaPPA-View (http://kpv.kazusa.or.jp/kappa-view/)
- KazusaAnnotation (http://a.kazusa.or.jp/))
- KNApSacK (http://kanaya.aist-nara.ac.jp/KNApSAcK/)
- PRIMe; The Metabolomics database at the PSC (http://prime.psc.riken.jp/)
- AtGenExpressJAPAN (http://pfg.psc.riken.jp/AtGenExpress/index.html)
- ATTED (http://www.atted.bio.titech.ac.jp/),
- RIKEN Arabidopsis Genome Encychclopedia RARGE (http://rarge.psc.riken.jp/)
- Phenome analysis of Ds transposon tagging line (http://rarge.gsc.riken.jp/phenome/)

Major funding sources for Arabidopsis functional genomics:

- CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
- Program of Promotion of Basic Research Activities for Innovative Biosciences (www.brain.go.jp/welcome-e.html)
- NEDO (www.nedo.go.jp/english/activities/1_sangyo/1/pro-sangi2e.html)
- Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT) (www.jsps.go.jp/english/e-grants/grants.html)

The Netherlands

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

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2008 Highlights for The Netherlands

In the extension of the Dutch Genomics Programme CBSG2 that was awarded in 2007, Arabidopsis research is again an essential ingredient. This provides additional resources to the Arabidopsis community in The Netherlands.

Marcel Dicke received the prestigious SPINOZA prize among others for his combination of a molecular genetic approach with an ecological approach in which Arabidopsis is used as a model for other brassicaceous plants. In recent work from his lab, a 70-mer Arabidopsis oligo array was successfully used to determine global transcriptional changes in Brassica oleracea in response to insect feeding.

For the identification of binding sites of the floral organ identity transcription factors SEP3 and AP1, Gerco Angenent's group performed Chromatin Immunopreciptation (ChIP) combined with deep sequencing. These ChIP-seq experiments yielded large numbers of binding sites for both proteins. The majority of the binding sites contain the consensus CArG binding site for MADS box transcription factors. The overlap in binding sites represents putative targets of the SEP3-AP1 dimer, controlling sepal and petal formation.

The Research prize of Wageningen University (Best publication of the university in the past 4 years) was awarded in 2007 to an Arabidopsis paper by Keurentjes et al. in Nature Genetics describing a global analysis of QTL for metabolites using natural variation.

Ben Scheres' group published two papers in the same September 2007 issue of Nature, one of them presenting evidence for the existence of a transcription factor gradient with dosage-dependent output and the other establishing a new framework for computational analysis of hormone transport in growing tissues.

Together with Remko Offringa from Leiden University and collegues from Austria, Germany and the US, Dolf Weijers of Wageningen University published in the September 2007 issue of Cell evidence that reversible phosphorylation controls polar sorting of PIN proteins.

Guido van den Ackerveken's PhD student Mireille Van Damme won the Leverhulme Trust Technology Transfer Award 2007 (70,000 euros) which awards particularly successful technology transfers between universities and private companies.

Major funding sources for Arabidopsis functional genomics:

- Netherlands Organization for Scientific Research (www.nwo.nl)
- The Netherlands Genomics Initiative (www.genomics.nl)
- The Netherlands Plant Genomics Network (www.cbsg.nl)
- Foundation for Technology funded by Ministries of Economic Affairs and Education (www.stw.nl)
- ERA-PG: 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

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

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Norway

The Norwegian Plant Functional Genomics Program (NARC, http://www.narc.no/) is 1 of 10 genomics technology platforms forming the national functional genomics program (FUGE). The plant platform includes service activities within transcriptional profiling, bioinformatics, genotyping and clone collection, *in situ* hybridization and yeast two-hybrid screening. Most of the activity involves *Arabidopsis thaliana*, and systems biology is an important topic in the FUGE II program (2008-2012), which has support for plant research. A small grant has been provided to keep the NARC microarray service going. In addition, four plant projects were granted. Overall, less money will be provided for plant science service activity and more money for plant science projects in FUGE II. More information at: www.forskningsradet.no/servlet/Satellite?cid=1088005968933&pagename=fuge%2FPage%2FHovedSideEng. A plant science initiative has started in Norway in 2007 with the goal to organize a joint Norwegian plant science program as a part of the Norwegian Research Council. Practically all organizations having plant science activity support this initiative. The report from this initiative is at present being evaluated by the national biology board and other authorities. In 2007, the 6th Norwegian Arabidopsis meeting was held at UIS in Stavanger. There will be a 7th Arabidopsis meeting in 2008 in Tromsø (UIT). Norway is a partner of the EU Plant Genomics network ERA-PG.

