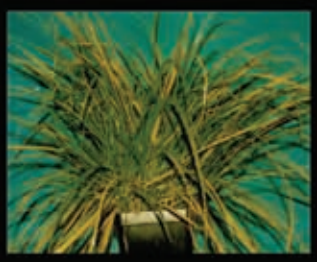
# The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

## Annual Report 2007

Applying *Arabidopsis*

*AtAP1 citrus flower*

*AtAP1 citrus fruit*



*Wildtype F. pratensis*

*Staygreen F. pratensis*

*Arabidopsis thaliana*

*Biosensor plants*

*Standard Canola*

*Anti-AtERA1 Canola*

*AtPHYB potato*

*Standard potato*

The Multinational *Arabidopsis* Steering Committee June 2007

# The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

# Annual Report 2007

**Ian Small** iansmall@cyllene.uwa.edu.au
Chair

**Xing Wang Deng** xingwang.deng@yale.edu
Co-chair

**Thomas Altmann** altmann@mpimp-golm.mpg.de
**Sacha Baginsky** Sacha.baginsky@ipw.biol.ethz.ch
**Ruth Bastow** ruth@arabidopsis.info
**Philip Benfey** philip.benfey@duke.edu
**David Bouchez** bouchez@versailles.inra.fr
**Jorge Casal** casal@ifeva.edu.ar
**Danny Chamovitz** dannyc@ex.tau.ac.il
**Bill Crosby** bcrosby@uwindsor.ca
**Ian Graham** iag1@york.ac.uk
**Klaus Harter** klaus.harter@zmbp.uni-tuebingen.de
**Marie-Theres Hauser** marie-theres.hauser@boku.ac.at
**Pierre Hilson** pierre.hilson@psb.ugent.be
**Eva Huala** huala@acoma.stanford.edu
**Jaakko Kangasjärvi** jaakko.kangasjarvi@helsinki.fi
**Sean May** sean@arabidopsis.info
**Peter McCourt** mccourt@botany.utoronto.ca
**Harvey Millar** hmillar@cyllene.uwa.edu.au
**Tom Mitchell-Olds** tmo1@duke.edu
**Ortrun Mittelsten- Scheid** ortrun.mittelsten_scheid@gmi.oeaw.ac.at
**Basil Nikolau** dimmas@iastate.edu
**Javier Paz-Ares** jpazares@cnb.uam.es
**Barry Pogson** barry.pogson@anu.edu.au
**Ben Scheres** b.scheres@uu.nl
**Randy Scholl** Scholl.1@osu.edu
**Heiko Schoof** schoof@mpiz-koeln.mpg.de
**Kazuo Shinozaki** sinozaki@rtc.riken.go.jp
**Willem Stiekema** willem.stiekema@cbsg.nl
**Chris Town** cdtown@tigr.org
**Klaas van Wijk** kv35@cornell.edu
**Paola Vittorioso** paola.vittorioso@uniroma1.it
**Wolfram Weckwerth** weckwerth@mpimp-golm.mpg.de
**Weicai Yang** wcyang@genetics.ac.cn

**Joanna Friesner** jdfriesner@ucdavis.edu
Coordinator and Executive Secretary

The Multinational *Arabidopsis* Steering Committee—June 2007

**Cover Photos:** A showcase of images exemplifying research that translates knowledge derived from basic *Arabidopsis* studies into real-world applications.

**Cover Design:** Joanna Friesner, MASC Coordinator, University of California, Davis, USA

**Center image:** *Arabidopsis thaliana* wild-type plant, *Cvi-0* (Cape Verde Islands) accession. Photo courtesy of the *Arabidopsis* Biological Resource Center (ABRC), Ohio State University, USA.

**Upper right images:** Drought-resistant Canola (*Brassica napus*)—the plant in the right image carries a construct (functional in Canola) that downregulates the *Arabidopsis ERA1* gene resulting in reduced water loss under drought conditions. The plant in the left image lacks the *Arabidopsis* construct and is more sensitive to drought stress. (See page 20). Photos courtesy of Yafan Huang, Performance Plants Inc., Queen's University, ON, Canada.

**Lower right images:** *AtPHYB* and standard potato plants—ectopic expression of the *Arabidopsis PHYB* gene in transgenic potato plants alleviates some of the negative growth responses caused by crowded field conditions. Transgenic *AtPHYB* potatoes had increased branching, higher rates of photosynthesis and higher overall yields when compared to non-transgenic plants. Left image: non-transgenic potato; Right image: *AtPHYB* expressing potato. (See page 23). Photos courtesy of Hernán Boccalandro, IFEVA, University of Buenos Aires, Argentina.

**Lower center:** Biosensor Plants—Nitrogenous compounds released from buried landmines are detected by transgenic *Arabidopsis* plants carrying a nitrogen-inducible construct which drives pigment production. This results in anthocyanin accumulation in leaf tissues producing dark purple-red plants when grown near buried landmines. The plants shown were grown in a landmine test-site; the plant on the right was grown at a distance from a buried landmine while the plant on the left was grown in close proximity to the landmine. (See page 21). Photo courtesy of Carsten Meier, Aresa Biodetection, Denmark.

**Lower left images:** Staygreen and wild-type grass—studies in *Arabidopsis* helped to pinpoint the gene underlying a naturally occurring grass mutation called *staygreen* (*sgr*). This knowledge will allow rapid breeding of new varieties of grass that are characterized by extended greenness. The left plant is wild-type at the *staygreen* locus and undergoes more rapid leaf senescence then the right plant which carries the *sgr* mutation. (See page 21). Photos courtesy of Howard Thomas and Paul Hilditch, IGER (Institute of Grassland and Environmental Research, United Kingdom)

**Upper left images:** Expression of *AtAP1* in citrus—the *APETALA1 (AP1)* gene from *Arabidopsis* is known to promote flowering initiation when expressed from a constitutive promoter. Ectopic expression of *AtAP1* in sweet orange accelerated the juvenile-to-adult transition allowing flower and fruit production to occur as early as one to three years rather than the typical 10-15 year timeframe for non-transgenic citrus plants. Left image: *AtAP1* citrus fruit; Right image: *AtAP1* citrus flower. (See page 22). Photos courtesy of Magdalena Cervera and Leandro Peña, Dpto. Protección Vegetal y Biotecnología, Instituto Valenciano de Investigaciones Agrarias (IVIA), Spain.

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# Foreword to the Report

This is the 2006/2007 annual report of the Multinational *Arabidopsis* Steering Committee (MASC) on the status of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. The primary goal of this 10-year program (initiated in 2001) is to determine a function for every *Arabidopsis* gene and thus begin to obtain a detailed and comprehensive understanding of a flowering plant. *Arabidopsis* 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 immediately apparent to most plant scientists and is easily justified by the huge strides forward in our understanding of basic plant science made since 2000. The intent has always been that the knowledge gained on this model organism 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.

Research on *Arabidopsis* (and most other closely studied organisms) can loosely be categorized into a series of phases, starting with genetic and physical mapping and progressing through genome sequencing, genome annotation, determination of gene function and, more recently, the study of networks formed by physical, genetic, metabolic or regulatory interactions between genes and proteins. These phases correlate very closely with steeply increasing amounts of data that need to be acquired and analyzed in order to reach meaningful conclusions. It is this predictable increase in the size and complexity of the 'big picture' that drove the creation of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project in 2001. Using the recently obtained genome sequence, researchers around the world were now equipped to investigate numerous facets of *Arabidopsis* biology at the molecular level. However, the scale and ambition of the project required a new focus on high-throughput technologies, novel experimental tools and comprehensive collections of plant resources. In addition, it was realized that the complexity of the task required much greater emphasis on data storage, analysis and visualization. To promote this revolution in research practices, the Multinational *Arabidopsis* Steering Committee, supported by a full-time staff member, was created and continuously evaluates the goals and needs of the research community. Via regular subcommittee meetings, national representatives and plenary meetings at annual International Conferences, it collects and weighs the opinions of the plant research community before making recommendations both to the scientists and the agencies that fund their research. It will have an important role to play over the next couple of years as the research community commences the essential 'phase-transition' beyond studies of the function of individual genes towards systems biology approaches applied to gene networks.

Establishing and maintaining world-wide collaboration is critical to the success of the project. Global resources need to be coordinated to maximize synergy and only sustained collaborations will enable the *Arabidopsis* community to achieve its ambitious goals. Since the start of the project, increasing numbers of countries have committed significant resources into coordinated efforts on *Arabidopsis* research. Following the US lead, first Germany then the UK (and later, other European countries) funded considerable efforts on *Arabidopsis*. More recently, Japan, China, Korea and now Australia have funded international-class collaborative efforts or research centers focusing on *Arabidopsis*. The Multinational *Arabidopsis* Steering Committee plays a key role in supporting this international coordination by collecting and disseminating information from the various initiatives and by promoting data exchange (via the development of standardized data formats and data exchange protocols). The high degree of friendly and effective international cooperation in the *Arabidopsis* research community is a major reason for its success and is extremely attractive to young scientists looking to develop new, exciting projects at the frontiers of current knowledge.

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.

**Research on *Arabidopsis* has provided most of the breakthroughs made in plant science over the last ten years and given the continuing rapid progress, will drive the major discoveries in plant science for the next ten. The resources and expertise are available to meet the goal of discovering a function for all the *Arabidopsis* genes of major significance within a reasonable timeframe. Given a high level of continuing support over several decades, the ultimate goal of obtaining a working understanding of how a flowering plant functions down to the molecular level is within sight. Such a working model would be of incalculable benefit to future generations of scientists, farmers, environmentalists and society at large.**

The Multinational *Arabidopsis* Steering Committee
June 2007

# Executive Summary

As the first plant to have its entire nuclear genome sequenced, *Arabidopsis thaliana* has become the most important model system for plant biology as well as an invaluable resource for the study of other multicellular organisms. Discoveries made using *Arabidopsis* are now driving many of the studies carried out in other plants including those of economic importance. The success of the multinational genome project and subsequent functional genomics projects are shaping similar efforts underway in other model plants such as rice, poplar, *Medicago truncatula* and the moss *Physcomitrella patens*. An increasingly comprehensive understanding of *Arabidopsis* biology encourages researchers from inside and outside the plant community to leverage *Arabidopsis* resources and data for comparative genomics and complex systems modeling.

The highly active and enthusiastic *Arabidopsis* community around the world continues to attract keen researchers; according to The *Arabidopsis* Information Resource (TAIR) there are currently about 16,000 *Arabidopsis* researchers in approximately 6,200 laboratories worldwide. The current high standards of collaboration and coordination across countries (particularly through timely sharing of data, stocks and other resources) must be maintained and further improved to meet the challenges ahead as the goals of *Arabidopsis* research become steadily more ambitious. At the same time, to justify future funding, care must be taken to maintain strong links to research on other organisms to clearly demonstrate the utility of *Arabidopsis thaliana* as the reference plant. The *Arabidopsis* community, despite its obvious success in advancing basic plant research, needs to remain aware that many funding agencies require proof of relevance to the everyday concerns of society.

## Highlights in *Arabidopsis* research

The past year has been a strong one for *Arabidopsis* research with a continuing increase in *Arabidopsis* publications including some notable breakthroughs. The hot areas in plant research at the moment are epigenetics and signaling, with *Arabidopsis* once again showing the way. Some highlights include:

- A global view of methylation patterns in *Arabidopsis* using high resolution whole genome tiling microarrays
- Transgenerational memory of stress in plants
- The crystal structure of the TIR1 auxin receptor
- Gene imprinting mechanisms in the plant embryo
- Cellulose synthesis guided by microtubules
- A high-throughput screen to improve fatty acid content

## Examples of applications arising from *Arabidopsis* research

Many patents worldwide acknowledge research on *Arabidopsis* but a widely-held myth is that few of these discoveries are ever turned into useful products. In reality, the time from discovery to application takes years and the pipeline is full of *Arabidopsis*-fueled discoveries heading for the marketplace. In this report we have chosen just a few examples of discoveries that have made it, to give a flavor of the different ways in which basic research in *Arabidopsis* can be translated into real-world applications.

## Major new initiatives announced this year

- AGRON-OMICS: European consortium of fourteen partners to develop a system-level approach to study leaf growth and development in *Arabidopsis*.
- UK: Three new centers specializing in systems biology have started up with a strong focus on *Arabidopsis*: The Centre for Plant Integrative Biology (Nottingham), the Centre for Systems Biology at Edinburgh and the Warwick Systems Biology Centre.
- US: NSF will fund the creation of a Plant Science Cyberinfrastructure Collaborative this year.
- Funding in Australia for a National Plant Phenomics Facility with areas specially designed for non-invasive measurements of *Arabidopsis* growth and function
- RIKEN Plant Science Center: A new Platform for the Analysis of the Metabolome and Hormonome

## Progress towards the goals of the Multinational Coordinated Functional Genomics Project

Since 2004, 'thermometer' illustrations have provided a visual way of tracking progress in gene function knowledge. Recent progress by the international community has allowed a more detailed picture of *Arabidopsis* resources and knowledge to emerge culminating in the expansion of the thermometers this year into two categories: Resources and Knowledge (see pages 16-19). These improvements reflect the increased specific knowledge generated by the community and are of vital importance to the continuing effort to track and fully describe a function for every *Arabidopsis* gene. The availability of high-quality genetic resources will facilitate future studies and contribute to our expanding pool of knowledge.

Biological Resources

- Availability of confirmed homozygous mutant plant lines for 6,388 genes, nearly triple the number from last year. As of May, seeds from 9,198 lines have been sent to

the *Arabidopsis* Biological Resource Center (ABRC) for preparation and distribution.

- Just over 93% of *Arabidopsis* genes (excluding pseudogenes) contain a sequenced insertion element.
- Availability of over 26,000 RNAi clones targeting at least 22,069 genes (including pseudogenes), or 21,671 genes (excluding pseudogenes); RNAi clones for 3,482 genes have been transformed into *Arabidopsis*.
- Isolation of full-length cDNAs for 20,338 of 27,589 genes; clones of 19,312 are currently being distributed.
- Availability of fully-sequenced ORF clones for 15,396 genes and partially-sequenced clones for 1,418 more.

Acquired knowledge of gene function

- 26,141 (nearly 95%) genes whose expression has been detected by cDNA, EST, MPSS, sage or microarray data.
- 2,637 genes experimentally determined to function in a known biological process.
- 3,944 genes for which the subcellular localization of the protein has been experimentally determined.
- 1,639 genes for which a molecular function of the protein has been experimentally determined.

## MASC subcommittees

The MASC subcommittees continue to actively promote international cooperation in a number of areas of functional genomics research. This year a new Systems Biology Subcommittee was formed which aims to facilitate the integration of *Arabidopsis* research at multiple levels as well as collaboration with other model systems.

- Bioinformatics—actively promoting and pursuing database integration via webservices workshops
- Clone-based functional genomics resources—many resources are now available, but the committee makes the point that funding has not been forthcoming so far to use these resources for genome-wide projects, limiting their impact
- Metabolomics—activity has focused on developing a set of minimum agreed standards for *Arabidopsis* research in line with the Metabolomics Standards Initiative recommendations.
- Natural Variation and Comparative Genomics—more effort is required to collect, store, distribute and analyze natural *Arabidopsis* genotypes. Forthcoming sequence data from the *A. thaliana* relatives *A. lyrata, Capsella rubella* and *Thellungiella halophila*, as well as data from Brassicas will be a big boost to comparative genomics studies.
- Phenomics—a number of new projects to isolate homozygous mutant plant lines will provide 'phenome-ready' resources, and artificial microRNAs complement this approach. It is expected that TAIR will transition to using the PO and PATO controlled vocabularies to describe phenotypes this year.
- Proteomics—databases (e.g. SUBA, ProMex) and tools for handling proteomics data have been developed and made accessible online. Work is ongoing to develop data format standards and a Proteomics subcommittee website aimed at integrating proteomics research worldwide is under development.
- Systems Biology—this new subcommittee is working to bring together *Arabidopsis* researchers interested in this new approach including the general *Arabidopsis* community and researchers of other model systems.

## Goals for the next year

- We need to start preparing now for the next 'phase' of *Arabidopsis* research after 2010. Internationally-organized workshops by MASC members in 2007-2008 will be devising the next 10 years of efforts and goals. To initiate this process a meeting will be held at the International *Arabidopsis* Conference in Beijing in June, 2007 to develop initial plans and coordinate future discussions. Input from the *Arabidopsis* community will be sought.
- Facilitate the work of the 'omics' subcommittees (Metabolomics, Proteomics, Phenomics) to develop and promote new data standards facilitating data sharing and analysis. It is imperative for future progress that researchers become as familiar and confident handling these types of data as they have become with transcript data.
- Expansion of our newest subcommittee, Systems Biology. The rapid uptake of systems approaches and the startling number of new research centers specializing in this new approach make it necessary for MASC to redouble its efforts to promote cooperation between these fledgling groups.
- Most *Arabidopsis* research is not carried out via high-throughput 'omics' approaches but by precise, methodical analysis of single genes or proteins. The literature is a huge repository of such high-quality data, often familiar to researchers within a chosen field but difficult to access by other researchers and even less accessible to machines. Current efforts to covert such data to a standard, machine-readable format need to be improved and expanded.

# Progress and Updates of Multinational *Arabidopsis* Functional Genomics Projects

## Progress and activities of the MASC in 2006/2007

In 2006/2007, Ian Small (University of Western Australia) succeeded Philip Benfey (Duke University) to become the MASC chair and Xing Wang Deng (Yale University) became co-chair. Dr. Deng will become the new MASC chair when Dr. Small steps down following the annual International Conference on *Arabidopsis* Research (ICAR) in June, 2007. At the annual MASC meeting during the ICAR in 2006, MASC members recommended that TAIR take over abstract submission for future ICARs. The MASC Coordinator worked with TAIR staff over the past year to design an abstract submission process that includes a request for submitters to voluntarily list the AGI codes for genes under study in their research. It is hoped that this will facilitate data gathering regarding the *Arabidopsis* genes under study in the global community. The database was developed in advance of the 2007 ICAR and was used for abstract submission beginning in February, 2007. This year Israel, represented by Danny Chamovitz of Tel Aviv University, became the newest member of the MASC bringing the number of countries represented on the MASC to twenty. The initial summary of *Arabidopsis* functional genomics efforts in Israel can be found in the reports from the International *Arabidopsis* Community.

MASC subcommittees, proposed at the 13th ICAR held in Seville, Spain in 2002, were established to help track progress towards the goals outlined in the 2002 Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. At the annual MASC meeting in 2005, several subcommittees were initiated and several were discontinued. Following the annual MASC meeting in 2006, in response to the increasing need for integrative approaches in research, a Systems Biology subcommittee was proposed by Philip Benfey. This year's report includes the initial Systems Biology report, along with reports of the current MASC subcommittees: Bioinformatics, cDNAs and Clone-based Functional Proteomics (ORFeomics), Metabolomics, Natural Variation and Comparative Genomics, Phenomics, and Proteomics.

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. They held a demonstration workshop at the 17th ICAR in June, 2006, and will hold a second workshop at the 18th ICAR in June, 2007. Following the 2006 meeting, work continued to advance the concept of a "one stop shop" by developing aggregator pages that will simultaneously query multiple locations for certain types of data. More project information and descriptions can be found in the Bioinformatics subcommittee report. Wolfram Weckwerth and other members of the Proteomics subcommittee worked to develop a new website that will include links to existing databases of *Arabidopsis* proteomics. The goals of the webpage are to disseminate standards for sample handling and data interpretation, provide a platform for the *Arabidopsis* community to exchange ideas and protocols, and allow discussions among interested researchers. The website will be accessible at TAIR (The *Arabidopsis* Information Resource, www.arabidopsis.org.) Subcommittee members have also been involved in several initiatives to develop databases and software tools for the exploitation of *Arabidopsis* proteomics data. Further information on these projects can be found in the Proteomics subcommittee report. In addition, a Proteomics Workshop will be held at the 18th ICAR.

A full-time MASC coordinator position was established in 2002 and funded for two years by the NSF (US), one year by the DFG (Germany), followed by another two-year grant from the NSF, which ended in February of 2007. At the 2006 Annual meeting, MASC members reaffirmed their support for the Coordinator position and recommended that funding for a Coordinator be continued. The current MASC coordinator, Dr. Joanna Friesner, submitted a new NSF grant with Dr. Charles Gasser at the University of California, Davis, and will continue for two more years after being awarded funding. It is expected that a new MASC member country will assume funding for a MASC Coordinator in spring 2009. 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, (3) producing and editing the annual MASC progress report and other MASC documents, (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. In the last year the MASC webpages at TAIR have been significantly updated and reorganized to increase usability and provide more current information. Additional updates are ongoing.

## Scientific Highlights of the Past Year

The number of peer-reviewed publications involving *Arabidopsis* continues to increase, undoubtedly a trend that can be attributed in large part to international funding efforts to support *Arabidopsis* research. In particular, initiatives that support resource development have provided useful tools that allowed many researchers to begin, or extend, *Arabidopsis* research programs. Only 20 years ago, when research in *Arabidopsis* was

limited to a few labs, just a few dozen *Arabidopsis* publications were produced per year. The release of the *Arabidopsis* genome sequence in 2000 was a landmark event whose success was largely due to the ten year genome sequencing collaboration by an international community of scientists. The availability of this first plant genome has facilitated rapid progress: in the five years preceding the genome release (1995-1999), peer-reviewed publications involving *Arabidopsis* were produced at an average rate of 847 per year; in the five years following (2001-2006), that number doubled to an average of 1,694 per year. In 2006 alone, more than 2,200 such publications were produced (figure 1). The increasing pool of knowledge and availability of resources for this reference plant has allowed truly top-quality studies to be proposed, producing exciting and new results at a quickening pace. 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.