Finland

The 16th Congress of the of the Federation of European Societies of Plant Biology (FESPB) will be held in Tampere, Finland in August 2008 (www.fespb2008.org/) The Congress is organized by SPPS (www.spps.dk), the Scandinavian Plant Physiology Society, an international society that promotes experimental plant biology. The chairman of the organizing committee is MASC representative Jaakko Kangasjärvi. Researchers studying Arabidopsis are highly represented in the program. Finland is a member in the European plant functional genomics network ERA-PG.

Sweden

The Umeå Plant Science Center (UPSC (www.upsc.se/)) is a center of experimental plant biology in Umeå. UPSC groups have also received National Center of Excellence status and funding for functional genomics. Their activities are mainly concentrated in trees (hybrid poplar). However, Arabidopsis functional genomics is heavily utilized for the determination of the function of poplar genes. The UPSC is also a partner in the European Complete Arabidopsis Transcriptome MicroArray (CATMA) project, www.catma.org/.

Denmark

In Denmark, a number of groups at the University of Copenhagen, Aarhus University, and Aalborg University work on Arabidopsis. The research, which in most cases is funded by the national research councils, involves studies of several aspects of plant life. The activities are coordinated through the Plant Biotech Denmark-network (www.plant-biotech.dk).

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 or by request to narc@bio.ntnu.no .
- University of Oslo: *in situ* hybridization and yeast-two-hybrid analyses (www.imbv.uio.no/gen/groups/narc/)
- UMB: *Arabidospsis* transformation, T-DNA genotyping, seed collection: (www.umb.no/?viewID=2552)

Arabidopsis Funding Sources

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

United Kingdom

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

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GARNet

GARNet, the Genomic Arabidopsis Resource Network was established in 2000 to provide public functional genomics resources, which now operate through "user pays" cost recovery. Coordination activities are funded for 2005-2009, to provide an information resource (http://garnet.arabidopsis.info/, newsletter, annual meeting) and point of contact for other UK research communities and international genomics programmes. Plant systems biology and translational research are now important parts of GARNet's activities.

New Funding Programmes in the UK during 2007

The Biotechnology and Biological Science Research Council, BBSRC, is the major funding agency for Arabidopsis Research. In 2007 the following funding schemes were open to Arabidopsis Researchers.

- Systems Approaches to Biological Research (SABR)

  The BBSRC previously funded 6 centres in Systems Biology, spread across the UK (http://www.bbsrc.ac.uk/organisation/institutes/systems_biology_centres.html). The SABR initiative with a budget of £25.8M aimed to promote further uptake of systems biology amongst research groups in the UK. Of 6 projects funded 3 involved Arabidopsis Research.

  1. Regulation of Biological Signalling by Temperature (ROBuST) – Universities of Edinburgh, Liverpool, Warwick and York. Lead PI, Dr. Karen Halliday - University of Edinburgh
  2. Elucidating Signalling Networks in Plant Stress Reponses – Universities of Warwick, Essex and Exeter. Lead PI, Prof. Jim Beynon – University of Warwick
  3. A multi scale approach to genes, growth and geometry – John Innes Centre and the University of East Anglia. Lead PI Prof. Enrico Coen - John Innes Centre

- ANR-BBSRC Systems Biology Collaborations

  This joint call between the Agence Nationale de la Recherche (ANR) France and the BBSRC was set up to support high quality research in systems biology between France and the UK. It aimed to facilitate the development of systems biology research both nationally and in Europe by encouraging a wide community to become involved in Systems Biology. 10 consortia were funded via this scheme including 3 that involve Arabidopsis/Plant research.