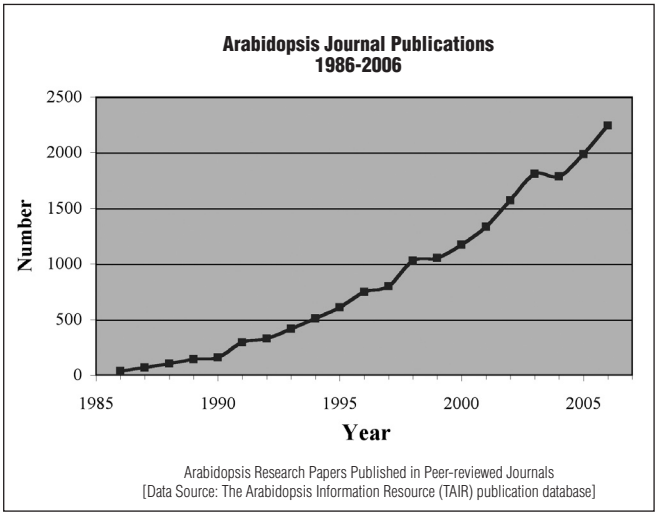



**Figure 1**

## The First Genome-wide Methylation Map

DNA methylation is involved in a number of important processes including regulation of gene expression, maintaining silenced transposons, and plant (and animal) development. A recent publication from Zhang *et al* describes the first genome-wide high-density methylation map of an entire genome using the reference plant *Arabidopsis thaliana.* The authors combined biochemical methods with a newly developed single chip, whole-genome tiling microarray to obtain a global view of methylation patterns in *Arabidopsis*. Using wild-type and methylation-deficient mutants they examined RNA expression profiles to determine the relationship between DNA methylation status and gene expression. Some of their findings confirmed, on a large scale, what was previously suggested in smaller studies. For example, they found that almost 19% of the *Arabidopsis* nuclear genome is methylated, with extensive methylation in heterochromatic regions including the centromeres, sites known to be rich in transposons and other repetitive sequences. However, they also found a significant level of methylation in euchromatic regions, with the highest levels seen in pseudogenes and non-expressed genes. Surprisingly they found that about 33% of all expressed genes are methylated within the transcribed region, excluding promoter sequences (the 'body-methylated' genes), and that about 5% of expressed genes are methylated within the promoter region. Analysis of the relationship between DNA methylation and gene expression patterns using microarrays revealed that the body-methylated genes had significantly higher expression levels than unmethylated genes, while expression levels of promoter-methylated genes were generally lower. Their findings also suggested that expression patterns of promoter-methylated genes tend to be highly tissue-specific while in general, body-methylated genes are expressed constitutively at a higher level. The data are available online along with a genome browser tool that allows researchers to seek methylated cytosines and compare methylation patterns in wild-type and methylation-deficient mutants.

*Reference: Zhang X, Yazaki, J, Sundaresan A, Cokus S, Chan SW, Chen H, Henderson JR, Shinn P, Pellegrini M, Jacobsen SE, Ecker JR, Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. Cell, Sept. 22 2006; 126 (6):1189-1201*

## Parental Stress Can Create Lasting Memories

Plants are continuously exposed to biotic and abiotic environmental stress and react to these conditions with a variety of physiological changes and modulations of gene activities. As a result plants may become tolerant to conditions such as excessive light, extreme temperatures, inadequate water supply and, most importantly, to pathogens. Genome changes, including the mobilization of transposable elements and homologous recombination, have also been reported in plants exposed to stress. A recent publication by Molinier *et al* reported another level of genomic change in populations of plants exposed to short-wave ultraviolet light (UV-C) or flagellin, an elicitor of plant defense. The authors found that not only did the plant population exposed to the stress conditions respond with elevated levels of somatic homologous recombination, but strikingly, the untreated descendants retained these increased levels for at least four generations. This finding was clearly due to an epigenetic change at (an) unknown locus/loci since the whole population was affected. If the phenomenon had been due to a mutation, only a tiny fraction of the plants would have shown a change in the tested trait. This dominant epigenetic change could be transmitted through both the maternal and paternal crossing partner. Increased recombination in the untreated generations proved to be independent of the presence of the transgene which was used to monitor recombination; the stimulus for increased recombination could be imposed *in trans* by a treated parent that lacked the transgene. At this point only speculations on the possible importance of the observed transgenerational phenomenon can be raised. It has been proposed that the environmental influences leading to increased genomic dynamics even in successive generations lacking exposure to biotic or abiotic factors may increase the potential for adaptive evolution.

*Reference: Molinier J, Ries G, Zipfel C, Hohn B, Transgeneration memory of stress in plants. Nature, Aug. 31 2006; 442(7106):1046-1049*

### The First Plant Hormone Receptor Structure Reveals That Auxin is the Glue

Auxin, a well-studied phytohormone, is known to be important for various aspects of plant growth and development by regulating gene expression. Previous studies demonstrated that auxin interacts directly with the TIR1 receptor, a ubiquitin ligase, in a signal transduction pathway that results in gene expression following proteolytic degradation of transcriptional repressors. Until the recent publication by Tan *et al*, the mechanism by which TIR1 perceives, and subsequently is activated by, auxin, was unknown. The authors purified full-length *Arabidopsis* TIR1 protein complexed with the ASK1 adaptor protein and determined a series of high resolution crystal structures of this complex alone, and in the presence of several auxin compounds, with or without a substrate peptide. The various crystallographic 'snapshots' of the complexes revealed that TIR1 isn't activated through conformational changes induced by auxin interaction distant from the TIR1 active site, but instead results from the increased substrate-binding affinity facilitated by auxin bound to the TIR1 active site. Auxin bridges the space between TIR1 and its substrate by promoting a continuous hydrophobic interaction, effectively 'gluing' TIR1 to its substrate. In the absence of auxin, TIR1-substrate complexes are not as stable. Unexpectedly the crystal structures also revealed the presence of an inositol hexakisphosphate cofactor which may be essential for TIR1-auxin-substrate interactions. The crystal structures also revealed that the TIR1 active site allows some flexibility in hormone binding suggesting that a variety of auxin compounds may form similar complexes with varying levels of stability. These findings may extend to regulation in other eukaryotic systems, potentially opening the door to the development of small compounds that could be used pharmaceutically to address disorders characterized by defects in ubiquitin ligase-substrate interactions.

*Reference: Tan X, Calderon-Villalobos L, Sharon M, Zheng C, Robinson, CV, Estelle M, Zheng N, Mechanisms of auxin perception by the TIR1 ubiquitin ligase. Nature, Apr. 5 2007; 446:640-5*

### Cutting Your Roots: Rethinking Regeneration

While the ability to regenerate organs is rare in animals it is quite common in plants. However, the molecular mechanisms underlying organ regeneration in plants are not clear. A recent publication by Xu *et al* looks at root development and regeneration in *Arabidopsis* and presents new and unexpected results. The authors used lasers to wound an important region of the root called the Quiescent Center (QC), which functions to maintain stem cell identify of surrounding cells and employed cell-specific markers to determine whether changes in cell fate surrounding the QC occurred. Wounding of the QC disrupted the flow of auxin, a plant hormone that regulates growth and development, and caused a rapid upregulation of the auxin response. Through the use of cell-specific patterning and polarity markers they determined that changes in identity in cells adjacent to the wounded QC had occurred indicating that disruption in auxin flow induced regeneration. They also examined whether the putative auxin efflux-facilitating membrane PIN proteins were affected by auxin disruption and found that new cell specification must first be established for new PIN expression and localization. Their findings also suggest essential roles for several important transcription factors, SHORTROOT (SHR), SCARECROW (SCR), and PLETHRORA (PLT), in re-establishing cell polarity. The authors propose a new model for root regeneration in which cell-fate changes leading to a new QC are initiated by auxin redistribution and changes in expression and activity of SHR, SCR, and PLT. Only after a new QC is established are changes in auxin flow polarity induced through new correctly polarized PIN expression. These findings challenge a traditional model that proposes that the first step in regeneration involves a flow of auxin that induces changes in the polarity of auxin transporters to set up a positive feedback signal to channel more auxin.

*Reference: Xu J, Hofhuis H, Heidstra R, Sauer M, Friml J, Scheres B, A molecular framework for plant regeneration. Science, Jan. 20, 2006; 311: 385–388*

### Transcription Factor Expression Regulation: What's Upstream is Key

The first-generation *Arabidopsis* root expression map generated with a technology that combines cell sorting with microarrays provided genome-wide information about cell-type specific expression in the root. A recent publication by Lee *et al* made advances in understanding how the expression of transcription factors is modulated, providing insight into global gene regulatory networks. The authors selected 61 transcription factors expressed in a tissue-enriched manner in *Arabidopsis* roots and created reporter constructs driven by each transcription factor's upstream non-coding sequence fused to a Green Fluorescent Protein (GFP) reporter gene alone, or together with the transcription factor's coding sequence. They compared the GFP patterns with mRNA expression patterns, and in parallel, developed an automated image analysis method for quantifying GFP signals in different tissues to validate the visual comparison method. From these combined analyses, it was found that (i) the upstream non-coding sequence was sufficient to recapitulate the mRNA expression pattern for 80% of the transcription factors, and (ii) 25% of the transcription factors undergo posttranscriptional regulation via microRNA-mediated mRNA degradation or via intercellular protein movement. These results suggest that, for *Arabidopsis* transcription factors, upstream non-coding sequences are major contributors to mRNA expression pattern establishment, but modulation of transcription factor protein expression pattern after transcription is relatively frequent. This study provided the first systematic overview of regulation of transcription factor expression at a cellular level in a multicellular organism. The updated root expression map is publicly available at http://www.arexdb.org/.

*Reference: Lee JY, Colinas J, Wang JY, Mace D, Ohler U, Benfey, PN, Transcriptional and posttranscriptional regulation of transcription factor expression in Arabidopsis roots. PNAS U S A, Apr 11 2006; 103(15):6055-60*

### Imprinting: a MEAns to an End

Gene imprinting is a phenomenon by which the activity of a gene depends on whether the particular allele is inherited from the male or female parent. Imprinting occurs during gametogenesis, often through the action of proteins that add methyl groups

to certain gene sequences, thereby marking them as being of paternal or maternal origin. A recent publication by Gehring *et al* provides insight on the mechanism of gene imprinting in *Arabidopsis*. The *MEDEA (MEA)* gene, which undergoes imprinting, is expressed only from the maternal allele in the endosperm of *Arabidopsis* seeds; the paternal allele is silenced. The authors found that this difference in activity depends on a DNA glycosylase, DEMETER (DME), which can remove methyl groups *in vitro* and when expressed in bacteria. DME is required for the hypomethylation and activation of the maternal *MEA* allele, presumably through its demethylase activity. Unexpectedly, the authors found that the silenced state of the paternal *MEA* allele is not due to its hypermethylation status but instead can be attributed to the action of a maternally-derived complex that includes the MEA protein itself. These data suggest that the complex directly regulates the chromatin structure of the paternal *MEA* allele to maintain it in a silenced state. The authors propose that imprinting regulation is achieved through demethylation of *MEA* in the female gametophyte by DME prior to fertilization, allowing the production of maternally-derived MEA proteins that assemble into complexes that target and silence the paternal *MEA* allele following fertilization. In this model *MEA* regulates its own imprinted state. Exactly how the paternal *MEA* allele is targeted, given that methylation status doesn't seem to be involved, remains to be discovered.

*Reference: Gehring M, Huh J, Hsieh T, Penterman J, Choi Y, Harada JJ, Goldberg RB, Fischer, DEMETER DNA Glycosylase Establishes MEDEA Polycomb Gene Self-Imprinting by Allele-Specific Demethylation. Cell, Feb 10, 2006: 124, 495-506*

### Microtubules Help Cellulose Synthesis Stay on Track

The cell walls of vascular plants are encircled by cellulose fibers (microfibrils) which are synthesized and deposited in an orderly fashion to provide structural support while simultaneously allowing cell growth. It has been known for decades that deposition of newly synthesized microfibrils often closely parallels the arrangement of cytoskeletal microtubules suggesting, although never proven, that microtubules somehow guide microfibril alignment. This close arrangement has led researchers to propose that during microfibril formation, either microtubules indirectly facilitate cellulose synthesis by acting as 'bumpers' that channel self-propelled cellulose synthase proteins or they actively participate by guiding synthases via direct interactions. A recent publication by Paredez *et al* provides direct evidence that microtubules guide the deposition of microfibrils and suggests a close, direct interaction between cellulose synthases and cortical microtubules. The authors tracked cellulose biosynthesis in *Arabidopsis* hypcotyl cells in live-cell imaging experiments using fluorescently-labeled proteins, CESA6 (a cellulose synthase component) and TUA1 (a microtubule protein), and confirmed the colinearity of synthase and microtubule movement. Importantly, a change in the direction of microtubule growth was followed by a correlated change in microfibril synthesis demonstrating the importance of microtubules in microfibril alignment. Neighboring synthases continued to move for a brief time following microtubule disruption suggesting synthase movement is powered by cellulose polymerization rather than microtubules, and that interactions with microtubules are not required for synthase motility. They also showed that while microtubules are important for synthase alignment and movement, when microtubules are absent, synthase complexes move in a non-random way suggesting an intrinsic ability to self-organize or the presence of another organizational pathway. Techniques such as live-cell imaging will allow further studies on this process, and perhaps lead to the identification of a physical link between CESA proteins and microtubules.

*Reference: Paredez AR, Somerville CR, Ehrhardt DW, Visualization of Cellulose Synthase Demonstrates Functional Association with Microtubules. Science, 2006: 312:1491-1495*

### When it Comes to Iron, What Matters is Location, Location, Location

Iron is critical for a number of processes, both in plants and animals, although it must be carefully sequestered due to its potentially damaging reactive properties. Understanding how and where plants sequester iron may help efforts to combat iron deficiency, a major nutritional problem particularly in areas where plant-based diets are common. A recent publication by Kim *et al* revealed that iron is stored in the developing vascular system of *Arabidopsis* seeds, and in the vacuole in particular, a plant cell's central storage site. The authors also learned that this localization depends on VIT1 proteins which act to transport iron into vacuoles, information obtained through the use of yeast and plant mutants. Using mass spectrometry they examined plants defective for VIT1 and found to their surprise there was no difference in iron content between *vit1-1* mutant and wild-type seeds or shoots. They next used a powerful noninvasive X-ray imaging technique to create a map of where iron is localized in both seed types and found that iron localization was aberrant in *vit1-1* seeds. In wild-type seeds iron is strongly localized to the provascular system while in *vit-1* seeds, iron is absent from those cells and is located diffusely in those and other cells. In contrast, the distribution patterns of zinc and manganese metals are similar in wild-type and *vit-1* seeds. They demonstrated that efficient iron transport and localization are important for plant growth as *vit1-1* seedlings grew poorly on iron-limited soil, although they grew normally on soil where iron was not limited. These results indicate the importance of the vacuole, and VIT1, in proper iron storage in seeds and contrast with many studies that focus on iron storage in ferritin proteins. The findings also suggest that the vacuole may be a promising target for increasing the iron content of seeds.

*Reference: Kim SA, Punshon, T, Lanzirotti A, Li L, Alonso JM, Ecker JR, Kaplan J, Guerinot M. Localization of Iron in Arabidopsis Seed Requires the Vacuolar Membrane Transporter VIT1. Science, Nov.24 2006; 314:1295-1298*

### Stop and Grow: Direction From the Outer Layer

The ability for plants to respond to environmental cues and modulate growth is critical to their survival. Extensive research has revealed the importance of a number of hormones, including the brassinosteroids, in plant growth and development. Plants that lack brassinosteroids are dwarfed in stature, but until now, a clear understanding of which part of the plant modulates growth in response to brassinosteroids has remained elusive. A recent publication by Savaldi-Goldstein *et al* provides compelling evidence that the epidermis, the outermost cell layer in higher

plants, is responsible for promoting and restricting shoot growth. Starting with plants defective in either brassinosteroid biosynthetic or receptor genes, the authors selectively introduced brassinosteroid synthesis and perception to discrete cell layers through the use of tissue-specific promoters. They found that brassinosteroid expression in the epidermal layer alone was sufficient to restore dwarfed plants to normal stature, even though the internal layers remained defective in brassinosteroid expression and signaling. In contrast, when brassinosteroid signaling was confined to the inner vasculature tissues, the plants remained dwarfed. They also provide evidence that the epidermis has a role in restricting growth; the majority of wild-type plants with brassinosteroids selectively depleted from epidermal cells through the activity of a brassinosteroid-inactivating enzyme were smaller than control plants suggesting that local brassinosteroid synthesis in the epidermis contributes to optimal leaf growth. These results suggest that the epidermis can act as a 'sensor' by communicating cues to internal tissues through an as-yet unknown non-autonomous signal, to both promote and restrict plant growth.

*Reference: Savaldi-Goldstein S, Peto C, Chory J, The epidermis both drives and restricts plant shoot growth. Nature, Mar 8 2007; 446(7132):199-202.*

### A High-throughput Screen to Develop a Fatter Bean

In an effort to create alternative sources of novel fatty acids to supplement the oleo-chemical industry, scientists have developed transgenic plants that over-produce important fatty acid biosynthetic enzymes. Unfortunately, the resulting transgenic seeds typically contained much lower levels of the novel fatty acids then the natural sources suggesting that over-expression of a single enzyme is insufficient to create transgenic plants that accumulate significant levels of specific fatty acids. In a recent publication by Lu *et al*. a high-throughput approach was employed to identify novel genes that increase fatty acid accumulation in *Arabidopsis* plants that already overexpressed the fatty acid hydroxylase *FAH12* gene from castor bean. Based on the knowledge that several genes are likely needed to synthesize fatty acids in castor, the authors generated the castor *FAH12* overexpressing *Arabidopsis* plants and then introduced the complete set of cDNAs derived from castor seed endosperm under the premise that positive interactions between *FAH12* and additional (unknown) castor genes may increase fatty acid content of transgenic seeds. The fatty acid composition of transgenic *Arabidopsis* seeds from about 4000 lines was analyzed using high-throughput gas chromatography allowing the identification of 8 transgenic lines with increased hydroxyl fatty acid content. Castor cDNAs from 3 single-insert candidate lines were then isolated and re-introduced into FAH-expressing *Arabidopsis* plants to confirm their ability to increase fatty acid content. The selected transgenic lines had moderate increases in hydroxy fatty acids (around 20%), and several of the lines contained multiple inserts of castor cDNAs. These results validate the novel high-throughput experimental design and suggest the approach may allow the identification of single, and combinations of, cDNAs that increase hydroxy fatty acid content. This method could be used to study other genes of interest and potentially allow the development of crops with increased nutritional value.

*Reference: Lu C, Fulda M, Wallis JG, Browse J, A high-throughput screen for genes from castor that boost hydroxyl fatty acid accumulation in seed oils of transgenic Arabidopsis. Plant Journal, 2006: 45, 847-856*

## Community Arabidopsis Projects and Resources

### European Integrated Project—AGRON-OMICS

Coordinator: Pierre Hilson; pierre.hilson@psb.ugent.be
Department of Plant Systems Biology, VIB, Ghent University
Project website: www.agron-omics.eu

AGRON-OMICS (Arabidopsis GROwth Network integrating-OMICS technologies) is a consortium of fourteen partners financed by the European Union (12 Million € project budget) within the 6th Framework Programme. It aims to develop a system-level approach to study leaf growth and development in *Arabidopsis*. This consortium will employ about 200 persons over the course of the project including about 40 new recruits over a period of five years (November 2006 – October 2011).

Growth is a complex trait regulated by the output of molecular networks that integrate intrinsic developmental programs and extrinsic environmental signals. At the cell level, leaves grow as a result of the coordination of proliferation and expansion in space and time. An increasing number of genes are functionally characterized and assigned to key modules involved in these two processes. The consortium builds on the expertise of the partners encompassing cell cycle, cell growth, cell signaling and cell metabolism to initially define a molecular scaffold specific for leaf growth and development yielding a framework for experimental and modeling work. Based on this knowledge and on the use of profiling and other technologies, the seven scientific work-packages of AGRON-OMICS have as main objectives:

- To survey systematically the molecular components driving growth;
- To explain and classify leaf growth phenotypes at the molecular level;
- To build coordinated molecular networks between pathway modules.

Experiments will combine profiling techniques, including the characterization of transcriptome, proteome and metabolome, with advanced and automated phenotyping protocols. In parallel, the consortium will explore novel high-throughput technologies for the functional analysis of plant genes, such as chemical screens and high-content cell assays. The plant material that will be studied comprises mutants, genotypes generated by reverse genetics protocols, ad-hoc transgenic and recombinant inbred lines. The large amount of data generated by the genetic, molecular profiling and phenotyping platforms require dedicated data repositories allowing access to data series for comprehensive analysis. In that context, the consortium's driving principles are to contribute to the improvement of existing standards (e.g., ontologies) and to develop reliable protocols for data integration. In parallel, AGRON-OMICS partners will build analytical, mathematical and visualization tools for functional genomics data intended for the elaboration of predictive models for complex systems. In turn, this computational scaffold is intended to shape emergent hypotheses to be tested and validated experimentally.

### Initiative to Establish an Australian Plant Phenomics Facility

The Australian Government has recently awarded funding

for the Australian Plant Phenomics Facility (APPF) to be established as a bi-nodal facility between the University of Adelaide and CSIRO Plant Industry and The Australian National University in Canberra. The APPF aims to be a state-of-the-art plant phenotyping facility with sophisticated plant growth facilities and cutting edge technologies for plant performance and function monitoring. Construction of the National Plant Phenomics Facility is expected to begin in 2007. A primary objective is the analysis of model species such as *Arabidopsis* and rice for gene function discovery (>50,000 plants screened per year) The University of Adelaide Waite Campus will develop a suite of glasshouse facilities with robotic monitoring of plant growth and performance with particular emphasis on application to agricultural species. The Canberra node will specifically establish a model species screening facility which will include a focus on *Arabidopsis* analysis. The technologies used for screening will include various imaging approaches including morphological growth and color analysis, chlorophyll fluorescence and hyperspectral reflectance. These will be coupled to robotic systems which will allow medium throughput screening of plant material grown under controlled environment conditions. See the Australia country report for further information.

## ERA-NET Plant Genomics

Contacts:
Christine Bunthof; bunthof@genomics.nl
Okker van Batenburg; batenburg@genomics.nl
ERA-PG Managing Office
Project website: www.erapg.org

ERA-NET Plant Genomics (ERA-PG) is a networking and coordination activity supported by the ERA-NET scheme under the EU's sixth Framework Programme for strengthening the European Research Area (ERA). Networking national funding organizations and coordination of national programs in Europe will facilitate a stepping up from national to multilateral coordination thereby reducing redundancy and maximizing the returns on investment in plant sciences. Close collaboration and synergy of research efforts and joint investments in large-scale technologies will create critical mass, contribute to the 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, the ERA-NET Plant Genomics was among the first of ERA-NET projects to start in 2004. ERA-PG is coordinated by NGI/NWO from The Netherlands and the founding members further 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 of ERA-PG two years after the start and Bulgaria joined the network as the first new EC member state in October 2006.