- Networks in Synthetic Biology

  This scheme was launched in 2007 to develop and establish communication and networking between researchers in the biosciences, engineering and the physical sciences in the area of synthetic biology, with associated input from the social sciences and humanities. 7 Networks in Synthetic Biology will be funded via this scheme, representing a total budget of £1M from BBSRC, EPSRC, AHRC and ESRC.

- European Research Area for Plant Genomics (ERA-PG)

  After a successful first call, that funded 29 projects across Europe, ERA-PG launched it is 2nd call for projects at the end of 2007: "Strengthening the European Research Area in Plant Genomics – integrating new technologies in plant science". http://www.erapg.org/everyone. Like the first call, applications for this round of ERA-PG must consists of research groups from 3 or more countries taking part in the call (Austria, Belgium, Finland, Germany, Israel, The Netherlands, Portugal, UK and Canada).

- Crop Science Initiative

  During 2007 the BBSRC put £13M into funding 18 research projects that aim to translate the excellent basic plant science base in the UK, into practical applications that will benefit farmers and consumers. Problems being tackled include:- improving willow biomass yields for bioenergy by transferring our current knowledge of shoot branching in Arabidopsis to willow.

- Sustainable Agriculture Research for International Development (SARID)

  In collaboration with the DFID, this initiative supports high-quality basic and strategic biological and biotechnological research in crop science and sustainable agriculture, which will establish productive partnerships between scientists in the UK and developing countries.

Noteworthy breakthroughs by UK researchers in 2007

- Control of plant organ size by KLUH/CYP78A5-dependent intercellular signaling.

  Anastasiou E, Kenz S, Gerstung M, MacLean D, Timmer J, Fleck C, Lenhard M, Dev Cell 2007 Dec 13(6):843-56

  UK researchers have discovered how plants control the size of organ such as leaves and flowers. Cells at the margin of an organ secrete a non-cell autonomous mobile growth signal (plant specific cytochrome P450) that keeps the cells throughout that organ dividing and thus growing larger. However, since the growth signal is only produced by the margins, the concentration within the organ reduces as the organs grows and once it has dropped below a critical threshold the organ stops growing. Interestingly this growth signal does not appear to influence the classical phytohormones, suggesting that there are still growth-promoting substances to be discovered in plants.

  Animals also use a similar 'dilution' principle to control size e.g a fly's wing; indicating that a common mechanism for size measurement has evolved in plants and animals.

- Light-quality regulation of freezing tolerance in *Arabidopsis thaliana*

  Franklin KA and Whitelan GC, Nat Genet. 2007 Nov;39(11):1410-3.

  Unlike animals, plants are not able to control their core temperature, yet they are require to cope with large temperature fluctuations. So how to plants deal with such changes in their environment? Recent work in the UK has shown that the two separate pathways, regulating light perception and temperature sensing, work together to protect plants against freezing temperatures. On their own either low temperatures or low light levels are not enough to induce the cold acclimation pathway but the combination of the two prevents plants from freezing. Such a mechanism is likely to help plants predict the oncoming winter during the autumn and help them to prepare for colder temperatures.

- Step-by-step acquisition of the gibberellin-DELLA growth-regulatory mechanism during land-plant evolution

  Yasumura Y, Crumpton-Taylor M, Fuentes S, Harberd NP, Curr Biol. 2007 Jul 17;17(14):1225-30.

  In this paper a team of UK scientists illustrates how plants have evolved the ability to adapt to changes in climate and environment. Higher plants are known to use the gibberellin signalling pathway to promote growth and take advantage of favorable conditions or repress growth in unfavorable conditions. Researchers show how this mechanism has involved in a series of steps that are associated with the key stages of flowering plant evolution.

- An ancient mechanism controls the development of cells with a rooting function in land plants.