ERA-PG has undertaken a large information gathering exercise leading to a shared information resource on research activities and the 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. On February 1, 2006 ERA-PG launched its first joint call for research '*Structuring Plant Genomic Research in Europe*' with a budget of over 30 million € which received more than one hundred applications, making it one of the largest coordinated multinational research programs in the ERA-NET scheme. The projects were selected and proposed to the funding institutions by a scientific advisory committee that had first assessed pre-proposals. In the second step they had selected experts from the international scientific community evaluate the full proposals through a peer review process. Applicants were given the opportunity to provide a rebuttal to the (anonymous) peer review reports. The ranking list was produced during a meeting of the scientific advisory committee and final decisions rested with the national funding institutions. A kick-off meeting with participation of the project coordinators will be held at Tenerife on October 2, 2007. The ERA-PG partners are exploring further possibilities for continuing their collaboration and have started preparations to open a second call in 2008. More information about the ERA-PG funded projects and other ERA-PG activities are available on our website.

## The Arabidopsis Information Resource

**(TAIR, www.arabidopsis.org)**

In October 2006, TAIR introduced the ability to search for genes, germplasms and polymorphisms based on associated phenotypes. The gene, germplasm and polymorphism search pages, along with their corresponding data detail pages were updated to display the new information. The locus and stock detail pages were also updated to display phenotype information, where available. Germplasm descriptions were curated, separating phenotype data from other kinds of seed stock information that were previously combined in this description. During this month, TAIR also released the final components of a new website design including portal pages which aggregate web-wide information and links for various major topics of interest into a central webpage, left navigation bars and a main header bar with dropdown menus. This new design provides a better organized and more intuitive user interface for TAIR.

On November 29, 2006 the TAIR database and website moved from hardware hosted at NCGR in Santa Fe, New Mexico to new hardware hosted at Stanford University. The new hardware has provided faster response times and better overall uptime. In February 2007, TAIR released version 3.5 of the AraCyc biochemical pathway database with 262 *Arabidopsis* biochemical pathways, including 51 newly added and 37 significantly updated pathways. In addition, 400 compounds were added from user submissions. Of the 262 total pathways, 79% are fully curated including a pathway summary, special significance if any and comments. For the fully curated pathways all available literature associated to the pathway enzymes has been reviewed and enzyme physiochemical properties and general comments about the enzymes have been added. In March 2007 TAIR released a new version of the *Arabidopsis* genome annotation, TAIR7, incorporating community submissions directly to TAIR and new cDNAs and ESTs submitted to GenBank since the previous

TAIR6 release. The new release includes 681 new genes bringing the total gene set to 32,041 genes, of which 26,819 are protein-coding, 3889 are pseudogenes or transposable elements and 434 are ncRNAs. The release also contains updates to 9755 genes, including 784 updates to protein sequences and addition of 1003 new splice variants as well approximately 10,700 updates to UTRs. A total of 34 gene merges and 41 gene splits were also carried out. TAIR7 has been released to GenBank and can be accessed from the NCBI Plant Genomes section as well as through TAIR. Over the past year (3/1/06-2/28/07) TAIR has curated 556 research articles, adding 4005 Gene Ontology and 2210 Plant Ontology annotations from the literature to 2181 genes and also updating gene summaries, aliases, phenotypes, alleles and germplasm information.

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

NASC distributes, collects and preserves seed and DNA resources of *Arabidopsis* and related species (but is also expanding to embrace tomato and other *Solanaceae*). In addition, we collect, generate and distribute transcriptomics data (especially Affymetrix) in the form of a primary repository; and have a mature integrated genome browser AtEnsEMBL (http://atensembl.arabidopsis.info) as part of ukcrop.net which incorporates both TAIR and MIPS genome annotations and links through to all of our other databases and resources (as well as external data such as Brassica gene information).

As the sister centre to ABRC, we have an ongoing mutual interchange of *Arabidopsis* and related species stocks which facilitates distribution to the research community worldwide. Ongoing recent donations to our centres include the Ecker homozygous T-DNA knockout lines routed through the ABRC, and 195,903 GABI-Kat lines (www.gabi-kat.de/), and 14,425 AGRIKOLA RNAi lines (http://www.agrikola.org) routed through NASC. Almost all known *Arabidopsis* genes are potentially available for transcript down-regulation using the AGRIKOLA RNAi clones (24,832 pEntry clones & 21,337 pDestination clones) made by members of the multinational AGRIKOLA consortium and available through NASC. For developers, the 24,864 CATMA DNA probes (www.catma.org/) used to generate these vectors are also available to order in plate form. Please note that most of our data is available through SOAP and BioMOBY web services. Funding for developing and training users in implementing web services has been funded at NASC for 4 years as part of the AGRON-OMICS EU project. If you need help in using these, please ask us or contact the MASC bioinformatics subcommittee. Our general BBSRC funding has been renewed this year to cover a further 5 years of the NASC seed service and a further 3 years for the GARNet transcriptomics and bioinformatics service. As part of this renewal, we will be offering several new services to be announced shortly. Please visit the NASC website for more information.

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

The ABRC distributes, collects and preserves seed and DNA resources of *Arabidopsis* and related species. Emphasis in 2007 is being placed on serving various post-genomic efforts, particularly phenomics. Distribution and organization of the homozygous insertions lines for various phenotypic investigations is proceeding. The Ecker laboratory (Salk Institute, http://signal.salk.edu/gabout.html) is genetically purifying to homozygosity 50,000 T-DNA insertion knockout lines. To date, 9,198 of these lines have been received, and the remainder will be arriving as they are generated. 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). Receipt and distribution of Entry and Expression ORFeome clones is also a priority. Entry clones are being received from the Ecker (SSP and SALK) and the C. Town projects as well several individuals in the research community. The extensive Expression ORF collections from S. P. Dinesh Kumar and S. Clouse are also being received, with 3,026 of these currently in-house. Present ABRC seed stock holdings include insertion lines covering 25,000 genes, the 10,000+ lines of the Arabidopsis TILLING service, 850 distinct natural accessions (now being genetically fingerprinted so that this entire collection will be marker-validated), 15 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 13,500 genes, BACs covering the entire genome, BACS of four related species, the AGRIKOLA RNAi Entry clones and various sets of Expression and Destination 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 donation of published mutants and clones, including purified insertion mutants and expression clones, are very welcome. The annual distribution of seed and DNA stocks exceeded 85,000 orders in 2006.

## Measuring Gene Function Knowledge

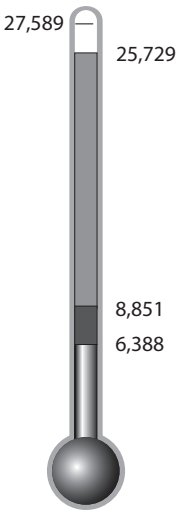
During the MASC annual meeting held during the 2003 International Conference on *Arabidopsis* Research members agreed that it would be useful to establish a better way to update gene function knowledge and quantify the number of genes with known function. Since the 2004 MASC annual report this was illustrated by thermometers to provide a visual illustration of the progress in *Arabidopsis* functional genomics efforts. This year the thermometers have been reorganized into two types: Resources and Knowledge. This change was undertaken to provide a more detailed view of the progress by the international community in generating resources and gene function knowledge. The four Resource thermometers are measured against the TAIR6 genome release and include (1) the number of genes containing sequence-indexed insertion elements, (2) the number of genes targeted by RNAi constructs, (3) the number of genes with full-length cDNA clones, sequencing status and availability, and (4) the number of genes with Open Reading Frame (ORF) clones produced. The four Knowledge thermometers, described in detail in the figure legend, quantify available information and evidence about gene function and include (1) gene expression detected, (2) subcellular localization, (3) biological process, and (4) molecular function. The thermometers are updated with data available at the end of February 2007 unless noted.

Given the expanding resources and knowledge base in the

*Arabidopsis* community, in the next four years it should be possible to collect at least one piece of data about every gene in the genome. As shown in the thermometers below, excluding pseudogenes, ORF clones are available as stocks for over 60% of genes and full-length cDNA information is known for nearly 75% of genes. Great strides have been made in developing resources to knockout, or knockdown, gene expression including the isolation of homozygous insertion mutants for 23% of genes just in the last year. In total, more than 93% of *Arabidopsis* genes (excluding pseudogenes) contain an insertion in an exon, intron, promoter, or 5' UTR. In addition, there are over 21,500 gene loci targeted by RNAi constructs including 3,482 loci with constructs transformed into plants (distribution of plant lines to stock centers is underway.) With this expanding set of resources and continued funding and strong international collaboration we can look forward to numerous insights and discoveries from the community over the next four years, substantiating the value of *Arabidopsis thaliana* as the foremost plant model system.

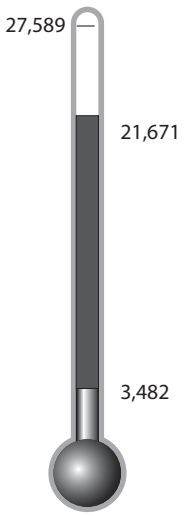
# Resource Thermometers

## Insertion Mutants



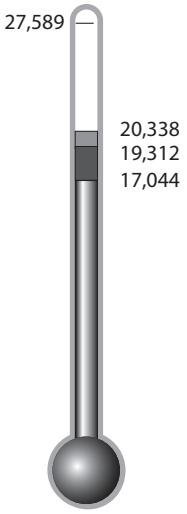

Loci with homozygous confirmed insertion sites
+ Loci with confirmed insertion sites, unknown zygosity
+ Loci with unconfirmed insertion sites, unknown zygosity

## RNAi



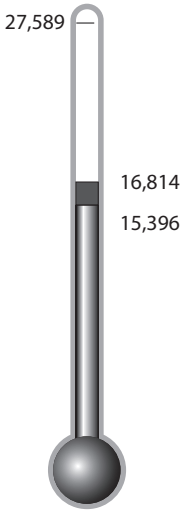

Loci with RNAi constructs transformed into plants
+ Loci with constructs made, not transformed into plants

## 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

## ORF




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

**Figure 2: Measuring *Arabidopsis* Genomics Resources.** All data are as of 2/28/07 unless otherwise indicated. For consistency, all resources are measured against the TAIR6 genome release (including noncoding RNAs and organelle-encoded genes but excluding pseudogenes, a total of 27,589 genes). Four resource categories are included: **Loci with insertion mutants** - 6,388 genes with homozygous confirmed insertion sites, an additional 2,463 genes with confirmed insertion sites and homozygous status unknown, and an additional 16,878 genes with unconfirmed insertions, homozygous status unknown (data from Huaming Chen, SIGnAL); **Loci with targeted RNAi knockdowns** –3,482 genes with RNAi constructs transformed into plant lines, an additional 18,189 genes with RNAi knockdown constructs made but not transformed into plant lines, (data from Ian Small, AGRIKOLA); **Loci with full length cDNA clones** - 17,044 genes with full length cDNAs fully sequenced and known to be available for ordering, an additional 2268 genes with cDNAs not fully sequenced but known to be available and an additional 1026 genes with fully sequenced cDNAs but stock availability unknown, (data from Huaming Chen, SIGnAL); **Loci with ORF clones** - 16,814 genes with fully-sequenced ORF clones and an additional 1,418 with partially sequenced ORF clones as of 5/15/07. An additional 4,630 genes are currently targeted by SIGnAL for ORF clone development, (data from Huaming Chen, SIGnAL). In the 2006 report about 3,500 loci were listed as 'targeted for ORF cloning'; however, in the past year the ATOME project (www.evry.inra.fr/public/projects/orfeome) has reprioritized its efforts to transfer existing SSP ORF clones into the recombinational Gateway® system. Because target gene lists are subject to change, the ORF thermometer now includes only completed clones.

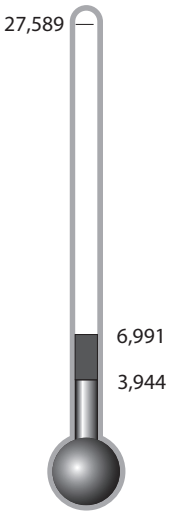
**Note:** Detailed information on ORF, cDNA, and RNAi clone projects can be found in the ORFeomics Subcommittee Report (page 25) and in the Tables of Major *Arabidopsis* Resources located at the end of this report (pages 62 to 65). One of these tables, the Table of Worldwide Genetic Seed Stock Resources, also indicates whether MTAs are required and/or if IP restrictions apply to each listed Seed Resource.

# Knowledge Thermometers

## Expression

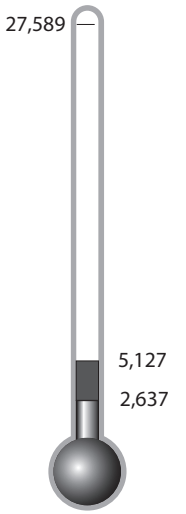

- Loci with cDNAs
- + Loci with ESTs
- + Loci with mpss or sage
- + Loci with microarray expression

## Subcellular Localization



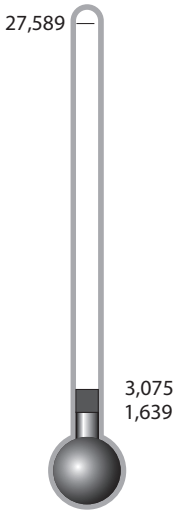

- Loci with experimental evidence
- + Loci with 'other' evidence

## Biological Process




- Loci with experimental evidence
- + Loci with 'other' evidence

## Molecular Function




- Loci with experimental evidence
- + Loci with 'other' evidence

**Figure 3: Measuring *Arabidopsis* Gene Function Knowledge.** Four knowledge categories are included, of which the last three correspond to Gene Ontology annotations and are broken down by type of evidence. 'Experimental' evidence includes direct assay of activity, genetic interaction, physical interaction, mutant phenotype, or expression profile. 'Other' evidence includes author statements not directly linked to experiments and knowledge inferred by a curator. Not included in these thermometers is gene function knowledge based on computational evidence, including sequence similarity to known proteins, presence of a protein domain with known function, or targeting predictions. **Expression detected** – 20,338 loci with cDNAs (data from SIGnAL), an additional 1,765 loci with ESTs (data from TAIR), an additional 2,912 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 1,126 genes with expression detected only by microarray analysis (data provided by GEO and TAIR); **Subcellular localizatio**n – 3,944 loci with experimental evidence and an additional 3,047 genes with other evidence (data from TAIR and Harvey Millar/ SUBA database); **Biological process** – 2,637 genes with experimental evidence and an additional 2,490 genes with other evidence (data from TAIR); **Molecular function** – 1,639 genes with experimental evidence and an additional 1,436 genes with other evidence (data from TAIR).

# Broader Impacts of Arabidopsis Research

## Impacts on Industry

In the 1990's, the availability of affordable, high throughput sequencing technologies provided an opportunity for the broader plant community to consider the "impossible"—to generate the nucleotide sequence of a plant genome. At that time, *Arabidopsis thaliana* was selected for use in extensive public and industry sequencing efforts because of its small genome and because of the wealth of available biological information and mutant resources that could be used to facilitate gene discovery and the elucidation of gene function. In 2000, the *Arabidopsis* genome sequence was completed, ushering in a new era of high throughput gene discovery and enabling technologies for systems-biology. Efforts in new and existing agricultural biotechnology companies were initiated in part because of the unique opportunity to rapidly isolate novel plant genes and assign gene function in *Arabidopsis* to commercialize and capture intellectual property. One measure of the intense use of *Arabidopsis* in gene discovery with potential commercial implications is the rapid increase from a few to over 700 utility patents referencing *Arabidopsis* that were issued by the United States Patent and Trademark Office over a 20-year period from 1986 – 2006 (Figure 4). Today, *Arabidopsis thaliana* stands alone as the premier model system for plant functional genomics. Over the years, its use for gene discovery has catapulted analogous efforts in plants of agronomic importance to discover novel genes involved in processes of economic value and to develop new strategies for commercialization using transgenic plants and marker-assisted breeding. The following illustrates some examples of research utilizing *Arabidopsis* that have translated to other plant species and/or led to a commercial product.

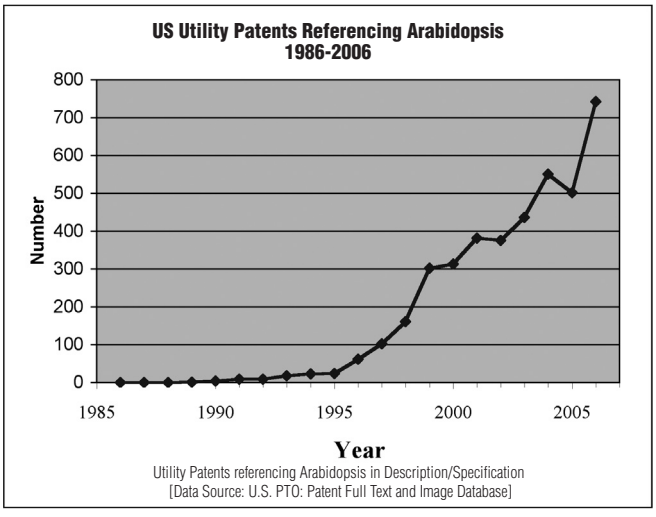



**Figure 4**

## Translational Research Examples Using Arabidopsis

### Improved Drought Tolerant Canola

Peter McCourt [1] and Yafan Huang [2]

[1] Dept. of Cell and Systems Biology, University of Toronto; Toronto, Canada; mccourt@botany.utoronto.ca

[2] Performance Plants Inc. Bioscience Complex, Queen's University; Kingston, ON, Canada

Protecting crops from various environmental stresses has always been a major challenge for modern agriculture. Drought, for example, imposed huge reductions in crop yields and now the era of climate change has added a new scale of urgency to this problem. Therefore, an understanding of the mechanisms of how a plant deals with water scarcity is not only of fundamental interest to plant biologists but possibly can be wedded with biotechnology to create molecular targets for plant breeding. In this respect, one promising target has been the plant hormone abscisic acid (ABA). Under drought conditions, endogenous ABA levels increase within the plant and this in turn leads to better water use efficiency through a variety of complex signaling pathways. Because ABA appears to coordinate many stress-regulated responses any genetic manipulation that increased ABA responsiveness, in principle, could improve on how plants deal with drought stress.

An *Arabidopsis* loss-of-function plant was identified that not only increased seed ABA sensitivity but also reduced wilting of whole plants under drought stress (1, 2). The gene defective in the mutant, *ERA1*, encodes one subunit of a protein farnesyl transferase suggesting that a negative regulator of ABA action needs to be farnesylated to function. Moreover, this also suggested inhibition of this post-translational modification by molecularly manipulating either protein subunit could be used to improved drought tolerance in crops. Transgenic *Brassica napus* (Canola) carrying an antisense *ERA1* construct under the control of a drought-inducible promoter were developed (3). As expected, the antisense downregulation of the canola farnesyltransferase significantly reduced water loss under drought conditions. Three consecutive years of field trials performed by Performance Plant Inc. (4) in Alberta, Canada showed that under moderate drought stress seed yields of antisense *ERA1* transgenic canola were 15-26% higher than the controls. Within ten years of its identification in the laboratory using *Arabidopsis*, molecular manipulation of *ERA1* is having profound impacts in the farmer's field.

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## Biodetection of Landmines by Arabidopsis thaliana

Carsten Meier[1] & John Mundy[2]
[1]Co-founder and CSO, Aresa Biodetection, Symbion Science Park, Copenhagen, Denmark; cm@aresa.dk
[2]Dept. of Molecular Biology, University of Copenhagen, Copenhagen, Denmark

Landmine Monitor has identified at least 84 countries contaminated with landmines and unexploded ordnance (UXO) and calculates that as of 2005, more than 200,000 square kilometers of the world's landmass is suspected to be contaminated by mines and UXO (1). Depending upon the environment and mine types, current de-mining programs employ vehicular detonation or manual removal after detection by radar/tomography, painstaking prodding by volunteers, or scenting by trained animals. Mine scenting by animals is possible because mines release detectable explosives, such as trinitrotoluene (TNT), and their degradation products including di-nitrotoluene (DNT) and nitrogen dioxide (NO2). Aresa (2) isolated the 5' upstream sequences of 15 *Arabidopsis* genes whose transcription is upregulated in plants grown in soil contaminated with explosives. These promoter(s) were candidates for developing biosensor plants that can detect chemicals released by soil-embedded landmines and respond by producing visible pigments.

Starting with *Arabidopsis* mutants blocked in an initial step of anthocyanin biosynthesis as the genetic background, Aresa introduced an inducible 'sensor' transgene that caused accumulation of high levels of anthocyanins in response to nitrogenous compounds. These biosensor plants appeared green when grown under standard conditions but accumulated anthocyanins and became darkly pigmented when grown on TNT-containing medium or soil. The plants were next tested to determine their detection capability in real-world situations. Buried landmines were covered with transgenic biosensor *Arabidopsis* seeds and resulting plants were sampled photographically and for anthocyanin content over a 3 month period. One transgenic line clearly responded to the landmines by exhibiting localized, visible pigment accumulation and increased anthocyanin content. An additional test facility exists at a military base in Denmark and similar test sites are under construction in Croatia and Bosnia Herzegovina. While Aresa has developed a basic system and methodology to explore field use, the first field test in 2006 indicated that initially engineered plants of the *Col-0* ecotype may not be robust or large enough for field work in all climates. Aresa has crossed experimental plants to other *Arabidopsis* ecotypes and their progeny will be tested in 2007 in Denmark, Croatia and Africa. The system warrants further testing and possible improvement using promoters exhibiting more stringent responses to explosives or their degradation products.