  Menand B, Yi K, Jouannic S, Hoffmann L, Ryan E, Linstead P, Schaefer DG, Dolan L, Science. 2007 Jun 8;316(5830):1477-80

  Land invasion by plants is significant step in evolution, which fundamentally changed the earth's ecosystem forever. Ancient plants such as moss exist with just one pair of chromosomes for the majority of their life cycle and don't have roots but instead grow cells such as rhizoids for anchorage. Whilst in higher plants the diploid phase dominates and roots are used to anchor the plant and absorb nutrients. In this paper UK researchers have discovered that the mechanism that controls the developmental of root hairs in Arabidopsis also controls the development of tip-growing cells with a rooting function in moss. This work would indicate the diversification of the body plan of plants for land colonization was dependent on the switch to a sporophyte dominant life cycle and recruitment of genes from the haploid to diploid phase.

- Pseudomonas syringae pv. tomato hijacks the Arabidopsis abscisic acid signalling pathway to cause disease.

  Torres-Zabala M, Truman W, Bennett MH, Lafforgue G, Mansfield JW, Rodriguez Egea P, Bögre L, Grant M., EMBO J. 2007 Mar 7;26(5):1434-43.

  Plant pathogens must manipulate their host to produce an environment conducive to their replication and dissemination. To do this many bacteria produce proteins, known as effectors that are targeted to the host cytoplasm. In this paper UK researchers have shown that the effectors of *Pseudomonas syringae* induced genes involved in the biosynthesis of and response to the plant hormone abscisic acid (ABA). They showed that in a successful colonization of a plant by the bacteria the levels of ABA rose. They also demonstrated that adding ABA increased host plant susceptibility whereas a mutant that disrupted the ABA synthetic pathway increased host resistance to the bacteria. These important data demonstrate that pathogens manipulate host hormonal balance to favour their growth and that specific pathogen effector proteins have evolved to exploit this route to suppress host defence mechanisms.

Relevant Meetings 2007

- GARNet 2007 - John Innes Centre Norwich.

  The aim of the annual GARNet meeting is to inform the UK Plant community of new advances, ideas and initiatives (http://www.sebiology.org/meetings/Notts08/Plant.html)

- Mathematics in Plant Science Study Group – University of Nottingham

  In collaboration with the Centre for Plant Integrative Biology (CPIB) GARNet hosted the inaugural Mathematics in Plant Science Study Group. This workshop brought together theoreticians and researchers to tackle 5 problems in plant science (http://cpib.info/workshop.shtml)

- Society of Experimental Biology – Annual Meeting

  This is an international conference comprising of high quality science, networking and education sessions, and techniques workshops (http://www.sebiology.org/meetings/index.php)

UK Funding Bodies

In addition to the BBSRC (http://www.bbsrc.ac.uk/), other relevant funding bodies include

- NERC (Natural Environmental Research Council) http://www.nerc.ac.uk/
- DEFRA (Department for Environment Food and Rural Affairs) http://www.defra.gov.uk/
- SEERAD (Scottish Executive Environment and Rural Affairs) http://www.scotland.gov.uk/topics/agriculture
- The Royal Society http://royalsociety.org/

United States

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

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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 early 2007 to develop a new vision to propel forward the next decade of Arabidopsis research in the US. In January of 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.

Participants felt that focusing on Arabidopsis has proven to be highly effective in facilitating numerous breakthroughs and advances in plant biology in a relatively short time. Evaluation of the AT2010 project thus far described several major accomplishments including the development of a large pool of genetic and genomic resources, the demonstration that rapid and groundbreaking achievements can be made using a reference plant system, and the growth of a vibrant research community. In particular, participants noted that over the last two decades, Arabidopsis has nucleated an energetic group of researchers drawing from a wide variety of disciplines, including significant international collaboration. The ability to develop theories and rapidly test them in Arabidopsis was seen as a major strength and it was noted that Arabidopsis may be unique for its capacity to enable investigation from the molecular to the ecosystem level. Recommendations and findings from the workshop will be presented at the MASC annual meeting during the 19th Arabidopsis Conference in July 2008. A summary report can be found on the MASC website: http://www.arabidopsis.org/portals/masc/workshop2020.pdf

New Plant Science Cyberinfrastructure Collaborative (PSCIC)