*References*
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## Staygreen in the Grass

Ian Armstead[1] and Ian King[2], and Joanna Friesner[3]
[1] Plant Genetics and Breeding Dept, IGER, UK; ian.armstead@bbsrc.ac.uk
[2] Plant Genetics and Breeding Dept, IGER, UK
[3] Edited by the MASC Coordinator, University of California, Davis

The staygreen trait, characterized by extended greenness in plant leaves and cotyledons, is caused by a gene mutation that disrupts chlorophyll degradation leading to delayed senescence. The trait also contributes to stress tolerance and productivity. A naturally-occurring staygreen variant was identified over two decades ago in the forage grass *Fetusca pratensis* and the phenotype has been incorporated into commercial grass varieties to produce greener landscape turf (1). However, the undetermined genetic basis of the staygreen mutation has hindered further use of this economically significant trait in breeding programs. To identify the genetic basis of the staygreen mutation, *sgr*, Armstead and colleagues first used chromosome introgression followed by mapping to identify a candidate region. Previous studies had established a syntenic relationship between this area and a region of a rice chromosome which also contained an *SGR* locus. Fine mapping indicated that *SGR* was likely to be one of about 30 genes on rice chromosome 9, including a promising candidate gene predicted to be a senescence-inducible chloroplast stay-green protein. To gain insight into a possible function for *SGR,* Armstead and colleagues turned to *Arabidopsis thaliana*. Analysis of temporal and organ-specific expression patterns of *Arabidopsis* genes orthologous to the 30 candidate rice genes identified one locus to be clearly upregulated for expression during the period of maximal senescence in leaves of *Arabidopsis*, placing gene activity in the right timeframe and tissue for involvement in leaf senescence (2). More convincing evidence was provided from RNAi experiments that silenced the *Arabidopsis SGR* gene, resulting in plants with a staygreen phenotype equivalent to the original staygreen *F. pratensis* plant. Chlorophyll degradation in the *Arabidopsis* RNAi lines was greatly reduced compared to control plants after dark incubation consistent with a role for *SGR* in chlorophyll catabolism (3). These results strongly suggested that the orthologous gene in *F. pratensis* is responsible for the staygreen trait.

After the *Arabidopsis* and rice *SGR* loci were identified, molecular techniques were employed to examine the defective *SGR* gene in staygreen grass lines revealing a four base-pair insertion in the gene sequence. This change is predicted to dramatically change the amino acid sequence of the SGR protein, and forms the basis of a molecular marker which co-segregates 100% with the staygreen trait in both existing mapping populations and breeding populations of *Lolium/Festuca*. The identification of this marker associated with *sgr* in grass will accelerate marker-assisted breeding programs, allowing additional varieties to be developed while significantly saving resources and reducing time-to-market.

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## Fruit in a Flash

Leandro Peña and Magdalena Cervera, Dpto. Protección Vegetal y Biotecnología, Instituto Valenciano de Investigaciones Agrarias (IVIA), Valencia, Spain; lpenya@ivia.es

The existence of a long juvenile phase in fruit trees has been one of the limiting factors for their genetic improvement because it prolongs in many years the time required to analyze mature traits. The juvenile phase in citrus ranges from 6 to 20 years; during this time, plants lack the meristematic competence to initiate flowering. The impracticality to evaluate fruit traits in individuals coming from controlled hybridizations or from transformation experiments using juvenile tissues restricts the potential of these technologies for genetic improvement of citrus. The *Arabidopsis thaliana* genes *LEAFY (LFY)* and *APETALA1 (AP1)* are known to regulate flowering initiation and have been shown to promote flower initiation and development when expressed from a constitutive promoter, suggesting that a similar approach might be successful in accelerating the juvenile-to-adult transition in economically important citrus species. Peña and colleagues reported that ectopic expression of *Arabidopsis LFY* or *AP1* induces early flowering in the hybrid Carrizo citrange. Both *LFY* and *AP1*-expressing transgenic citrange plants produced fertile flowers and fruits as early as the first year, notably through a mechanism involving a dramatic shortening of their juvenile phase. Furthermore, expression of *AP1*, being as efficient as *LFY* in the initiation of flowers, did not produce any severe developmental abnormalities. Both types of transgenic trees flowered again in consecutive years, and sexual and nucellar derived transgenic seedlings had a very short juvenile phase, flowering in their first spring (1). Based on these promising results in Carrizo citrange, which is used as a rootstock, the authors chose to investigate whether this strategy could be used to accelerate flowering in economically important *Citrus* varieties. Transgenic *AP1* plants of the commercially relevant Pineapple sweet orange cultivar were produced. The plants were phenotypically normal but flower and bear fruit after 3 years of growth instead of the 10-15 years typically needed under Mediterranean climate conditions.

Current studies involve using *AP1* sweet orange transgenic plants as parents in crosses with non-transformed diploid and tetraploid clementine genotypes that presumably will yield progeny where 50% will flower and set fruit in 1-2 years, thus providing the opportunity to evaluate fruit features very early and to rapidly advance generations. Additional studies include re-transforming *AP1* transgenic citrus plants to test the effects of expression of certain transgenes and flowering-promoting *Arabidopsis* genes in modifying fruit quality traits and improve understanding of flowering and phase change with the goal of controlling generation time in this important tree crop.

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## Plants that Synthesize Altered Protein Patterns

Herta Steinkellner and Richard Strasser, Institute of Applied Genetics and Cell Biology, BOKU-WIEN, Vienna, Austria; herta.steinkellner@boku.ac.at

In recent years plants have become an attractive alternative for the production of recombinant proteins. However, their inability to perform authentic mammalian N-glycosylation may cause a limitation for the production of therapeutics, as most therapeutically relevant proteins need this important protein modification for *in vivo* activity and plant glycan patterns are immunogenic in mammals. Since plant glycans have carbohydrate linkages one approach is to specifically inhibit glycosyltransferases in plants. Studies by Steinkellner and Strasser aim to understand and modify the N-glycosylation pathway in plants to allow synthesis of mammalian-like structures. A compelling prerequisite to reach this aim is the characterization of the entire N-glycosylation pathway in plants, including cloning and molecular characterization of the involved enzymes. In previous and ongoing work they were able to identify and characterize all enzymes involved in the pathway and elucidate the molecular mechanism of this important cellular process in *Arabidopsis thaliana*. This knowledge is now being transferred to biotechnologically more relevant species.

One example of these efforts was the generation of viable *Arabidopsis* mutants that lack several important plant glycosyltransferases and instead, synthesize a human type N-glycan profile (1, 2). Subsequently this knowledge was transferred to *Nicotiana benthamiana*, a species widely used for recombinant protein production, and RNAi lines in the aquatic plant *Lemna minor*, able to produce human monoclonal antibodies with a human-like N-glycan profile were generated (3). The antibodies lacked detectable plant-specific N-glycans and performed better than antibodies expressed in cultured mammalian cells. This result provides a major step towards quality improvement of therapeutically relevant antibodies.

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## TILLING for New Mutants

Abdelhafid Bendahmane, and Michel Caboche, URGV, Evry, France; michel.caboche@evry.inra.fr

The ability to isolate mutants in an organism of interest is clearly of great value to understanding gene function. In *Arabidopsis*, where directed gene mutagenesis is not feasible, one highly successful approach has been to apply insertional mutagenesis to generate randomly-placed insertions. This approach often generates so-called 'knockout mutants' that have complete loss-of-function in the mutated gene. This is frequently a useful outcome but can be a limitation if the interrupted gene is essential, or if a more subtle gene defect gives a desired outcome. Furthermore, systematic inventories of 'knocked out' mutants have been made in *Arabidopsis* and a few other plants species such as rice, but this painstaking effort relies on the fact that these plants have relatively small genomes. To overcome these limitations a process known as TILLING was developed which uses chemical mutagenesis to yield a series of individually-mutated DNA bases in virtually all genes (1). This process is of particular value for essential genes where sublethal alleles are needed.

TILLING requires a special enzyme that detects the mutated DNA, and is often performed using Cel1, an enzyme extracted from celery. However, the Cel1 enzyme is inefficient, reducing its potential to accurately screen DNA samples isolated from mutagenized plants. Researchers in France isolated a similar enzyme from *Arabidopsis*, Endo-1, which performs the TILLING reaction at a consistently high level of efficiency and accuracy (2). The enzyme will allow not only the identification of additional *Arabidopsis* mutants, but also will facilitate identification of mutations in plants with larger genomes, such as crop plants. This enzyme is currently used as a diagnostic tool to discover new mutations in DNA, and is produced by the French company Serial Genetics (3).

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## Convincing Plants to 'Love thy Neighbors'


Jorge J. Casal, IFEVA, Universidad de Buenos Aires, Argentina; casal@ifeva.edu.ar


The global demand for food increases along with the world population, however, at the same time the amount of suitable land for growing crops is shrinking. In order to meet future needs, greater and consistently higher quality yields are needed from cultivated plants; needs that may be addressed in large part through genetic manipulation. Selection of favorable traits occurs on the level of individual plants, however, when plants are grown as commercial crops, the yield of the entire population is of primary importance. Therefore, characteristics that confer an advantage to the individual may be detrimental for the productivity of the crop as a whole. An example of this is the 'shade avoidance response' whereby plants use photoreceptors to detect and respond to the reduced proportion of red (R) compared to far-red (FR) light transmitted through dense canopies. In response to the altered R to FR ratio, plants adjust their growth patterns to avoid crowding, a process that can result in reduced yields. It has been suggested that disabling this response through the manipulation of photoreceptors might increase yields in crop plants. *Arabidopsis* mutants have helped to elucidate the functions of different members of the phytochrome family of photoreceptors. These studies identified *PHYB* as the most important member in plant responses to the R/FR ratio signal. Based on this knowledge, studies were performed to examine the effect of ectopically expressing *Arabidopsis PHYB* in transgenic potato plants. When grown in the field, transgenic plants showed reduced responses to low R/FR light, including increased branching, greater number of tubers produced, higher rates of photosynthesis, and higher yield overall compared to control plants (1). A low R/FR signal normally reduces the amount of active PHYB in plants, but ectopic expression of *Arabidopsis PHYB* provided an additional pool of active PHYB that ameliorated the response. Strikingly, the greatest reduction in response to low R/FR occurred when the plants were grown at very high densities. Despite the overall positive effect of *PHYB* expression, the transgenic potatoes had some limitations as they failed to use the light signals to optimize the position of foliage and light interception. Current studies use *Arabidopsis* to find genes acting downstream of *PHYB* with the goal of selectively reducing negative responses to low red to far-red ratios and retain positive responses (e.g. foliage positioning).

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# Reports of the MASC Subcommittees

## Bioinformatics

Prepared by Chris Town (Co-chair, cdtown@tigr.org) and
Heiko Schoof (Co-chair, schoof@mpiz-koeln.mpg.de)

The main activities in the last year have been a continuation 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). Two developers' workshops were held in the spring of 2006, one at MPIZ-Cologne and one at TIGR. During the workshops, an increasingly detailed set of notes on how to set up the appropriate IT environment and how to implement web services was developed and made available on the project web site. Three of the participants at the Cologne workshop went on to develop their own services once back at their home institution. At the TIGR workshop, several simple web services were set up and deployed from the participants' home institutions during the course of the workshop. One additional service was deployed later. In addition, by remote consulting, a new web service for SeedGenes was deployed without any face-to-face interaction between the project personnel and the SeedGenes informaticians. A "show-and-tell" workshop was held at the International Conference on *Arabidopsis* Research in Madison, 2006 to demonstrate and promote web services. Following the meeting, work continued at MPIZ to advance the concept of a "one stop shop" by developing aggregator pages that will simultaneously query multiple locations for certain types of data. Their essential feature is that relevant web services are discovered automatically: once a data provider makes a BioMoby web service public, that data will be included in the aggregator automatically. Currently, the two best examples of these are tAIGa and LitRep (http://bioinfo.mpiz-koeln.mpg.de/araws/searchtools). tAIGa is short for 'the Arabidopsis Image Gallery' and acts as aggregator for services which take an AGI locus code as input and return one or more image(s). Currently, tAIGa queries seven services giving access to image data from SeedGenes, ABRC, RAPID, ATIDB, AtNoPDB, ProtLocDB and Arex. Like tAIGa, litRep requires the input of an AGI locus code and returns publications as PubMed or PubMedCentral identifiers. Currently four services are integrated, most notably the manually curated collections of bibliographic references of the project partners TAIR and Aramemnon. It will be important in the future both to enrich these pages by encouraging the deployment of additional web services for these data types as well as to begin to aggregate new types of data. One application is enriching databases with external content, as can be seen in MAtDB (http://mips.gsf.de/proj/plant/jsf/athal/index.jsp) where GeneOntology terms, literature references and images are retrieved from BioMoby web services and displayed in the gene report. An important activity during the project has been supporting data providers in updating and maintaining their web services through (mostly remote) consulting with specific BioMoby know-how. In this way, dozens of services hosted e.g. by NASC, the major provider of web services, were reactivated after changes in BioMoby had rendered them inoperable. A list of all services implemented and/or updated can be found at http://bioinfo.mpiz-koeln.mpg.de/araws/web-services/public-ws.

*Lessons Learned and Challenges Faced*

The project has (two) long-term goals:

1a. To educate data providers in the value of web services for data dissemination and to provide the instruction and tools necessary to accomplish this in a relatively straightforward fashion and, ultimately, without the need for a high level of technical expertise;

1b. To encourage the use of web services by an increasing number of data providers;

2. To acquaint and educate users in the potential benefits of web services, initially through the use of aggregator-type "one stop shop" interfaces, but also progressively by introducing them to the concept of workflows through the use of tools such as Taverna.

There are several challenges, but the most significant is identifying a group of data providers who will be proactive both in developing web services *and in maintaining them*. Based upon our experience to date, we believe that the combination of an instructional workshop that provides an overview of Biomoby, its implementation in Perl and Java, its deployment in a test environment and the use of Taverna to develop workflows, segueing into a hackathon where first services are implemented will be the most productive for future efforts.

Instructional media combined with remote consulting is a workable model but the "flying geek" approach has not been tested. Compared with pure remote consulting, workshops provide a stimulating and synergistic environment. Future workshops should be structured around groups of providers that host datasets that are complementary and potentially synergistic. It is important to deploy services during the workshop, since people tend to lose focus on web services very quickly after a workshop is finished. We think this is due in large part to insufficient priority granted to this method of data sharing by the PIs which in turn reflects the lack of community interest or pressure to provide data in this form. To address this, we will strive for better visibility of the achievements of the project as well as to provide novel integration of services that can currently only be performed manually by visiting multiple web sites. We intend to create links to the clients from prominent sites like TAIR and TIGR, preferably integrating remote results in report pages. Also, a paper summarizing our results and experiences is being considered. In

the remaining time of the project, we will try to motivate partners to set up more services and enlist new partners. A list of planned services is available on the project home page.

## Clone-based Functional Genomics Resources

Prepared by Pierre Hilson (Chair, pierre.hilson@ugent.be)

A number of consortia and individual laboratories have created clone resources that they chose to share with the research community at large via stock centers located in the USA, Europe and Japan:

- the Arabidopsis Biological Resource Center (ABRC, USA) http://www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm
- the RIKEN BioResource Center (BRC, Japan) http://www.brc.riken.jp/lab/epd/Eng/catalog/pDNA.shtml
- the GABI Primary Database (GABI/RZPD, Germany) http://gabi.rzpd.de/
- the National Resources Centre for Plant Genomics (CNRGV, France) http://cnrgv.toulouse.inra.fr/ENG/index.html
- the Center for Eukaryotic Structural Genomics (CESG, USA) http://www.uwstructuralgenomics.org/
- the European Arabidopsis Stock Centre (NASC, United Kingdom) http://arabidopsis.info/
- the BCCM/LMBP Plasmid and DNA library collection (BCCM/LMBP, Belgium) http://bccm.belspo.be/db/lmbp_gst_clones/
- The table below provides an overview of the type of clones these stock centers distribute including full length cDNAs, ORFs and silencing vectors. Most of the collections have been created in format compatible with recombinational cloning protocols.
- Access to well-documented and cheap clones undoubtedly boosts *Arabidopsis* research projects. These clones are exploited by scientists interested in the functional characterization of only a few genes. They also enable more systematic approaches focusing on the analysis of large gene sets. But despite these great assets, and unlike developments in other eukaryotic model species, *Arabidopsis* clone-based functional genomics datasets are still rare. Future progress in this area will depend on the funding of ambitious projects and on the development of novel technologies for the high-throughput analysis of genetic perturbations introduced in plant cells.

| Creator | Format | Focus | Validation | Count | URL | Stock center |
|---|---|---|---|---|---|---|
| ***ORF clones*** | | | | | | |
| SSP consortium & Salk Institute | Univector pUNI51 | Random | Full sequence | 14,154 | signal.salk.edu/2010/index.html | ABRC |
| Salk Institute | Gateway entry | Random | Full sequence | 1,012 | signal.salk.edu/2010/index.html | ABRC |
| TIGR | Gateway entry | Hypothetical genes | Full sequence | 2,110 | www.tigr.org/tdb/hypos/TargetGeneList.shtml | ABRC |
| Peking-Yale Joint Center | Gateway entry | Transcription factors | 5' and 3' end seq. | 1,150 | | ABRC |
| Dinesh-Kumar et al. | Gateway Expression (from Peking-Yale JC) | TAP-tagged transcription factor | | 1,100 | | ABRC |
| REGIA | Gateway entry | Transcription factors | 5' and 3' end seq. | ~ 1,000 | gabi.rzpd.de/materials/ | GABI/RZPD |
| CESG | Gateway entry c | Potential new fold | Full single pass seq. | ~ 1,500 | www.uwstructuralgenomics.org/cloning.htm | CESG |
| ATOME 1 | Gateway entry | Random | 5' and 3' end seq. | ~ 2,000 | http://www.evry.inra.fr/public/projects/orfeome/orfeome.html | CNRGV |
| ATOME 2 | Gateway entry, no stop | Random (from SSP) | 5' and 3' end seq. | ~ 3,500 | same | CNRGV |
| Doonan et al. | Gateway Expression (from SSP) | 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 | 50 | http://genetics.mgh.harvard.edu/sheenweb/category_genes.html | ABRC |
| ***cDNA clones*** | | | | | | |
| RIKEN/SSP/ Salk Institute | λ ZAP or λ PS | Random | Full sequence | 16,913 | http://www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml | BRC |
| RIKEN/SSP/ Salk Institute | λ ZAP or λ aPS | Random | Single pass | 246,640 | same | BRC |
| MPI-MG | Gateway expression | Random | 5' end seq. | 4,500 | gabi.rzpd.de/materials/ | GABI/RZPD |
| Génoscope/LTI | Gateway entry | Random | Full single pass seq. | 28,743 | www.genoscope.cns.fr/Arabidopsis | CNRGV |
| ***RNAi clones*** | | | | | | |
| AGRIKOLA | Gateway entry | Random | PCR sized insert | 28,049 | www.agrikola.org | NASC, ABRC |
| AGRIKOLA | Gateway entry | Random | Pure, seq. validated | 368 | http://bccm.belspo.be/db/lmbp_gst_clones/ | BCCM/LMBP |
| AGRIKOLA | hp RNA expression | Random | PCR sized insert | 26,318 | www.agrikola.org | NASC |
| CFGC | ds RNA expression | Chromatin remodel. | Single pass seq. | 162 | www.chromdb.org | ABRC |

## Metabolomics

Prepared by Ian Graham (Co-chair: iag1@york.ac.uk) and Basil Nikolau (Co-chair: dimmas@iastate.edu)

The Metabolomics Subcommittee's primary activity of the past year has been focused on fully integrating into the Metabolomics Standards Initiative (MSI) (http://msi-workgroups.sourceforge.net/). The MSI effort lead by Dr. Oliver Fiehn (University of California, Davis) has established minimum standards for the reporting of metabolomics experiments. This has been achieved by a number of MSI-subcommittees with foci on issues associated with: 1) Biological Sample Context; 2) Chemical Analysis; 3) Data analysis, 4) Ontology, and 5) Data exchange.

Each sub-committee drafted documents that outlined the minimum standards. Reactions to these drafts were sought, first from a small group of metabolomics practitioners. Subsequently, reactions to these drafts were sought from attendees at two major metabolomics conferences (the 4th International Congress on Plant Metabolomics, held in Reading, England in April, 2006; and the Metabolomics Society Annual Scientific Meeting, held in Boston, USA in August, 2006). After integrating comment received from these reactions, manuscripts that describe the standards have been prepared, which are currently in the midst of the publication process.

## Natural Variation and Comparative Genomics

Prepared by Tom Mitchell-Olds (Chair, tmo1@duke.edu)
*Note: expanded reports will be available online at http://www.arabidopsis.org/portals/masc/masc_docs/masc_sub_rep.jsp*

### Natural Variation

*Arabidopsis* offers a resource for studying not only gene function but also ecological processes in modern contexts. One important benefit of studying natural variation in *Arabidopsis* is the extension of gene function and effects from the individual to the species level. Additionally, plants provide the best system for studying environmental responses. Since plants have adapted to different environments, they are particularly good system for studying environmental adaptation. These analyses have clear relevance for evolutionary studies in general, as well as providing benefits for agriculture, understanding of biological responses to global climate changes, and other economically important problems. However, there are a number of challenges facing researchers studying Natural Variation in *Arabidopsis*. Even with the ever-growing set of resources available, the ability to study variation between *Arabidopsis* accessions requires more resources than most areas of *Arabidopsis* research. Seed collections of *Arabidopsis* accessions maintained by individual labs should be deposited in public stock centers. Furthermore, recent expansion and internationalization of this research community creates increasing needs for electronic and institutional facilitation of communication among research groups. Funding for *Arabidopsis* research has been declining in some regions making the competition for resources greater each year. These issues can be partly addressed through greater coordination of resources and effective communication.

*Major obstacles to Natural Variation studies*

(1) Seed contamination is a consistent problem. A genetic fingerprint of relevant lines and a fast assay would be an excellent development. Several labs are working towards solutions to this problem. This approach also should be deployed at the stock centers.

(2) Limited availability of viable seeds from related species restricts comparative studies.

*Key needs in the field*

(1) Accession Resources: Recombinant inbred lines (RILs), near isogenic lines (NILs), and other pedigreed, genotyped populations are of enormous value as are genetic and molecular resources for efficient mapping and genotyping. Widespread collections of natural accessions, collections suitable for association studies and comparative sequence information from related species are needed. It would be extremely valuable to have RIL sets bulked and densely genotyped, and common sets of densely genotyped accessions are needed for genome-wide association mapping. Efforts are needed to collect and characterize populations in ancestral habitats. In the longer term, complete genomic sequences from many accessions will be extremely valuable.

(2) Genetic tools appropriate for ecological studies are needed: The lack of ecological information on the public seed stocks is a severe impediment to our understanding of natural variation. More seed collections are needed from refugial locations and from recently introduced populations, a thorough characterization of the geographic and ecological range of *A. thaliana* is needed, and ecological information from sites of collection is essential. In addition, a series of maintained field sites that span latitude, longitude, and habitat would be extremely valuable. It would be extremely useful to have a dedicated resource for *Arabidopsis* field research in Europe and North America—European sites representing both ancestral and introduced sites, and North American sites representing unambiguously introduced sites.

(3) Genetic resources using an appropriate genetic background for ecological studies need to be developed: Currently, many mutant lines and transgenic materials have been constructed in the Landsberg *erecta* (Ler) mutant background, however, Ler is not the most appropriate ecotype for natural variation studies and a suite of ecotypes is needed.

(4) Discussion regarding appropriate growth conditions and phenotyping protocols, especially relating to environmental variation among natural populations, is needed: It is important to emphasize the environment-dependence of phenotypes, and the utility of standardizing phenotypic measurements across different environments.

(5) Community databases for sharing of phenotype and QTL information are needed to allow direct comparison among studies: WebQTL/The Gene Network (http://www.genenetwork.org/) provides an early example, including data from *Arabidopsis* RILs. Likewise, a centralized web resource listing current and past grants on *Arabidopsis* research would be very useful.

*Relevant Natural Variation databases*
In addition to TAIR, most relevant databases belong to individual labs (e.g., http://naturalvariation.org/, http://www.dpw.wau.nl/natural/, http://www.inra.fr/internet/Produits/vast/, http://www.genenetwork.org/, http://www.mpiz-koeln.mpg.de/masc/index.html); it would be desirable to have all information on genotyping and phenotypes of accessions and mapping populations coordinated at TAIR.

### Comparative Genomics

Comparative genomic data have been used to improve annotation of genes in *A. thaliana* and will allow development of more appropriate models for traits important in agricultural or natural habitats, such as apomixis, or tolerance to drought, heavy metals, or high salt concentrations. Comparative genomics with *Arabidopsis* relatives will be facilitated by rapid advances in new sequencing technologies and by three high-quality genome sequences that are pending (*A. lyrata*, *C. rubella*, and *Thellungiella halophila*). In *Brassica*, coordinated international efforts are moving forward with BAC by BAC sequencing of *B. rapa*. The genome sequence of papaya will serve as an outgroup for comparative genome analysis of the family *Brassicaceae.* Examples of other developing areas include *Thellungiella* (*T. halophila* has been approved for sequencing at JGI), heavy metal-resistant *Thlaspi* genus and *Arabidopsis halleri*, and *Boechera*, a model for ecological studies among *Arabidopsis* relatives.

*Major Obstacle to Comparative Genomics*
Limited financial resources for *Brassicaceae* comparative genomics is a fundamental problem. Among the close *Arabidopsis* relatives, only *Brassica* is an economically important crop plant. Consequently, funding sources which focus on *A. thaliana* or on crop species provide little support for many aspects of *Brassicaceae* comparative genomics.

*Key needs in the field*
(1) Establishment of phylogeny of related species is needed: Although many clusters of closely related species are known in the *Brassicaceae*, the ordering of tribes within the family contains many unresolved nodes. This large-scale framework is essential for planning and interpretation of comparative genomics experiments. In order to resolve phylogenetic relationships across the family, information is required from multiple loci from the major groups in the crucifers. An important unsolved problem is to determine optimal evolutionary distances for genomic comparisons examining a range of evolutionary and functional questions.

(2) Discussion and agreement on the goals for model systems and the species to develop is needed: Genomic models should be selected carefully and democratically. Important factors include phylogenetic position, interactive user communities, unusual physiological and morphological traits, and groups for which ecology is well studied. Experimental advantages include conserved orthologous markers, integrated linkage and physical maps which can be anchored to genome sequences, efficient transformation, rapid cycling lines, physiological and anatomical studies, multi-species and multi-tissue transcriptome datasets, informatics, inbred lines for sequencing, suitability for interspecific crosses and genetics, and well-documented and accessible germplasm collections.

(3) Integrated bioinformatics tools that can move between *Arabidopsis* and other *Brassicaceae* genomes are desperately needed for the crucifer genomics community. There is also need for more taxonomic and morphological information for the evolutionary and genomics communities.

*Relevant Comparative Genomics databases*
Existing databases in Britain and Korea focus on *Brassica* resources (accessible via www.brassica.info) TAIR (and others) focus on *Arabidopsis* (www.arabidopsis.org). A papaya genome database is being developed by Andrew Paterson's lab.

## Phenomics

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

*New Phenotyping Facility Approved in Australia*
The Australian Government has recently awarded funding for a new Australian Plant Phenomics Facility (APPF) to be established. The APPF aims to be a state-of-the-art plant phenotyping facility with sophisticated plant growth facilities and cutting edge technologies for plant performance and function monitoring. Construction of the Facility is expected to begin in 2007. A primary objective is the analysis of model species such as *Arabidopsis* and rice for gene function discovery. The technologies used for screening will include various imaging approaches including morphological growth and colour analysis, chlorophyll fluorescence and hyperspectral reflectance. These will be coupled to robotic systems which will allow medium throughput screening of plant material grown under controlled environment conditions. See the Australia country report for further information.

*Updates on Phenomics Resources*
- Homozygous Mutant *Arabidopsis* Collection
    1. This project at the Salk Institute aims to create a 'phenome-ready' genome through the identification of two T-DNA homozygous mutants for every *Arabidopsis* gene. As of March, 2007, the project has sent seeds from 9,198 plant lines representing 7,105 individual genes to the ABRC (US) for distribution. (http://methylome.salk.edu/cgi-bin/homozygotes.cgi). Seeds of the Salk homozygous lines are being prepared at ABRC for forward screening. Pools of lines will be available, and the feasibility of distributing sets of individual lines is being investigated.
    2. The Homozygote Collection Gene Family Viewer is a new resource that groups genes by gene family, and lists the corresponding homozygous plant lines currently available, or that are being targeted, for each gene. Selecting a gene reveals a diagram of the sequence and the insertion location(s) and line(s) available for that gene. Genotyping primer sequences are included, and you can select lines to order. (http://methylome.salk.edu/gene_fam/)

- At the RIKEN Plant Science Center (Japan) two types of mutant resources are being developed for phenome analysis:
  1. Ac/Ds type transposon lines containing single gene insertions. A recent publication describes phenomic analysis of 4000 Ds mutants. (RAPID: http://rarge.gsc.riken.jp/phenome/ and Kuromori *et al*, Plant J. (2006) 47:640-651). Homozygous Ds mutant lines are also being generated.
  2. Full-length cDNA overexpression (FOX) lines: gain-of-function mutant resource overexpressing *Arabidopsis* flcDNAs in *Arabidopsis* plants. Over 10,000 FOX lines were made out of around 10,000 independent full-length cDNAs. A database including these mutant lines is under preparation. (Ichikawa *et al*, Plant J. (2006) 25:974-985
- The AGRIKOLA consortium has constructed a collection of 26,318 plasmids each capable of triggering RNAi against a defined target sequence in an *Arabidopsis* transcript. The collection covers at least 22,087 different genes. 3,848 of these plasmids were used to transform *Arabidopsis* and up to 12 transformants from each transformation were visually inspected for putative RNAi-induced phenotypes. Four individual lines from 322 of these transformations were more thoroughly phenotyped in the T2 generation. The data obtained give valuable insights into the efficacy, specificity and stability of RNAi-induced phenotypes in plants for a very wide range of target genes. Ontological descriptions of mutant phenotypes have been generated for plants carrying constructs against 250 different target genes.
- Artificial microRNAs: a complementary tool for gene silencing. A new versatile tool for gene knockouts that complements T-DNA insertions and TILLING lines are artificial microRNAs (amiRNAs). AmiRNAs allow highly specific and predictable gene silencing, from constitutive, inducible or tissue-specific promoters. A particular advantage of amiRNAs is that they allow the simultaneous inactivation of several, sequence-related genes. An important application is the analysis of tandemly duplicated genes, which are difficult to knock out by conventional means, as well as knockout of genes in accessions other than the standard Columbia strain. A web-based platform for the design of amiRNAs has been developed by the Max Planck Institute for Developmental Biology (http://wmd.weigelworld.org). The platform includes automated primer design for cloning into the pRS300 vector. In addition, Cold Spring Harbor Laboratory has obtained NSF Arabidopsis 2010 funding to generate multiple amiRNAs against all genes in the *A. thaliana* genome, including pairs of segmentally duplicated genes and tandemly duplicated genes (AT2010 award #0617983.) The corresponding ~80,000 amiRNAs were also designed by the Max Planck Institute for Developmental Biology. Preliminary user feedback indicates that amiRNAs are successful in about 75% of all cases.

*New Phenotype data and tools at TAIR*

In the last 12 months TAIR has separated phenotype data from other germplasm information and now stores phenotype descriptions for 1768 genes, including 417 genes identified as mutants but lacking sequence information and 1351 sequenced genes with AGI codes. TAIR has also added the capacity to search for genes, germplasms, and polymorphisms using associated phenotype information. The gene, locus, germplasm, polymorphism and stock detail pages were also updated to display phenotype data. When available, the reference that describes the phenotype is cited. TAIR curators will continue to extract phenotype descriptions along with other types of data from the current literature and add them to TAIR. It is expected that TAIR will transition to using the GO (Gene ontology), PO (Plant Ontology) and PATO (phenotypic quality) controlled vocabularies to describe phenotypes in the coming year.

*NCBiO develops phenotype curation tool*

A curation tool designed to annotate phenotypes using an EQ model (entities represented by Gene Ontology or Plant Ontology terms combined with qualities such as absent, abnormal, decreased length, etc. represented by the PATO ontology) has been developed by Mark Gibson for NCBiO. Genotypes and publications can also be associated with each phenoytpe annotation. The standalone tool, called Phenote, is available for download from http://www.phenote.org/. The PATO ontology is undergoing rapid development, see http://www.bioontology.org/wiki/index.php/PATO:Main_Page for more information and to submit new terms.

*Publications / presentations / workshops relating to Arabidopsis PO/ PATO and phenotyping*

- The Plant Ontology Consortium (POC, http://www.plantontology.org), formed in 2003 and headed by Lincoln Stein, presented a summary "The Role Of Plant Ontology In Comparative Plant Genomics And Gene Discovery" at Plant & Animal Genome XV (available at http://www.intl-pag.org/15/abstracts/PAG15_P08a_841.html). For contact purposes, the coordination of PO has passed from Katica Ilic (ex-TAIR) to Chih-Wei Tung (Cornell University).
- A subset of the PO consortium published a definitive paper (Plant Structure Ontology. Unified Vocabulary of Anatomy and Morphology of a Flowering Plant. Ilic *et al* Plant Phys. Dec 2007); describing the rationale and development of the ontology for *Arabidopsis* by TAIR, and subsequent integration into a range of databases (including a description of the PATO implementation at NASC).

*Open Workshops*

- Ontologies, Standards and Best Practice, PSB, Gent (Belgium), May 21-23, 2007 - including a practical by NASC on the laboratory use of PO and PATO; talks on the integration of PO/PATO into NASC (since 2005 but now including web-services); and presentations on the development and applications of PO as a coordinated program by Katica Ilic and Chih-Wei Tung. See: http://www.agron-omics.eu/
- Growth Phenotyping and Imaging in Plants, LEPSE, Montpellier (France), July 17-19, 2007 - including presentations of automated phenotype analysis, growth imaging and modeling for leaves and roots. See: http://www.agron-omics.eu/

## Proteomics

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

Proteomics using *Arabidopsis thaliana* as a model system has made great progress in recent years. The throughput and accuracy of protein identification techniques relies strongly on the availability of whole genome sequences. The availability of both a complete genome sequence and high quality genome annotation makes *Arabidopsis* an ideal system to develop new proteomics technologies and identify candidate genes for development and differentiation of plant cells. Furthermore, *Arabidopsis* proteomics research may serve as a paradigm for other plant proteomics research projects and the advancement of plant proteomics in general. And finally, *Arabidopsis* proteomics enables the development of a unique platform for plant systems biology by integrating proteomics databases with existing transcriptomics and novel metabolomics and bioinformatics initiatives. Due to the enormous complexity of a dynamic proteome, different approaches have to be combined to measure protein expression and dynamics, stress- and developmental responses, posttranslational protein modifications and protein interaction. Although the *Arabidopsis* functional proteomics projects are progressing well in general, technical obstacles still remain to be overcome. The development of proteomics techniques for plant biology applications is showing strong progress, and some of these are probably groundbreaking methods that will be generally applicable to work in other model species. However, proteomics has not yet reached its goal. We are still in the process of initial data generation, and in the face of the enormous complexity of the dynamic proteome, substantial method development is still needed, especially in the fields of quantitative proteomics and the dissection of signaling pathways involving post-translational modification. Therefore, this working group devoted to *Arabidopsis* proteomics aims to combine the efforts of different research groups to develop programs which will consolidate databases, technique standards and experimentally validated candidate genes and functions. The subcommittee plans to build a continuing presence at the International Conference on *Arabidopsis* Research (ICAR) in the form of a workshop. This would aim to discuss methods/practice of proteomics, to inform the community, make new contacts, and to develop initiatives for new activities of the subcommittee. In the future symposia with invited speakers will be organized where proteome analysis in *Arabidopsis* is a key theme. The first proteomics workshop took place at the 2004 Berlin meeting before the subcommittee was formed. The next workshop is planned for the 2007 ICAR in Beijing, and then on a regular basis.

*Subcommittee activities in 2006/2007*

We have developed a proteomics subcommittee webpage that includes links to existing databases of *Arabidopsis* proteomics. The goal of this webpage is to disseminate standards for sample handling and data interpretation. Furthermore, we consider it a platform for the *Arabidopsis* community to exchange ideas and protocols and to spark discussions among interested researchers. Developed in the spirit to facilitate scientific networking, this webpage will foster interactions between plant proteomics researchers by providing contact information of proteomics laboratories and assembling information on meetings. Furthermore, we will crosslink the MASC efforts with a recently launched European COST initiative on Plant Proteomics using our webpage as an information exchange platform. The website will be available at the TAIR website (http://www.arabidopsis.org/portals/masc/Subcommittees.jsp)

Subcommittee members have been involved in several initiatives to develop databases and software tools for the exploitation of *Arabidopsis* proteomics data:

- A database for the subcellular location of *Arabidopsis* proteins (SUBA). The database houses large scale proteomic and GFP localisation sets from cellular compartments of *Arabidopsis*. (www.suba.bcs.uwa.edu.au).
- A repository of searchable MS/MS spectra as a protein/peptide-reference library for the Arabidopsis thaliana proteome integrating different levels of molecular organization including metabolites, pathways, and transcript expression (ProMex) (http://promex.mpimp-golm.mpg.de/cgi-bin/peplib.pl)
- Tools for the protein database-independent identification of MS/MS spectra in order to allow improving genome annotation with proteomics data (http://cvs.sourceforge.net/viewcvs.py/sashimi/qualscore/
- Further activities and web resources will be found at the MASC proteomics website (http://www.arabidopsis.org/portals/masc/Subcommittees.jsp).

*Subcommittee future goals*

- Establishment of a high density proteome map of *Arabidopsis thaliana* using different tissues and high-throughput mass spectrometry as a basis for future systems biology approaches
- Discuss international network grant proposals for plant proteomics.
- Develop standards for two-dimensional gel-electrophoresis, shotgun proteomics, and quantitative proteomics.
- Write guidelines for minimal requirements for different types of proteomic studies and distribute these to plant journals (especially: Plant Molecular Biology, Plant Physiology, Plant Cell, and the Plant Journal) for their consideration of publication standards—issues include experimental method, data analysis and call of identifications.
- Work towards a central international database of MS/ MS spectra derived from *Arabidopsis* samples.
- Collaborate with other interested parties on *Arabidopsis* proteomic data storage.
- Seek funding opportunities for the exchange of students and young researchers between different labs in order to develop a common training initiative

## Systems Biology

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

A primary goal of the subcommittee is to further the use of Systems Biology among *Arabidopsis* researchers to elucidate

the structure, dynamics, and organizational principles of the regulatory and metabolic networks that support living cells. Although there is no widely agreed upon definition of Systems Biology, most work in this field can be characterized as an effort to identify the molecular interactions that underlie cellular function and to integrate them in a coherent model. What distinguishes Systems Biology from fields like Molecular Genetics, which have the same ultimate goal, is the approaches that are used and the perspective taken. Systems Biology uses high-dimensional data that are usually acquired through high-throughput approaches such as microarrays, together with more focused high-resolution and high-content data, particularly time series. The elements within the large datasets are seen as a parts list and an initial goal is to find the connections among the parts. This leads to the identification of modules that frequently have properties that would be difficult to predict from the collection of parts. These are referred to as emergent properties. When connections are found between modules it can lead to the identification of networks. Once networks are identified, Systems Biologists seek to determine how the networks function. This is done by perturbing them with external stimuli or by removing or increasing the activity of one of the parts. Perturbation of the network can lead to an understanding of the dynamics "over" the network - for example how information flows through a signaling network.

Systems Biology also seeks to understand the dynamics of networks in the sense of how networks become modified as cells alter their states. A salient feature of Systems Biology is the tight integration of quantitative reasoning with biological experimentation. Modeling approaches are drawn from statistics, dynamic systems, linear algebra and topology, to name a few. The reliance on modeling approaches is driven by the high dimensionality of the data and the complexity of the networks that govern cellular function. Most Systems Biology today is carried out by interdisciplinary teams of scientists with backgrounds in Computer Science, Mathematics, Physics, Engineering, Statistics, and Biology.

- Given the shortage of theoreticians currently working on questions in plant science, a short-term goal of the subcommittee is to bring together additional researchers from primarily quantitative backgrounds with experimentalists working on *Arabidopsis* to address Systems Biology questions.
- A second goal is to promote public data repositories and benchmark data sets, which allow theoretical work with wider scope and on larger scales.
- A medium-term goal is to facilitate the development of international consortia in *Arabidopsis* systems biology by promoting communication among emerging national Centers and research programs.
- A long-term goal will be to promote the application of Systems Biology approaches to a wide range of plant science problems.

*Subcommittee plans*

- The subcommittee will plan a workshop to coincide with the next International *Arabidopsis* Conference (Montreal, 2008).
- It will also work with the other MASC subcommittees that interface closely with work in Systems Biology, and build links to the relevant community organizations in Systems Biology, theoretical and computational biology. One aim here is to recruit theoretical researchers by publicizing some of the contemporary questions in *Arabidopsis* research, and making the relevant *Arabidopsis* data very easily accessible.
- Another aim is to benefit from existing models and modeling expertise in other organisms and fields. The subcommittee also will seek input from the rest of the plant community at the next Plant Biology Conference to identify what their needs are, and how *Arabidopsis*, as a model system, can best assist systems biology efforts in other species and benefit from experience of modeling in other areas of plant science. This will facilitate the investigation of agronomically-important and medicinal species. It is anticipated this would the first of many such discussions.

*Recommendations of the Subcommittee*

The amount of *Arabidopsis* experimental data being generated by high throughput methods is growing at a tremendous pace. Indeed, data integration is one of the biggest challenges that we face today in systems biology research. Achieving effective data integration for data analysis and interpretation is crucial to advance plant systems biology.

- This subcommittee will work closely with the MASC Bioinformatics subcommittee to promote the creation of software platforms and data sharing standards to allow systems biology research to be carried out effectively by the *Arabidopsis* community. A key set of challenges center around the creation of experiments and experimental data in a form that is maximally accessible to bioinformatics analysis, biologist-mining and mathematical modeling, and in parallel, the promotion of model-building as a central component of *Arabidopsis* research.
- Comparisons of analysis of the same benchmark data sets by different groups could facilitate our understanding of the strengths and weaknesses of different computational methods in different contexts. For example, one idea, is a systems biology competition, where an *Arabidopsis* dataset is given out with "known information" intentionally missing, and a prize is given to the student who can best predict the missing data.
- Integration of systems biology approaches into teaching, by updating the mathematics content of undergraduate courses in biology (to include modeling, not just statistics) and by updating the plant science examples used in mathematics courses (to include functional genomics and development, not just agronomics).

# Analysis and Recommendations

The goals originally presented in 2002 for the Multinational Coordinated *A. thaliana* Functional Genomics Project covered 5 areas:

(1) Development of an expanded genetic toolkit, including new technology development that enables a broad community of scientists to conduct functional genomics research in *Arabidopsis*

(2) Whole-systems identification of gene function, including global analyses of gene expression, the plant proteome, metabolite dynamics, molecular interactions, and comparative genomics

(3) Expansion of the role of bioinformatics

(4) Development of community and human resources

(5) Promotion of international collaboration

Progress in each of these areas has been generally very good, with just a few areas where more effort needs to be concentrated. A more complete analysis and set of recommendations will be produced following the MASC coordination meeting to be held at the International *Arabidopsis* Conference in Beijing in June 2007.

## An expanded genetic toolkit

Considerable progress has been made through the use of several complementary technologies, including T-DNA insertion collections (covering up to 93% of *Arabidopsis* genes), RNAi constructs (available for 78% of *Arabidopsis* genes) and full-length cDNA or ORF clones (available for 74% and 61% of *Arabidopsis* genes respectively). These resources have proved invaluable for reverse genetics projects, with TILLING resources as a further addition to the arsenal. Natural variation in *Arabidopsis* is also proving to be a powerful aid to functional studies and comprehensive resources in terms of ecotype collections, recombinant inbred lines and SNP data (over 500,000 unique SNPs identified in 20 accessions) are now available. Projects underway include the generation of comprehensive collections of artificial microRNAs and the construction of homozygous mutant lines for at least 25,000 *Arabidopsis* genes, including T-DNA and transposon insertions.

*Recommendations*

- The resources available are superb, but efforts to complete these collections should continue to be supported.
- The emphasis should start to shift from generating new resources towards analyzing those that already exist. Much more effort needs to be put into profiling and phenotyping the current genetic resources whose full potential is not being realized due to a lack of well-funded projects capable of systematically analyzing sufficient numbers of plants.
- In the same vein, insufficient use of the clone resources has been made so far. One area where *Arabidopsis* research has lagged behind that in other model organisms is in molecular interaction data. Protein-protein, protein-DNA and protein-RNA interaction data for *Arabidopsis* are sketchy and poorly integrated with other functional genomics data. Strong efforts are needed in this area before credible network analyses can take place. The ORF libraries available for *Arabidopsis* allow these types of experiments to be envisaged on a genome-wide scale.