The PSCIC, also known as the iPlant Collaborative (iPC) is a major new NSF-funded project that began in spring 2008. The iPC is centered at the University of Arizona with several additional partner institutions and is funded at the level of 50 million USD for 5 years, with the possibility of a second 5 year funding period. The project goal is to develop a cyberinfrastructure collaborative for the plant sciences that would enable new conceptual advances through integrative, computational thinking. Importantly, the iPC intends to be fluid and dynamic and community-driven. The project encompasses all of the plant sciences. Arabidopsis, with its advanced resources, datasets and extensive research community, is expected to play an integral part. The project's opening conference, held in April, included over 400 participants, including approximately 100 via direct, live participation webcast. The conference included presentations by iPC members, computational and plant scientists, and education experts, as well as a number of smaller, focused discussion sessions. All presentations from the conference are available for public viewing at the iPC website: http://iplantcollaborative.org/home.

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. The definition of a 'Grand Challenge' (GC) is an evolving concept but several ideas from the discussion groups include that GCs should have a compelling solution, have a well defined measure for success, give some predictive power, be both visionary and realistic, be compelling to the general public, and motivate and include many different types of researchers. GCs will be proposed by the community and selected by the iPC Board of Directors. The iPC will not directly fund data collection or researchers but is funded to develop the cyberinfrastructure that successfully approved GC proposals require. International collaboration is encouraged but compensation is limited to expenses. In the first year, in addition to GC proposals, the iPC will consider proposals to develop 'foundational tools' which have obvious benefit to the plant biology community and potentially to one or more future GCs. The iPC expects to begin reviewing workshop proposals as early as June 1, 2008 (for up to 6 workshops a year) and anticipates two rounds of reviews annually. Broader impacts of the iPC project are expected to extend beyond simply addressing grand challenge questions on a scientific level as the iPC will involve extensive community building and educational outreach.

Textpresso Scientific Literature Text Mining System for Arabidopsis

Textpresso is a text-mining system for scientific literature (http://www.textpresso.org). Its two major elements are (1) access to full text, so that entire articles can be searched, and (2) introduction of categories of biological concepts and classes that relate two objects (e.g., association, regulation, etc.) or describe one (e.g., biological process, etc). A search engine enables the user to search for one or a combination of these categories and/or keywords within an entire literature. The system was initially developed as part of Wormbase for *C. elegans* but more recently has been extended to additional organisms including Arabidopsis, which now has its own site (www.textpresso.org/arabidopsis). TAIR was heavily involved in developing the Arabidopsis Textpresso system; most of the Arabidopsis scientific literature comes from TAIR which sent around 15,000 in-house articles. In addition, TAIR provided the Arabidopsis vocabularies and categories. Currently, Textpresso for Arabidopsis contains information on these data types (data counts in parentheses): abstract (25,877), body (15,276), title (26,834), totaling 67,987 entries.

The system allows users to perform targeted searches of Arabidopsis literature, for example, using gene names, GO terms, or a combination of search terms. The results page lists literature citations containing the search query specified and the entire set can be downloaded into Endnote, or displayed for printing or in xml format. Although the system does not provide the full text of articles it does provide abstracts, and perhaps most useful, displays several sentences from each article that contain the search term(s). This quickly reveals the context of search terms which can help users determine the usefulness of the reference. Gene names or other entities mentioned only in the supplementary materials will not be retrieved because these documents are not currently included in the set of documents indexed and searched by Textpresso. Reference: *Textpresso: an ontology-based information retrieval and extraction system for biological literature* ; Müller HM, Kenny EE, Sternberg PW (2004) Textpresso: An Ontology-Based Information Retrieval and Extraction System for Biological Literature. PLoS Biol 2(11): e309

AT2010 Project

The National Science Foundation (NSF)-sponsored 2010 project aims to determine a function for all genes in *Arabidopsis thaliana* by the year 2010. Since its inception the project has funded proposals in two main areas: proposals that address gene function directly and proposals that develop enabling tools and resources for functional genomics research. Since the first awards were granted in 2001, approximately $185 million has been allocated for 135 awards encompassing 111 diverse projects, ranging from studies of gene families, development of research tools, analysis of natural variation, transcriptomics, widely-used reverse genetics resources such as sequence-indexed insertion lines, and many others. In 2007, NSF committed approximately $18 million for 16 awards spanning 12 projects. Project descriptions and funding levels can be found at the NSF AT2010 award page: www.nsf.gov/bio/pubs/awards/2010awards.htm.