## Global molecular profiling

Abundant resources are now available for transcript profiling in *Arabidopsis* including multiple formats of whole transcriptome arrays from several commercial suppliers and the ability to make custom microarrays at affordable prices. Whole genome tiling arrays are commercially available. High-throughput quantitative RT-PCR analysis of transcripts is proving increasingly popular, especially for low-abundance transcripts. Transcriptome data from large collaborative experiments (such as AtGenExpress, CAGE) are being made available and being pooled with many smaller studies from individual labs in interactive databases such as Genevestigator, NASCArrays or Expression Angler. These resources are extremely popular with researchers and have greatly facilitated gene expression analysis. Further improvements in transcript analysis will come from increased precision in collecting RNA samples to obtain cell-type specific or even single-cell samples, or samples from particular cell compartments, or samples bound to particular proteins. A full understanding of gene expression control will require this precision.

Proteomics and metabolomics profiling are still in their preliminary stages, although metabolite profiling is being increasingly used in many laboratories with much success. Proteomics profiling is currently mostly limited to inventories of proteins in specific parts of the cell, such as those brought together in the SUBA database. Some promising technologies for quantitative proteomics are under development but not yet widely available. Metabolite profiling has enormous promise but is still limited by the difficulty in developing methods to comprehensively extract and identify all metabolites. Despite these drawbacks, the future for both of these profiling technologies is bright. It is urgent to further develop standards and software for storing and analyzing mass spectra such that data from many laboratories can be pooled in the same way as has been achieved for transcript data.

*Recommendations*

- Tools and approaches for molecular profiling of cell-type specific samples need to be further developed and brought

into the mainstream of research
- Effective protocols are required for analyzing nucleic acids bound to particular proteins (e.g. chIP-chip and RIP-chip approaches)
- Standards for proteomics and metabolomics data need to be further developed and promoted, together with the development of centralized repositories of tools and data. Usage of these approaches by the community will depend upon the data quality and the ease of use of the analysis tools reaching the same standards as now available for transcript data.

## Expansion of the role of bioinformatics

*Arabidopsis* researchers have a central information portal in the form of The *Arabidopsis* Information Resource (TAIR), a highly regarded and much-appreciated source of data about everything to do with *Arabidopsis*. The recent 7th release of the genome annotation from TAIR will maintain the status of *Arabidopsis* as having probably the best-annotated genome sequence of any multicellular organism. The culture of plant researchers has changed over the last five years, with an easily observable shift from wet-work in the lab towards an increasingly larger proportion of time spent at the computer. The training of young scientists has not always kept pace, and too many still arrive ill-equipped for the informatics side of their research projects. Nevertheless, outside TAIR, many admirable databases, websites, software and other informatics resources exist. A challenge is to bring these disparate resources together to allow seamless integration. The Multinational *Arabidopsis* Steering Committee is promoting pilot projects in 'web services' designed to do just this.

*Recommendations*
- Maintain TAIR at the forefront of the data repositories for model organisms
- Continue to develop approaches to integrate other data sources via webservices or other technologies
- Redouble efforts to convert published literature into machine-readable form for integration into functional genomics and bioinformatics projects
- Promote initiatives to integrate multiple types of profiling data, such as transcript, protein and metabolite profiles

## Development of community and human resources

As described above, a great deal of effort has gone into creating research resources in the form of biological stocks and databases, with an extremely stimulating effect on *Arabidopsis* research. Less visible but equally laudable efforts have been undertaken via web portals (e.g. TAIR Education and Outreach), workshops (e.g at the annual International Conference on *Arabidopsis* Research or organized by MASC subcommittees and other community members), mailing lists and newsgroups to create a true sense of community by providing valuable educational and social services to researchers, especially those joining the field. Such services include making experimental protocols easily accessible, training and discussion workshops on new approaches, job listings and outreach material for use in schools or in presentations to the general public.

Undoubtedly more could be done if additional resources were available for this type of activity. The *Arabidopsis* research community needs to redouble efforts to present the advantages of working on a model plant to the lay public, relevant end-users (representatives of the biotech industry, farmers), funding agencies, and government members. Such initiatives are currently under-resourced and poorly coordinated worldwide. MASC would be the logical organization to carry out such work but lacks the human resources and economic/legal expertise to build a strong case in terms that industry and government agencies can easily relate to.

*Recommendations*
- Improve liaisons with the biotech and agricultural industries to promote fundamental research and obtain data and case studies supporting the utility of such research on *Arabidopsis*.
- Establish better coordination of worldwide public outreach efforts in the same way that the research effort is being successfully coordinated.

## Promotion of international collaboration

International collaboration within the *Arabidopsis* community is exemplary and the envy of research communities working on many other species. From the genome sequencing project onwards, multinational collaboration has been frequent and largely effective. MASC has been successful in advising large collaborative research projects and providing a forum for discussion, both promoting new projects and preventing unwitting duplication of effort. Funding agencies are generally keen to fund international collaborations and there exist many highly successful bilateral and trilateral projects. What is needed now are mechanisms to support large, intercontinental projects that make best use of truly exceptional facilities, expertise or resources wherever they are found.

*Recommendations*
- Maintain MASC's role to coordinate worldwide research on *Arabidopsis*
- Continue recent efforts to globalize MASC by holding International Conferences (*e.g.* once in North America, once in Europe, once in Asia, in three year cycles)
- Work with funding agencies to coordinate funding of large intercontinental projects

# The International *Arabidopsis* Functional Genomics Community

## Country Highlights

### Argentina

- 9th Edition of the Buenos Aires Plant Biology Lecture Series: Scientists and students from Argentina and neighboring countries attend these annual lectures given by international speakers including (in 2006): Phillip Benfey (Duke Univ.), Brian Staskawicz (Univ. of California, Berkeley), James Carrington (Oregon State Univ.), Ottoline Leyser (Univ. of York), and Sheila McCormick (Univ. of California, Berkeley).
- The number of *Arabidopsis* research papers from Argentineans is steadily increasing. Compared to the three year period from 1998-2000, there was a 30% increase in publications during 2001-2003, and a 100% increase between 2004-2006.

### Australia: Plant Phenomics Facility (APPF)

A new initiative by the Australian Government to fund major national infrastructure and facilities includes a Plant Phenomics Facility to be located at ANU Plant Energy Biology and CSIRO Plant Industry in Canberra and at ACPFG in Adelaide. It will implement technology platforms for rapid and detailed noninvasive phenotyping and imaging of crops and model plants, and allow relation of phenotype to genetic make-up. A primary objective is the analysis of model species such as *Arabidopsis* and rice for gene function discovery. The APPF will be available in 2008 for projects from national and international researchers. For more information see the Australia report.

### Austria: Opening Symposium of the New Gregor Mendel Institute

In 2000, a new international research institution was proposed and later selected to be a new plant research center, the first of its kind in Austria. The Gregor Mendel Institute of Molecular Plant Biology held its Opening Symposium on September 29th and 30th, 2006. Internationally renowned plant scientists from Europe and the US met at the GMI to present their latest research results using *Arabidopsis thaliana*. Speakers included Elliot Meyerowitz, Philip Benfey, Maarten Koornneef, Barbara Hohn, Detlef Weigel, Ottoline Leyser, and Ueli Grossniklaus, among others. For more information: http://www.gmi.oeaw.ac.at/en/home/

### Belgium: Scientists Propose New 5 Year Arabidopsis European Integrated Project

Pierre Hilson and Dirk Inzè of the Department of Plant Systems Biology, VIB at Ghent University initiated a new program, AGRON-OMICS (*Arabidopsis* GROwth Network integrating-OMICS technologies), a consortium of fourteen partners whose aim is to develop a system-level approach to study *Arabidopsis* leaf growth and development. The European Union will provide support under its 6th Framework Programme at a level of 12 million €. The official program start date was November 1, 2006. For more information, see the Community *Arabidopsis* Resources and Projects section of this report.

### Canada: Arabidopsis Interactions Viewer at Botany Array Resources

The Arabidopsis Interactions Viewer is a new tool for exploring more than 20,000 known and predicted *Arabidopsis* protein-protein interactions. These interactions can be displayed in tabular format and also as outputs from Expression Browser and Expression Angler to help guide hypothesis generation. The confirmed *Arabidopsis* interacting proteins come from BIND, the Biomolecular Interaction Network Database and from high-density *Arabidopsis* protein microarrays. The interactions in BIND were identified using several different methods, such as yeast two hybrid screens, but also via traditional biochemical methods. For more information see the Canada report.

### China: Host of the 18th International Conference on Arabidopsis Research

In June, 2007, the 18th International Conference on *Arabidopsis* Research (ICAR) was held at the Jiuhua Spa and Resort in Beijing, China. This year's meeting is notable because it is the first time that the ICAR was held in an Asian country. Over 1,500 people attended the conference jointly organized by five local institutions. For more information see the China report.

### France: New Genoplante 2010-funded initiatives

An initiative was launched in April 2005 to sustain research in plant genomics to the year 2010. GENOPLANTE 2010 is a six year initiative involving seven partners from the public sector and private companies. Although a large part is devoted to crop plants, several *Arabidopsis* projects are funded through the "New Tools" committee. Newly funded research projects (2006) are described at: http://www.genoplante.com/doc/File/Projets 2006.pdf. For more information see the France report.

### Germany

- In 2006, the *Arabidopsis* Functional Genomics Network (AFGN) finished AtGenExpress, the worldwide largest and internationally cooperative *Arabidopsis* transcriptome project. The AFGN part of the project includes data sets for *Arabidopsis* development and response to its biotic and

abiotic environment and for several natural accessions. This open access database provides an experimental base for many open access bioinformatics tools such as the Germany-based AtGenExpress Visualisation Tool (AVT) and MapMan.

- Support for five years, beginning January, 2007, will be provided by the Potsdam-Golm BMBF-Research Project on Systems Biology for four research centers to address the quantitative comprehension of biological networks and regulation. GoFORSYS proposes a Systems Biology approach towards the study of photosynthesis and its enhancement in crop plants. Comprehensive systems analysis will be done first in the alga *Chlamydomonas reinhardtii*, followed by efforts in *Arabidopsis* and tomato (http://www.goforsys.de/).

### Israel: New MASC Country

This year Israel joined the MASC with Danny Chamovitz of Tel Aviv University as the country's representative. The major centers of *Arabidopsis* research are in Tel Aviv University (8 groups with funded research), The Hebrew University of Jerusalem (primarily at the Faculty of Agriculture, 6 groups with funded research) and the Weizmann Institute of Science (4 groups with funded research). For more information see the Israel report.

### Italy: A Compelling Report on Cytokinin's Role in the Root

A recent paper from the Sabatini lab at Università La Sapienza sheds light on the role of the plant hormone cytokinin in root meristem differentiation. The authors provide evidence that cytokinin acts primarily in a particular tissue and developmental stage to control the rate of meristematic cell differentiation and the size of the root meristem. (Dello Ioio *et al.* Cytokinins determine Arabidopsis root meristem size by controlling cell differentiation. Current Biology 17(8):678-82, April, 2007)

### Japan

- At the RIKEN Plant Science Center a Metabolomics platform has been established to analyze complex metabolic networks in *Arabidopsis* and rice (PI Kazuki Saito). By using mass spectroscopy and NMR, hundreds of plant metabolites can be analyzed. A Horomonome platform has also been established to analyze various hormones in one sample for the analysis of crosstalk in hormone regulation (PIs Yuji Kamiya and Hitoshi Sakakibara.)
- Systematic Phenotypic Analysis of Knockout Mutants: A RIKEN Plant Science Center publication details the phenome analysis of 4,000 Arabidopsis Ds tagging mutants. (Kuromori et al. A trial of phenome analysis using 4000 Ds-insertional mutants in gene-coding regions in Arabidopsis. Plant Journal 47: 640-651, 2006)

### The Netherlands

- Ben Scheres of Utrecht University was awarded the NWO/ Spinoza price in 2006. The prize, which some regard as the 'Dutch Nobel Prize', is awarded to Dutch scientists who are at the very top of the research profession. The award to Scheres, who studies pattern formation in *Arabidopsis* roots, is notable as it is the first bestowed upon a plant scientist.
- The 15th Crucifer Genetics Workshop: Brassica 2006 was held Sept. 30-Oct. 4, 2006 in Wageningen.

### The Nordic *Arabidopsis* Network

- The Academy of Finland has recently funded a number of activities on *Arabidopsis* systems biology related to stress biology and photosynthesis, including two national Centres of Excellence - one in Helsinki and one in Turku. A Finnish national graduate school on Plant Biology, focusing mainly on *Arabidopsis*, was established and started its activities at the beginning of 2006.
- In November 2006 the 5th Norwegian *Arabidopsis* meeting was held at NTNU in Trondheim by the Norwegian *Arabidopsis* Research Centre, NARC. NARC is part of the national functional genomics program (FUGE), and is expected to be extended until 2012. More information in the Nordic report, Norway section.

### United Kingdom: New *Arabidopsis* Systems Biology Initiatives

The Biotechnology and Biological Science Research Council (BBSRC) has recently funded a number of initiatives that build upon functional genomics to develop integrative and predictive understanding including (1) the Centre for Plant Integrative Biology (CPIB, Nottingham; http://www.cpib.info/) which aims to create a virtual *Arabidopsis* root as an exemplar of Systems Biology in multi-cellular systems, and (2) the Centre for Systems Biology at Edinburgh (CSBE; http://csbe.bio.ed.ac.uk/) which aims to streamline the modelling of dynamic intracellular processes including the plant circadian clock. For more information see the UK report.

### United States

- Plant Science Cyberinfrastructure Collaborative: In November 2006, the NSF initiated a new program whose goal is to create a cyberinfrastructure collaborative for plant science that will enable new conceptual advances through integrative, computational thinking. The community-driven collaborative, involving plant biologists and other experts, will be fluid and dynamic, utilizing new computer, computational science and cyberinfrastructure solutions to address an evolving array of grand challenge questions in plant science. For more information see the US report.
- Chris Somerville (Carnegie Institution, Stanford) and Elliot Meyerowitz (California Institute of Technology) were co-awarded the 2006 Balzan Prize in Plant Molecular Genetics. The scientists were recognized "for their joint efforts in establishing *Arabidopsis* as a model organism for plant molecular genetics." The Balzan prize is awarded annually for outstanding achievements in humanities, social sciences, physics, mathematics, natural sciences, and medicine. For more information: http://www.balzan.it

# Argentina

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

## Current Research Projects

- Transcriptome analysis in plant-pathogen interactions: plant genes required for susceptibility to fungal infection. Malena Alvarez, malena@dqb.fcq.unc.edu.ar; CIQUIBIC-CONICET, Facultad Ciencias Quimicas, Universidad Nacional de Cordoba. Province of Córdoba; http://www.ciquibic.gov.ar/
- The genetic network involved in plant responses to the light environment: transcriptome analysis in phytochrome and cryptochrome mutants. Jorge J. Casal, casal@ifeva.edu.ar; IFEVA, Facultad de Agronomía, Universidad de Buenos Aires. Buenos Aires; http://www.ifeva.edu.ar/en/staff/casal.htm
- Functional analysis of genes involved in the biogenesis of the cytochrome c-dependent respiratory chain. Daniel H. Gonzalez, dhgonza@fbcb.unl.edu.ar; Facultad de Bioquímica y Ciencias Biológicas. Universidad Nacional del Litoral. Province of Santa Fe
- Role of senescence associated genes in the formation of lytic vacuoles during senescence. Juan José Guiamet,; jguiamet@museo.fcnym.unlp.edu.ar; Instituto de Fisiología Vegetal, Universidad de La Plata. Province of Buenos Aires
- Genes involved in Potassium and Sodium transport. Guillermo E. Santa-Maria, gsantama@pop.unsam.edu.ar; Instituto de Investigaciones Bioteconológicas, Universidad Nacional de San Martin. Province of Buenos Aires
- Regulatory genes involved in the control of transcription of genes of the photosynthetic antenn*a.* Roberto J. Staneloni, RStaneloni@Leloir.org.ar; Instituto Leloir. Buenos Aires
- Functional analysis of oxidative stress-regulated genes. Estela M. Valle, evalle@fbioyf.unr.edu.ar; Instituto de Biología Molecular y Celular de Rosario (IBR-CONICET), Facultad Ciencias Bioquimicas y Farmaceuticas, Universidad Nacional de Rosario. Province of Santa Fe
- Identification of key components for retrograde signaling between mitochondria and nucleus in higher plants by transcriptomic, proteomic and functional analyses of respiratory complex mutants in Arabidopsis. Eduardo Zabaleta, ezabalet@mdp.edu.ar; Universidad de Mar del Plata. Province of Buenos Aires
- Regulatory genes involved in the biogenesis of mitochondrial Fe-S proteins. Metabolic analysis of Arabidopsis mutants deficient in enzymes involved in carbon metabolism. Diego Gómez-Casati, diego.gomezcasati@intech.gov.ar; Instituto de Investigaciones Bioteconológicas, Universidad Nacional de San Martin, Province of Buenos Aires

## *Arabidopsis* genomics tools and resources:

- Recombinant inbred lines (RILs) between Landsberg *erecta* and Nossen produced by Jorge J. Casal in collaboration with the groups of Allan Lloyd (University of Texas) and Javier Botto (University of Buenos Aires), are available at the Arabidopsis Biological Resource Center (ABRC), Ohio State University, USA.
- The first Affymetrix workstation in Latin America has gone to Arabidopsis research groups. ANPCYT has granted an Affymetrix workstation (at IFEVA) to a consortium integrated mainly by research groups listed above.

## 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/
- FIRCA (NIH), http://www.fic.nih.gov/programs/firca.html
- 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 of Australia having some research involving *Arabidopsis* as a model system. Major areas of *Arabidopsis* research and functional genomics are Canberra, Melbourne and Perth. Major sites of plant science with foci on crops such as grains, grapes and legumes include Queensland, Tasmania, South Australia and NSW. Increasing numbers of New Zealand plant scientists are incorporating *Arabidopsis thaliana* into their research, and several are using functional genomics approaches. Funding is principally available through the Royal Society of New Zealand's Marsden Fund and the New Zealand Foundation for Research, Science and Technology. In addition to the projects being conducted at the universities, research programs are carried out at the Government-owned Crown Research Institutes, including Horticulture and Food Research Institute of New Zealand (HortResearch), and the New Zealand Institute for Crop & Food Research Limited (Crop & Food Research).

The number of peer reviewed publications in 2006 utilizing Arabidopsis that listed Australia or New Zealand was 189.

## Key new development during 2006

*Establishment of the Australian Plant Phenomics Facility*
The Australian Government has recently awarded funding for the Australian Plant Phenomics Facility (APPF) to be established as a bi-nodal Facility between the University of Adelaide in Adelaide and CSIRO Plant Industry and The Australian National University in Canberra. The APPF will aim to be a state-of-the-art plant phenotyping facility with sophisticated plant growth facilities and cutting edge technologies for plant performance and function monitoring. It will have the following broad scientific targets and objectives:

- The high throughput phenotypic analysis of agricultural species, particularly cereals (>100,000 plants screened per year).
- Analysis of model species such as *Arabidopsis* and rice for gene function discovery (>50,000 plants screened per year)
- Application of the phenotyping data for the more rapid discovery of molecular markers and faster germplasm development, aimed at improving the tolerance of major crops and other agriculturally important plants to biotic and abiotic stresses, including drought, salinity and a broad spectrum of plant diseases
- Deployment of emerging technologies in plant phenotyping. The University of Adelaide Waite Campus will develop a suite of glasshouse facilities with robotic monitoring of plant growth and performance with particular emphasis on application to agricultural species. The Canberra node will specifically establish a model species screening facility which will include a focus on Arabidopsis analysis. The technologies used for screening will include various imaging approaches including morphological growth and colour analysis, chlorophyll fluorescence and hyperspectral reflectance. These will be coupled to robotic systems which will allow medium throughput screening of plant material grown under controlled environment conditions. The APPF will be available on a fee for service basis in 2008 for research projects from national and international researchers. Contact Murray Badger (murray.badger@anu.edu.au) or Mark Tester (mark.tester@acpfg.com.au) for any inquiries.

## 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. This new knowledge will aid improvement of plants by enabling better management of: (1) the timing and rate of plant growth and development; (2) biomass and yield; (3) efficient use of water and mineral nutrients; (4) tolerance of plants to environmental stresses such as excess light and drought; and (5) synthesis of plant metabolites important for human nutrition. Investigators are: Ian Small , Murray Badger, David Day , Barry Pogson , Harvey Millar , Jim Whelan and Steven Smith .
- CSIRO Plant Industry (www.pi.csiro.au). Major Programs on Genomics, microRNAs and Plant Development. This program investigates several aspects of plant function and, importantly, is developing major facilities for *Arabidopsis* functional genomics work. Work on microRNAs, funded as a CSIRO emerging science initiatives, involves a number of researchers (including Peter Waterhouse, Iain Wilson, Frank Gubler). Other Projects include activation tagging and CHP on Chip (Chris Helliwell), reproductive development (Abed Chaudhury), floral initiation and epigenetic regulation (Jean Finnegan), genetic engineering for plant improvement (Jeff Ellis ) and fruit initiation (Anna Koltunow).

### Examples of Australian and New Zealand Universities and Institutions with substantial research on Arabidopsis

- University of Auckland: (www.auckland.ac.nz/ )
- Association of Crown Research Institutes, including AgResearch and HortResearch: (www.acri.cri.nz/ )
- University of Otago: (www.otago.ac.nz/)
- Monash University (www.biolsci.monash.edu.au/)
- University of Melbourne (www.unimelb.edu.au/)
- The Australian National University (www.anu.edu.au/bambi/ ; www.rsbs.anu.edu.au/ )
- The University of Queensland (www.uq.edu.au/)
- The University of Adelaide (www.adelaide.edu.au/)

### Genomics Companies

- CAMBIA (www.cambia.org )
- Diversity Arrays Technology Pty Ltd (www.diversityarrays.com).

### Examples of Research Projects Using Functional Genomics Approaches

- Aluminum and manganese stress tolerance—Peter Ryan, CSIRO
- Arabinogalactan proteins—Carolyn Schultz and Tony Bacic, U. Adelaide
- Boron tolerance— Robert Reid, U. Adelaide
- CesA—related genes and cellulose synthesis—Richard Williamson, ANU
- Chloroplast development and function, oxidative stress and photoprotection—Barry Pogson, ANU
- Dehydrin genes and Myb gene function—Roger W. Parish, La Trobe U.
- Defense gene expression - Karam Singh, CSIRO
- Defining microRNA function—Tony Millar, ANU
- Fimbrin gene family—David McCurdy, U. Newcastle
- Flowering—Alan Neale, John Hamill, John Bowman, David Smyth, Monash
- Heterotrimeric G-proteins—Jimmy Botello, U. Qld
- Mechanical impedance in roots—Josette Masle, ANU
- Mitochondria—Jim Whelan, David Day, Harvey Millar, UWA and U. Syd.
- Nodulation related control mechanisms—Peter Gresshoff, U. Qld
- Peroxisomes and Metabolomics—Steve Smith, UWA
- Phosphorus-use efficiency—Peter Ryan, CSIRO
- Photosynthetic capacity regulation—Murray Badger, ANU
- Plant Development, John Golz, U. Melb
- Plant Natriuretic Peptide immunoanalogues (PNPs)—Helen R. Irving and David Cahill, Deakin U
- Plasmodesmata functional proteomics—Robyn Overall, U. Syd
- PPR proteins—Ian Small, UWA
- Respiration: non-phosphorylating pathways associated with the mitochondrial electron transport chain—Kathleen Soole, Flinders U.
- Sodium efflux systems in the plasma membrane—Ian A. Newman, U. Tas

### 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).

- Discovery Grants and Fellowships - supporting fundamental research
- Linkage Grants - supporting projects between academic institutions and industry
- 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
Contacts:
Marie-Theres Hauser
University of Natural Resources and Applied Life Science Vienna
Email: marie-theres.hauser@boku.ac.at
Ortrun Mittelsten-Scheid
GMI, Austrian Academy of Sciences
Email: ortrun.mittelsten_scheid@gmi.oeaw.ac.at

In Austria 25 groups are undertaking functional genomic research projects with *Arabidopsis* on specialized topics from development, epigenetics, chromosome biology, RNA metabolism, stress responses and signaling, plant-pathogen interactions and the functional analysis of gene families. The research activities are clustered at four institutions in Vienna and one in Salzburg and have been bundled in four consortia.

## University of Natural Resources and Applied Life Science Vienna (BOKU),

**Department of Applied Plant Sciences and Plant Biotechnology (DAPP)**

- Institute for Applied Genetics and Cell Biology (IAGZ)
- Gerhard Adam (www.dapp.boku.ac.at/5499.html): *plant-pathogen interactions, detoxification of Fusarium mycotoxins*
- Marie-Theres Hauser (www.boku.ac.at/zag/AG_hauser.htm): *root development, cell wall biosynthesis, cytokinesis, vesicle trafficking, functional analysis of the ARIADNE gene family*
- Christian Luschnig (www.dapp.boku.ac.at/5499.html): *Polar auxin transport, ubiquitination and degradation, chromatin architecture*
- Herta Steinkellner (www.dapp.boku.ac.at/5499.html): *investigation and manipulation of the N-glycosylation pathway*

**Institute of Plant Protection (IPS)**

- Holger Bohlmann (www.dapp.boku.ac.at/2238.html): *expression analysis of syncytia*
- Florian Grundler (www.dapp.boku.ac.at/2238.html): *plant nematode interaction, sugar transport in syncytia*
- Georg Seifert: *Arabinoglactan proteins and programmed cell death*

## Gregor Mendel Institute of Molecular Plant Biology (GMI)

- Werner Aufsatz (www.gmi.oeaw.ac.at/waufsatz.htm): *histone deacetylase in RNA silencing and stress adaptation*
- Thomas Greb (www.gmi.oeaw.ac.at/tgreb.htm): *development of vascular tissue*
- Claudia Jonak (www.gmi.oeaw.ac.at/cjonak.htm): *stress signaling and physiological responses, functional analysis of the GSK gene family*
- Antonius and Marjori Matzke (www.gmi.oeaw.ac.at/amatzke.htm): *epigenetics*
- Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/oms.htm): *epigenetic changes in polyploids*
- Karel Riha (www.gmi.oeaw.ac.at/rkriha.htm): *telomers and genome stability*
- Dieter Schweizer (www.gmi.oeaw.ac.at/dschweizer.htm): *chromosome biology, meiosis*
- Hisashi Tamaru (www.gmi.oeaw.ac.at/htamaru.htm): *Asymmetric cell division and chromatin reshaping during pollen development*

## University of Vienna, Max F. Perutz Laboratories (MFPL)

**Department of Plant Molecular Biology**

- Erwin Heberle-Bors (www.mfpl.ac.at/index.php?cid=397): *epitope-tagging of MAP kinases*
- Fritz Kragler (www.mfpl.ac.at/index.php?cid=52) *nature and function of systemic non-coding RNAs, proteins/RNA movement by plasmodesmata*.
- Irute Meskiene (www.mfpl.ac.at/index.php?cid=53): *Specificity and functional analysis of a PP2C protein phosphatase gene subfamily*
- Brigitte Poppenberger: *brassinosteroid biosynthesis*
- Tobias Sieberer: *development of the shoot apcial meristem*
- Markus Teige (www.mfpl.ac.at/ index.php?cid=55): *Calcium-dependent protein kinases*

**Department of Chromosome Biology**

- Peter Schlögelhofer (www.mfpl.ac.at/index.php?cid=54): *Analysis of meiotic recombination*

## Medical University of Vienna, Max F. Perutz Laboratories (MFPL)

**Department of Medical Biochemistry**

- Andrea Barta (www.mfpl.ac.at/index.php?cid=68): *RNP complexes, spliceosome and small non-coding RNP complexes*
- Elisabeth Waigmann (www.mfpl.ac.at/index.php?cid=57*): intra- and intercellular transport of plant viral genomes*

## University of Salzburg

**Department of Cell Biology**

- Raimund Tenhaken (http://www.uni-salzburg.at/zbio/

tenhaken): *Biosynthesis of nucleotide sugars for cell wall polymers, programmed cell death*

## Current Research Consortia

**APAR** (A Platform of *Arabidopsis* Research) is funded by the *Austrian Science Fund FWF* and aims to promote sciences on Arabidopsis in Austria.

Consortium members:

- Marie-Theres Hauser: *Functional characterization of gene families involved in root morphogenesis*
- Heribert Hirt (www.heribert-hirt.at): *Stress signal transduction*. Since February 2007 Heribert Hirt joined the Unité de Recherche en Genomique Végétale—URGV as future Director (http://www.evry.inra.fr/public/index.html)
- Claudia Jonak: *Analysis of glycogen synthase kinase/shaggy-like kinases*
- Irute Meskiene: *Specificity and functional analysis of a PP2C protein phosphatase gene subfamily*
- Karel Riha: *Functional study of the Ku complex at Arabidopsis telomeres*
- Markus Teige: *Calcium-dependent protein kinases in Arabidopsis signal transduction*

**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 Bundesministerium für Wissenschaft, Bildung und Kultur

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

**Integrative Analysis of Stress Response Mechanisms to Improve Plant Performanc**e is funded by the *Vienna Science and Technology Fund WWTF*:

The project elucidates the role of protein kinases, viral-interacting host factors and micro RNAs in response to a combination abiotic and biotic stresses. The aim of these studies is to provide the molecular basis for breeding novel sustainable crop varieties of broad resistance against abiotic and biotic stresses.

Consortium members: Andrea Barta (coordinator), Heribert Hirt, Claudia Jonak, Elisabeth Waigmann,

**GYKOdesign in Plants** is funded by the *Vienna Science and Technology Fund WWTF*:
The goal of the project is the production of plant lines that are capable of producing pharmaceutically relevant glycoproteins which are, among other things, applicable in human therapy.

Consortium members:Herta Steinkellner (coordinator), Friedrich Altmann (University of Natural Resources and Applied Life Sciences Vienna, Institute of Chemistry), Renate Kunert (University of Natural Resources and Applied Life Sciences Vienna, Institute for Applied Microbiology)

### Meetings

The 4th Tri-National *Arabidopsis* Meeting (TNAM) 2007 will be held at University of Natural Resources and Applied Life Science (BOKU) in Vienna between the 12th—15th of September (http://www.gmi.oeaw.ac.at/tnam2007/)

### 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)
- Translational and applied reseach: FFG (Österreichische Foschungsförderungsgesellschaft mbH) (www.fff.co.at)

### Public relations - education

Several of the research groups have been participating and opened their labs for the GEN-AU SummerSchool, an educational program for high school students. www.gen-au.at/artikel.jsp?id=68&base=vermitteln&lang=de

# Belgium

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

Belgian *Arabidopsis* projects are funded via university-, regional- or federal-level grants, but not within calls specifically targeting this model plant species or plants. In addition VIB, the Flanders Institute for Biotechnology, provides significant support to the Department of Plant Systems Biology (about 5 million Euro 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. Perlieux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project.
- Other current *Arabidopsis* research topics in Belgium include the cell cycle (D. Inzé, L. De Veylder), root and leaf growth and development (T. Beeckman, G. Beemster, M. Van Lijsebettens), brassinosteroids (J. Russinova), abiotic stress (F. Van Breusegem), genome annotation and evolution (Y. Van de Peer, P. Rouzé), computational biology (M. Kuiper), modelling (R. Merckx), functional genomics (P. Hilson), proteomics (G. De Jaegher), quantitative biology (M. Vuylsteke), lignin biosynthesis (W. Boerjan), ethylene signaling (D. Van Der Straeten), hormone biology (Harry Van Onckelen), membrane proteins (M. Boutry), salt stress and tolerance to heavy metal (N. Verbruggen), 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 the Belgian Coordinated Collections of Microorganisms (BCCM/LMBP), PSB set up a service for the sequence validation and dissemination of AGRIKOLA resources; visit http://bccm.belspo.be/db/lmbp_gst_clones/ to order purified and sequence validated clones; visit http://www.psb.ugent.be/reva/index.php?o=/reva/main to request the validation of specific 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 (see page 12).

# Canada

http://www.arabidopsis.org/portals/masc/countries/Canada.jsp
Contact: W.L. Crosby
University of Windsor, Ontario, Canada
Email: bcrosby@uwindsor.ca

In 2006, 57 laboratory groups known to be conducting research with *Arabidopsis* were polled by Email for contributions to the MASC report. Of these, approximately 30 responded and their contributions are summarized in this report.

The past two years have witnessed a period of rapid turnover and new hires among University Faculty in Canada—in part due to the retirement of those Faculty hired in the late 1960's and early 70's. As a result, a number of new and exciting young scientists have joined the plant science research cadre, including a significant number of *Arabidopsis* researchers.

## Reports

- François Belzile—l'Université Laval (fbelzile@rsvs.ulaval.ca) The Belzile lab studies *Arabidopsis* DNA mismatch rep air (MMR) in regards to both microsatellite instability and homoeologous recombination.
- Thomas Berleth—University of Toronto (thomas.berleth@utoronto.ca) The Berleth lab developed approximately 4,000 indirect enhancer trap lines, together with ~ 70,000 indirect activation tags (among them ~30,000 conditional activation tags) for use in the study of very early vascular genes. In addition, they are conducting a study to map QTLs defining *Arabidopsis* fibre properties.
- Malcolm Campbell—University of Toronto (campbell@botany.utoronto.ca) The Campbell lab investigates (1) the perception of sugars, amino acids and water, and how this affects the allocation of resources to key facets of metabolism and development, (2) comparative genomic analyses with the model woody perennial genus *Populus*.
- Jin-Gui Chen—University of British Columbia (jingui@interchange.ubc.ca) The Chen lab investigates signal transduction networks using both forward- and reverse-genetic, molecular and cellular biological, and biochemical approaches.
- William Crosby—University of Windsor (bcrosby@uwindsor.ca) The Crosby lab investigates the role of E3 ubiquitin ligase (E3) complexes in the regulation of patterning and development in *Arabidopsis*.
- Raju Datla—NRC Plant Biotechnology Institute (raju.datla@nrc-cnrc.gc.ca) The Datla lab investigates gene expression dynamics during embryo development, currently focusing on genes in *Arabidopsis* as well as the closely related *Brassica napus*.
- Michael Deyholos—University of Alberta (deyholos@ualberta.ca) The Deyholos lab applies genetic analysis and functional genomics of *Arabidopsis* to two areas of research: vascular development, and abiotic stress responses.
- Brian Ellis—University of British Columbia, Vancouver (bee@msl.ubc.ca) The Ellis lab studies regulation of secondary wall deposition and lignification (Collaborators: Carl Douglas, Lacey Samuels, Shawn Mansfield (UBC)). A second project concerns the functional analysis of the Arabidopsis MAPK phosphatase gene family (Collaborators: Geoff Wasteneys (UBC), Dominique Bergmann (Stanford)). Finally, the group is undertaking the functional analysis of the Arabidopsis MAPKK gene family (Collaborators: Jin-Gui Chen (UBC); Igor Kovalchuk (Lethbridge); Dominique Bergmann (Stanford).
- Sonia Gazzarrini—University of Toronto, Scarborough, (gazzarrini@utsc.utoronto.ca) The Gazzarrini group uses functional genomic, molecular and chemical genetic approaches to study the molecular mechanisms that regulate early developmental phase transitions and plant resistance to abiotic stresses in *Arabidopsis*.
- Vojislava Grbic—University of Western Ontario (vgrbic@uwo.ca) The Grbic lab investigates the diversification of plant forms by studying a set of late-flowering *Arabidopsis* accessions with naturally occurring variant morphology.
- George Haughn—University of British Columbia (haughn@interchange.ubc.ca) The Haughn laboratory studies regulation of plant morphogenesis and seed coat differentiation in *Arabidopsis* and oversees the Canadian reverse genetic TILLING facility, CAN-TILL (http://www.botany.ubc.ca/can-till/).
- Shelley Hepworth—Carleton University (shelley_hepworth@carleton.ca) The Hepworth lab focuses on determining how positional information is translated into morphological asymmetry, an important aspect of developmental patterning in plants.
- Ljerka Kunst—University of British Columbia (kunst@interchange.ubc.ca) The Kunst laboratory studies lipid metabolic pathways in higher plants, focusing on two specific areas of lipid metabolism: cuticular wax biosynthesis and secretion.
- Xin Li—University of British Columbia (xinli@interchange.ubc.ca) The Li group is studying R-protein signaling pathways that play central roles in recognizing pathogens and initiating downstream defense cascades.
- Jaideep Mathur—University of Guelph (jmathur@uoguelph.ca) The Mathur lab studies sub-cellular dynamics and organelle interactions in order to understand the early responses of plants to various abiotic / biotic stimuli.

- Doug Muench—University of Calgary (dmuench@ucalgary.ca) Research in the Muench laboratory is aimed at understanding the role of the plant cytoskeleton, specifically microtubules, in subcellular mRNA localization, protein sorting, and low temperature stress signaling.
- Roger Lew—York University, Toronto (planters@yorku.ca) The Lew lab is interested in the electrical properties of *Arabidopsis* root hairs. Current studies involve ion transport in cellular expansion and plant cell stress response.
- Nicholas Provart—University of Toronto (nicholas.provart@utoronto.ca) The Provart lab oversees the Botany Array Resource (see Functional Tools at the end of this section.) In addition, the wider *Arabidopsis* research group at the University of Toronto has generated 10,000 DEX inducible random insertion lines which will be deposited to the stock center in the future.
- Przemyslaw Prusinkiewicz—University of Calgary (pwp@cpsc.ucalgary.ca) The Prusinkiewicz group focuses on simulation modeling of *Arabidopsis*, including the multiple roles of auxin in plant morphogenesis, general methods of modeling plants across multiple scales of organization, and further development of simulation software.
- Dan Riggs—University of Toronto at Scarborough (riggs@utsc.utoronto.ca) Research in the Riggs laboratory focuses on two distinct but interrelated processes: factors which affect plant architecture and factors that regulate chromatin condensation.
- Owen Roland—Carleton University (owen_roland@carleton.ca) The Roland lab studies the synthesis of cuticular waxes and their deposition onto plant surfaces via map-based cloning and reverse genetic and biochemical approaches.
- Kevin Rozwadowski—Agriculture and Agri-Food Canada, Saskatoon (rozwadowskik@agr.gc.ca) The Rozwadowski group is interested in DNA double-strand break repair in vegetative and meiotic cells. The lab uses *Arabidopsis* as a model to characterize the details of the repair process and evaluate plant responses to genotoxic stress.
- Lacey Samuels—University of British Columbia (lsamuels@interchange.ubc.ca) The Samuels lab is conducting a multi-disciplinary research project to study the plant cuticle. The project involves characterizing biosynthetic mutants (Kunst Lab), studying wax export and the cell structure of these mutants (Samuels Lab) and analyzing the chemical composition and biosynthetic pathways of cuticular lipids (Jetter Lab).
- Dana Schroeder—University of Manitoba (shroed3@cc.umanitoba.ca) The Schroeder group works on the regulation of light signaling and DNA repair by DET1, DDB1A, and DDB2 in *Arabidopsis*.
- Randall Weselake—University of Alberta (randall.weselake@afhe.ualberta.ca) The Weselake group is (1) assessing the functionality (in this case the ability to impart tolerance to abiotic stress) of a number of oilseed rape genes using *Arabidopsis*, and (2) researching novel methods for modifying the fatty acid composition of seed oils.
- Tamara Western—McGill University (tamara.western@mcgill.ca) The Western lab focuses on the seed coat mucilage secretory cells as a model system to study multiple aspects of cellular differentiation, including: (1) the regulation of cell wall production and modification, (2) polar secretion, and (3) plasma membrane-cell wall interactions.
- Stephen Wright—York University (stephenw@yorku.ca) The Wright lab is interested in (1) understanding the forces driving gene and genome evolution in the genus *Arabidopsis*, (2) testing for the accumulation and increased activity of transposable elements in the allopolyploid genome of *Arabidopsis suecica*, and (3) sequencing of the genomes of *Arabidopsis lyrata* and *Capsella rubella*.
- Hugo Zheng—McGill University (hugo.zheng@mcgill.ca) The Zheng lab is studying how intracellular membrane trafficking is regulated as cell morphology changes during plant development and in response to environmental stresses. The approach is to use reverse genetics combined with in vivo imaging approach to exploit the regulatory role of Rab-A and Rab-E GTPases and forward genetics to identify novel genes that are involved in plant-specific membrane trafficking.
- Jitao Zou—NRC Plant Biotechnology Institute (jitao.zou@nrc-cnrc.gc.ca) The Zou lab is mainly interested in lipid and carbon metabolism. They study enzymatic components of the lipid metabolic network and are interested in exploring natural variation in wild type accessions to dissect regulatory components of seed oil deposition.

## Arabidopsis genomics tools and resources

- Canadian reverse genetic TILLING facility, CAN-TILL (http://www.botany.ubc.ca/can-till/).
- Botany Array Resource (http://bbc.botany.utoronto.ca): Contains more than 1000 gene expression data sets consisting of more than 24.6 million data points. Tools available include: [1] an Expression Browser for performing electronic Northerns [2] a new Fluorescent Protein Browser tool, which paints gene expression information from the Gene Expression Map of *Arabidopsis* Development onto a diagrammatic representation of the developmental series used, [3] Expression Angler, to identify genes that are co-expressed with genes of interest in a specified data set, and [4] Promomer for the identification of potential *cis*-regulatory elements in the promoter of a given gene, or in the promoters of a set of co-regulated genes. Additional tools include a database of genome-wide predicted CAPS markers across 96 accessions, based on sequence data from Magnus Nordborg and colleagues (2005, PLoS Biol. 3:e196).

**New for 2007 is the Arabidopsis Interactions Viewer** for exploring more than 20,000 known and predicted Arabidopsis protein-protein interactions, with output in tabular or Cytoscape format.(http://bbc.botany.utoronto.ca/interactions/cgi-bin/arabidopsis_interactions_viewer.cgi) **Another development for 2007 is the Cell eFP Browser** for generating pictographic representations of protein subcellular localization from the SUBA database (Heazlewood et al., 2007, NAR 35:D213).

# China

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

*Arabidopsis* research takes place mainly in the Beijing and Shanghai areas, including Peking University, China Agricultural University, Tsinghua University, and Chinese Academy of Sciences. Funding for *Arabidopsis* research is improving in China as the National Science Foundation of China (NSFC), the main funding agency for basic research, will double its budget in the next five years. On December 3, 2006, more than 200 participants from 20 institutions attended the annual Workshop on *Arabidopsis* Research, held at Shanghai Institutes for Plant Physiology and Ecology, Shanghai.

In June of 2007, the 18th International Conference on *Arabidopsis* Research (ICAR) was held at the Jiuhua Spa and Resort in Beijing, China. Xing Wang Deng, lead conference organizer, is the chair-elect of the Multinational *Arabidopsis* Steering Committee and a member of the North American *Arabidopsis* Steering Committee. Dr. Deng holds a professorship position at Yale University in the U.S. and has extensive interactions and collaborations with scientists in a number of institutions in China. This year's meeting is notable because it is the first time that the ICAR was held in an Asian country. Over 1,350 people attended the conference. Five local institutions jointly organized the conference: the National Institute of Biological Sciences, The Institute of Botany and Institute of Genetics and Developmental Biology of the Chinese Academy of Sciences, Peking University, and China Agricultural University. Conference website: www.arabidopsis2007.com

## Current Research Projects

- In 2006, NSFC granted three key projects to Dr. Lijia Qu (www.pepge.pku.edu.cn/each_lab/biotech/Qu/quindex.htm) of Peking University on auxin metabolism, Dr. Lixin Zhang (http://english.ibcas.ac.cn/info_www/news/detailnewsb.asp?infono=65), Institute of Botany of CAS on photosynthesis, and Dr. Chunpeng Song (www.bio.henu.edu.cn/ReadNews.asp?NewsID=202) of Henan University on ABA signaling, using the *Arabidopsis* model plant.
- To promote group research effort on plant epigenetics, the NSFC funded a team project headed by Dr. Xiao-Feng Cao (www.genetics.ac.cn/xywwz/Faculty/CaoXiaofeng.htm) at the Institute of Genetics and Developmental Biology (www.genetics.ac.cn/xywwz/main.html), Beijing.