This year, as in 2007, the Program will focus on (1) research on exemplary networks using high throughput methods and integrating modeling with experimental data to understand the gene circuitry underlying basic plant processes; (2) projects that will develop experimental and computational methods, tools, and resources for enabling a broad community of scientists to conduct functional genomics research on Arabidopsis; and (3) projects to perform genome-wide analyses of the gene function. Changed for 2008 is that the project will be an NSF-only activity, proposals will not be jointly reviewed by the German Arabidopsis Functional Genomics Network Program. International collaboration is still encouraged.

The abundance of knowledge, and especially, community resources, generated so far by the 2010 project have helped facilitate rapid advances in elucidating the function of many Arabidopsis genes. It is clear that cooperation and collaboration were key factors in the past success of the Arabidopsis Genome Project, and for the success of the current 2010 Project and other large-scale international Arabidopsis functional genomics projects. To maximize the return from such efforts, future projects must similarly be integrated and coordinated. It is also critical that funding levels are maintained.

NAASC and the 18th and 19th International Conferences on Arabidopsis Research

The eight member North American Arabidopsis Steering Committee (NAASC, www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp) is composed primarily of US 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. Mark Estelle (Indiana University) and Jane Glazebrook (University of Minnesota) were recently elected to serve a four year NAASC term starting this July. Judith Bender and Xing Wang Deng conclude their term at the 2008 International Conference on Arabidopsis Research (ICAR). Additional continuing committee members include Xuemei Chen, Joe Kieber, Julian Schroeder, Caren Chang, George Haughn, and Scott Poethig.

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. Since 1995 the meeting had been in the US approximately 2 of every 3 years. In 2005 the NAASC changed the format of North American meetings to include sites to alternate with the usual location in Madison, Wisconsin. At the annual MASC meeting held during the 2007 ICAR in Beijing, the MASC adopted a 3 year conference site rotation: North America, Europe, and Asia/Pacific Rim.

The 18th ICAR, held in 2007 in Beijing, marked the first time the meeting took place in an Asian country and nearly 1500 attendees participated. NAASC member/MASC co-Chair Xing Wang Deng was the lead scientific organizer for the conference. Building upon increasingly global research efforts, the 19th Conference will mark another milestone: in 2008, the 19th ICAR will be held in Montreal, Canada, the first time the ICAR has come to Canada. The conference organizing

committee is chaired by NAASC members Joe Kieber and Xuemei Chen, and includes local researchers at McGill University as well as other NAASC members. Joanna Friesner, the MASC Coordinator from UC Davis, provided overall organization of each conference held between 2006-2008. The 2009 ICAR will be held in Edinburgh, Scotland, with lead organization provided by GARNet in the UK and assistance from the MASC Coordinator. The ICAR is expected to be held in Asia in 2010 and to return to the US in 2011.

TAIR/Plant Physiology Collaboration: A unique partnership has been formed between the journal Plant Physiology and TAIR to ensure that Arabidopsis gene function data published in the Journal are reliably captured in TAIR's database. This collaboration provides a mechanism for authors to submit Arabidopsis gene function information to TAIR as part of the publication process. It is anticipated that similar collaborations with additional journals will be established in the future.

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 10 graduate students. The program will continue until the end of May, 2009. More information on the US program: www.arabidopsis.org/portals/masc/NSF_Arabidopsis_research_program.pdf

Grant information: www.nsf.gov/awardsearch/showAward.do?AwardNumber=0529918_

More information on the German program: www.uni-tuebingen.de/plantphys/AFGN/yrep.htm

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The 2008 MASC report, and previous reports, are available online at:

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

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

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