## Chinese Arabidopsis research community links

- Epigenetics

  Dr. Xiaofeng Cao:
  microRNA biogenesis (www.genetics.ac.cn/xywwz/Faculty/CaoXiaofeng.htm)

  Dr. Huishan Guo:
  microRNA (www.im.ac.cn/en/new/PI/026E04 Prof Huishan Guo.doc)

  Dr. Xiujie Wang:
  noncoding RNA (www.genetics.ac.cn/xywwz/Faculty/wangxiujie.htm)

- Hormone signaling

  Dr. Hongwei Guo:
  Ethylene signaling (www.bio.pku.edu.cn/collegereview/scholarinfo.jsp?name=guohw)

  Dr. Xiangdong Fu:
  GA signaling and development (www.genetics.ac.cn/xywwz/Faculty/fuxiangdong.htm)

  Dr. Yuxin Fu:
  Auxin and development (http://cstm.ibcas.ac.cn/HuYuxin_lab_en.htm)

  Dr. Chuanyou Li:
  JA signaling and biotic stress (www.genetics.ac.cn/xywwz/Faculty/LiChuanyou.htm)

  Dr. Lijia Qu:
  Auxin and leaf development (www.pepge.pku.edu.cn/each_lab/biotech/Qu/quindex.htm)

  Dr. Qiguang Wen:
  Ethylene signaling (www.nlpmg.labs.gov.cn/ewenqg.doc)

  Dr. Hongwei Xue:
  Auxin and brassinosteriod signaling (www.nlpmg.labs.gov.cn/xhw.html)

  Dr. Daoxin Xie:
  Jasmonic acid signaling (www.biosci.tsinghua.edu.cn:8001/english/index.html)

  Dr. Jianru Zuo:
  Cytokinin signaling (www.genetics.ac.cn/xywwz/Faculty/ZuoJianru.htm)

- Development

  Dr. Shunong Bai:
  Root development (www.pepge.pku.edu.cn/each_lab/bai_sn/research.htm)

  Dr. Hai Huang:
  Leaf development (www.nlpmg.labs.gov.cn/ehuangh.doc)

Dr. Chunming Liu:
Embryogenesis and peptide signaling (http://cstm.ibcas.ac.cn/LiuChunming_lab_en.htm)

Dr. Yongbiao Xue:
Pollen and pollination (http://plantbiol.genetics.ac.cn/the_xue_lab/index.htm)

Dr. Weicai Yang:
Female gametogenesis (www.genetics.ac.cn/xywwz/Faculty/YangWeicai.htm)

Dr. De Ye:
Pollen development (www.cau.edu.cn/sklppb/sysry/yede.htm)

Dr. Dabing Zhang:
Anther development (http://zhanglab.sjtu.edu.cn/english/index.php?option=com_contact&Itemid=3)

- Environmental responses

  Shouyi Chen:
  Salt stress (www.genetics.ac.cn/xywwz/Faculty/ChenShouyi.htm)

  Dr. Kang Chong:
  Cold response (www.genetics.ac.cn/xywwz/Faculty/ChenShouyi.htm)

  Dr. Zhizhong Gong:
  Salt stress (www.cau.edu.cn/bio/shizi/gongzhizhong.htm)

  Dr. Zhuhua He:
  Biotic stress (www.nlpmg.labs.gov.cn/ehezh.doc)

  Dr. Chunpeng Song:
  ABA and stress (www.bio.henu.edu.cn/ReadNews.asp?NewsID=202)

  Dr. Weihua Wu:
  Potasium uptake (www.cau.edu.cn/sklppb/sysry/wuwh.htm)

  Dr. Hongquan Yang:
  Stomata and light response (www.nlpmg.labs.gov.cn/research groups.html)

  Dr. Lixin Zhang:
  Photosynthesis (http://english.ibcas.ac.cn/info_www/news/detailnewsb.asp?infono=65)

  Dr. Jianmin Zhou:
  Biotic stress (www.nibs.ac.cn/english/index.php?act=view&id=13)

## Major funding sources for Arabidopsis functional genomics

- National Science Foundation of China

  83 Shuangqing Road, Haidian District, Beijing 100080, China, www.nsfc.gov.cn/

# France

http://www.arabidopsis.org/portals/masc/countries/France.jsp
Contact: David Bouchez
Institut Jean-Pierre Bourgin, SGAP-INRA Centre de Versailles, Versailles
Email: bouchez@versailles.inra.fr

## Major funding sources for *Arabidopsis* functional genomics

- Genoplante : http://www.genoplante.com/
- French National Research Agency (ANR): www.gip-anr.fr/
- ERA-PG: www.erapg.org/

A major source of funding in France for *Arabidopsis* functional genomics projects is Genoplante, a federative program for plant genomics research created by public institutions and several French ag-biotech companies. Created in 1999, it has supported research on the genomes of crop plants, and also has directed over €62 million of research on *Arabidopsis*, supporting creation of high throughput genomics tools and resources as well as functional genomics studies. An initiative was launched in April 2005 to sustain research in plant genomics to the year 2010: "GENOPLANTE 2010" is a 6 year initiative involving seven partners from the public sector (INRA, CNRS, CIRAD, IRD) and private companies (Biogemma, Arvalis, Sofiproteol). This program is now administered by the French National Research Agency (ANR: Agence Nationale de la Recherche). The annual budget for the program for the next few years is around 30 million Euros per year. Although a large part is devoted to crop plants, several *Arabidopsis* projects are funded through the "New Tools" committee. The ANR also contributes significantly to funding *Arabidopsis* research through its "white programs" for fundamental research.

## Newly funded research projects (2006)

http://www.genoplante.com/doc/File/Projets 2006.pdf
http://www.agence-nationale-recherche.fr/documents/aap/2006/selection/blanc.pdf

*Examples of newly funded projects :*

- Cyclic nucleotide-gated cation channels involved in hypersensitive cell death in *Arabidopsis thaliana*, PI: Claudine Balague, CNRS Toulouse
- Natural variation for drought tolerance: from QTL for Targeted traits to functional polymorphisms, PI: Olivier Loudet, INRA Versailles
- Identification of signals controlling the protein trafficking between the secretory pathway and the chloroplast, PI: Patrice Lerouge, CNRS Rouen
- Initiation, synthesis, and degradation: an integrated approach toward the understanding of starch metabolism and formation in plants, PI: Christophe D'Hulst, CNRS Lille
- MicroRNA Transcription and Activity: uncovering and exploiting the genes between the genes, PI: Olivier Voinnet, CNRS Strasbourg
- Design and exploitation of a versatile *Arabidopsis* whole-Genome Tiling Array, PI: Michel Caboche, INRA Evry
- RNA dependent RNA Polymerases involved in epigenetic silencing in plants, PI: Patrice Crété, Marseille University
- Cell calcium signatures regulate plant phenypropanoid metabolic phenotype, PI: Raoul Ranjeva, CNRS Toulouse
- Control of cellulose synthesis in higher plants, PI: Samantha Vernhettes, INRA Versailles
- Epigenetic role of histone methylation in environmental adaptation in *Arabidopsis*, PI: Wen-Hui Shen, CNRS Strasbourg
- Analysis of the cross-talk between transcriptional and post-transcriptional small RNA pathways in *Arabidopsis*, PI: Herve Vaucheret, INRA Versailles
- The TOR/PTEN signalization pathway in plants, PI: Christian Meyer, INRA Versailles

## Genoplante and ANR projects funded in 2005 and before

http://www.genoplante.com/doc/File/pdf/Projets 2005.pdf
http://www.agence-nationale-recherche.fr/documents/aap/2005/finances/financeBLANCSAE2005.pdf

Other ongoing Genoplante projects (January 2006 update) : http://www.genoplante.com/doc/File/pdf/Projets en cours.pdf

## European projects

http://www.genoplante.com/doc/File/pdf/Projets collaboratifs.pdf

- French-Spanish-German projects and ERA-PG: Several Génoplante projects are jointly funded with similar German and Spanish initiatives in the frame of bi- and tri-lateral collaborations. (www.genoplante.com/doc/File/pdf/Projets collaboratifs.pdf
- Génoplante and ANR are participating in ERA-PG, a European network of research funding organizations responsible for the development of national or regional plant genomics research programs. The network concentrates on creating a stimulating and fruitful environment for European plant genomics. ERA-PG started in 2004 with twelve member organizations from eleven countries funded

through the EU's 6th Framework Program. In 2005, four new countries have joined.

## *Arabidopsis* genomics tools and resources

**The Plant Genomics Unit** (URGV, Evry), runs large generic programs on *Arabidopsis* functional genomics (http://www.evry.inra.fr/public/scientific/functional.html), including

- FLAGdb++: an *Arabidopsis* genomics database including amongst many other things an inventory of flanking sequence tags from the Versailles *Arabidopsis T*-DNA collection. Also includes the rice genome and its annotation. (www.evry.inra.fr/public/projects/bioinfo/flagdb.html)
- CATMA and CATdb : A complete *Arabidopsis thaliana* microarray containing more than 24000 gene-specific tags (http://www.evry.inra.fr/public/projects/transcriptome/transcriptome.html). This program involves several EU countries (www.catma.org). CATdb (http://www.evry.inra.fr/public/projects/bioinfo/catdb.html) is a relational database developed to contain the description of Biological experiments (plant species, growth conditions, treatments...); Micro-arrays used (sequences, clones...); Hybridizations (protocols, results, statistics...)
- ATOME: *Arabidopsis thaliana* ORFeome whose goal is to create expression vectors. ATOME, in collaboration with Invitrogen, aims to clone up to 5000 Arabidopsis ORFs into Gateway entry vectors. (http://www.evry.inra.fr/public/projects/orfeome/orfeome.html)

The **Institut Jean Pierre Bourgin** (INRA Versailles, www-ijpb.versailles.inra.fr/en/) houses the French Resource Centre for *Arabidopsis* (www-ijpb.versailles.inra.fr/en/sgap/equipes/variabilite/crg) which distributes insertion lines, natural accessions and several populations of recombinant inbred lines. Nested core-collections of 8, 16, 24, 32, 40, 48 *Arabidopsis* accessions maximizing diversity has been established. All relevant information can be found at :

- VNAT: A database on *Arabidopsis* natural variation (http://dbsgap.versailles.inra.fr/vnat/
- Agrobact +: A database for the Versailles T-DNA lines (http://dbsgap.versailles.inra.fr/agrobactplus/English/Accueil_eng.jsp)

The **National Resources Centre for Plant Genomics** (CNRGV) in Toulouse distributes *Arabidopsis* cDNA and BAC clones. They also provide services including high density colony arrays, genomic pools, custom screening, robotic services and large scale PCR amplification.

- CNRGV: (http://cnrgv.toulouse.inra.fr/ENG/)

# Germany

http://www.arabidopsis.org/portals/masc/countries/Germany.jsp
Contacts
**MASC** German representative: Thomas Altmann; University of Potsdam; E-Mail: taltmann@rz.uni-potsdam.de
**AFGN** (*Arabidopsis* Functional Genomics Network, DFG funded): Coordinator: Klaus Harter; University of Tuebingen; E-Mail: klaus.harter@zmbp.uni-tuebingen.de

Research on *Arabidopsis thaliana* has a long history in Germany, and many individual research groups have used this reference plant for analysing different aspects of plant biology. Two independent programs support research on plant functional genomics in Germany, namely the *Arabidopsis* Functional Genomics Network (AFGN), supported by the German Research Foundation Deutsche Forschungsgemeinschaft (DFG), and the more crop, and therefore application oriented plant genomics research program, GABI, funded by the Federal Ministry of Education and Research (BMBF). Both programs work together in close cooperation, with intensive links at both the scientific and the contributor level.

## The AFGN

The AFGN was founded in 2001 as a basic research program and is supported by the DFG. The AFGN currently funds 25 projects in Germany and has been organized in close coordination with the NSF 2010 Project, including a joint reviewing process. Together with many other research programs throughout the world both programs aim to elucidate the function of all *Arabidopsis* genes in the near future. The main activities of the ongoing research projects concentrate on the analyses of members of selected multiprotein families and cover the elucidation of their structure, activity, interaction partners, gene expression, intracellular localisation, post-translational regulation and function. In addition, the AFGN and the 2010 Project implemented the collaborative AFGN-2010 Young Researcher Exchange Program (AFGN-2010-YREP, http://www.uni-tuebingen.de/plantphys/AFGN/yrep.htm). The program provides funding for 1 to 3 month research visits of young scientists to the US and *vice versa*.

In 2006, the AFGN finished the worldwide largest and internationally cooperative *Arabidopsis* transcriptome project called AtGenExpress. The AFGN part of the project includes data sets for *Arabidopsis* development and response to its biotic and abiotic environment and for several natural accessions. This open access database provides an experimental base for many open access bioinformatics tools such as the Germany-based AtGenExpress Visualisation Tool (AVT) and MapMan. Together with colleagues from Austria and Switzerland the AFGN has initiated a yearly international conference on *Arabidopsis* functional genomics. In 2006, the 3rd meeting was hosted in Tübingen, Germany, and visited by over 200 hundred scientists from Europe, Asia and the US. In 2007, the 4th meeting will be held in Vienna, Austria.

The third funding period of the AFGN will start in the autumn of 2007. The AFGN program will continue to support basic functional genomics research in *Arabidopsis thaliana*, thereby contributing to the accelerated acquisition and utilization of new knowledge and innovative approaches in order to elucidate fundamental biological processes in higher plants. Two areas of research were identified which future support should concentrate on:

*Functional Genomics of Biological Processes:* The focus of the AFGN will move towards the genomic analysis of multigene networks whose members functionally interact with each other to accomplish a given biological process. Such a network may consist of members of the same or of different *Arabidopsis* multiprotein families.

*Tools and Resources for Plant Functional Genomic Research*: The development of novel and, especially, quantitative genome-wide tools and technologies (e.g. in cell imaging, protein modification and intracellular localisation, protein-protein interaction), and additional resources in plant functional genomics to address unmet needs (e.g. conditional expression collections of *Arabidopsis* for the characterisation genes with yet unknown function, intracellular protein localisation and protein-protein interaction databases).

## AFGN-related Arabidopsis tools and resources

- AFGN: http://www.uni-tuebingen.de/plantphys/AFGN/AFGNHome2.html
- AtGenExpress: http://www.uni-tuebingen.de/plantphys/AFGN/atgenex.htm
- AtGenExpress-related publications: Schmid et al. (2005) Nat. Genetics 37, 501-506; Kilian et al. (2007) Plant J., in press.
- AVT: http://www.weigelworld.org/resources/microarray/AtGenExpress/
- MapMan: http://gabi.rzpd.de/projects/MapMan/
- 4th Tri-National *Arabidopsis* Meeting, Vienna, Austria, 2007: http://www.gmi.oeaw.ac.at/tnam2007/
- AFGN-2010-YREP: http://www.uni-tuebingen.de/plantphys/AFGN/yrep.htm

## GABI programs

GABI, a BMBF funded German plant genome research program is now in its seventh year. With an annual budget of 10 million Euros plus an additional 20% from industrial partners GABI

is the biggest research program in plant genomics in Germany. Approximately 30% of the total budget supports research on *A. thaliana*. In its second program period translational research was introduced: topic-oriented research clusters combine basic research on *A. thaliana* with research activities on crops. Since the start of GABI, *A. thaliana* has also served to deepen international cooperation through bilateral as well as trilateral research projects between France (Génoplante), Spain and GABI.

Within GABI, important resources such as the GABI-KAT lines, the world's second largest T-DNA insertion line population, were generated and are available to the global research community. The transfer of the confirmed insertion lines from Cologne to the Nottingham Stock Center (U.K.) began in 2005 and will continue until the conclusion of the GABI-KAT project. The generation of plant resources for the analysis of natural diversity (natural accessions and experimental populations such as F1's, F2's, RIL's, NIL's), as well as their geno- and phenotyping to provide characterized biological material for researchers, is coordinated between colleagues from Génoplante (France) and GABI. A database summarising genetic and experimental data is under construction, and data warehousing, management and visualisation are primary foci for bioinformatics activities in GABI. GABI-Matrix at MIPS (GSF Munich) and the GABI-Primary Database (RZPD Berlin) are the two big centres for bioinformatics in GABI, flanked by many decentralized bioinformatics groups within the research institutions. ARAMEMNON, one of the world largest databases on *Arabidopsis thaliana* membrane transport proteins, was generated to aid in the identification, classification and characterization of novel transporters. The GABI TILLING facility is an example of a coordinated technological development that expands the worldwide capacity for TILLING screens in *Arabidopsis*.

Discussions have also started within the GABI community on how to continue research and development activities. GABI-FUTURE (2007-2013), the third funding phase of the national plant genomics program, is underway and is expected to increase the research budget significantly. GABI-FUTURE will continue to bundle fundamental and applied, but still pre-competitive, research activities within a single program. Public-private-partnerships, the backbone of the program, will continue and more partners will be needed for the gradual creation of a knowledge based bio-industry. Furthermore, basic research on crops will be improved to close the gaps in knowledge and to ease the technology transfer from *A. thaliana* to important crop plants. GABI and the AFGN played an important role during the establishment of the European Research Area Network on plant genomics (ERA PG). Out of the total annual budget of approximately 10 million Euros for the first joint call of the ERA PG, the two German funding agencies support German research groups with more than 3 million Euros per year.

## GABI-related Arabidopsis tools and resources

- GABI: (www.gabi.de) 12 million €/year from the Federal Ministry of Education and Research (www.bmbf.de) and a Business Platform promoting GABI Plant Genome Research e.V. (WPG) (www.wirtschaftsverbund-gabi.de)
- GABI-KAT: (www.gabi-kat.de/)
- GABI-Matrix: (http://mips.gsf.de/projects/plants/)
- GABI-PD: (http://gabi.rzpd.de/)
- GABI-ARAMEMNON: (www.uni-koeln.de/math-nat-fak/botanik/bot2/agflue/HOME/projects/GABI_rkunze/index.html)
- GABI-TILLING: (www.gabi-till.de/index.de.html)

# Israel

http://www.arabidopsis.org/portals/masc/countries/Israel.jsp
Contact: Danny Chamovitz
Tel Aviv University
Email: dannyc@ex.tau.ac.il

*Arabidopsis* projects in Israel are funded via national and binational grants. Currently there are no national funding initiatives specifically targeting *Arabidopsis* functional genomics. A major German-Israel binational consortium studying chemical-genetic platforms for the study of plant biology was funded by the German-Israel Coorporation Foundation (DIP). This consortium includes groups at The Hebrew University Faculty of Agriculture, Hebrew University, Tel Aviv University, and the Max Planck Institute für Züchtungsforschung.

The major centers of *Arabidopsis* research are in Tel Aviv University (8 groups with funded research), The Hebrew University of Jerusalem (primarily at the Faculty of Agriculture, 6 groups with funded research) and the Weizmann Institute of Science (4 groups with funded research). These three centers have recently upgraded, or are in the process of upgrading, *Arabidopsis* growth facilities. For example, the Manna Center for Plant Biosciences at Tel Aviv University received a $1,000,000 donation this past year for renovating and developing the *Arabidopsis* growth facility infrastructure.

## Funded research programs, 2006

| | PI | Institute | Research title | Main Collaborator |
|---|---|---|---|---|
| 1 | Abed Azzem | TAU | Function of chloroplast chaperones in *Arabidopsis* | |
| 2 | Adi Avni | TAU | A protease-like protein involved in ethylene biosynthesis | |
| 3 | Alon Samach | HUJI | Chemical-genetic platforms for the study of plant biology | George Coupland, MPI. Cologne |
| 4 | Alon Samach | HUJI | Analysis of the effects of light on the stability and activity of constants, a protein that mediates the photoperiodic control of flowering | George Coupland, MPI, Cologne |
| 5 | Amnon Lers | VI | Dark-induced Reactive Oxygen Species Accumulation and Inhibition by Gibberellins: Towards Inhibition of Postharvest Senescence | Sucheng Gan, Cornell |
| 6 | Avi Levy | WIS | Enhancing the Rate of Meiotic Crossing-Over for Plant Breeding | Clifford Weil, Purdue |
| 7 | Bernard Epel | TAU | Molecular and functional analysis of plasmodesmotal proteins | |
| 8 | Daniel Chamovitz | TAU | Structure-function analysis of COP9 signalosome subunit 7 | |
| 9 | Daniel Chamovitz | TAU | eif3 Complexes and the eif3e Subunit in *Arabidopsis* Development and Translation Initiation | Albrecht von Arnim, Univ. Tennessee |
| 10 | David Weiss | HUJI | Mechanisms of interaction between the gibberellin and cytokinin signaling pathways | |
| 11 | David Weiss | HUJI | The Role of Serine/Threonine O-glcnac Modifications in Signaling Networks | Neil Olszewski, Univ. Minnesota |
| 12 | Gadi Galilil | WIS | Genomic approaches to revealing networks of amino acid metabolism | |
| 13 | Gadi Gallili | WIS | Genetic, Genomic and Biochemical Analysis of *Arabidopsis* Threonine Aldolase and Associated Molecular and Metabolic Networks | Georg Jander, BTI, Cornell |
| 14 | Gadi Schuster | WIS | Integration of phosphorus and chloroplast mRNA metabolism through regulated ribonucleases | David Stern, BTI, Cornell |
| 15 | Hillel Fromm | TAU | Targets and regulation of a novel family of plant transcription factors | |
| 16 | Naomi Ori | HUJI | Genetic dissection of dissected leaves | Detlef Weigel, MPI, Cologne |
| 17 | Nir Ohad | TAU | Elucidation of the roles of the atyy1-like polycomb proteins in plant development | |
| 18 | Nir Ohad | TAU | Evolution of composition and function of the polycomb protein group (pcg) complexes, regulators of developmental programs from *Physcomitrella* to *Arabidopsis* | Prof. Dr. Ralf Reski, - Universitaet Freiburg |
| 19 | Nir Ohad | TAU | Regulation of plant development by polycomb group proteins | Robert Fisher, UC Berkeley |
| 20 | Orit Shaul | BIU | The molecular basis of resistance and storage of heavy metals in plants | |
| 21 | Orna Elroy-Stein | TAU | Mechanism of Internal Initiation of Translation in Plants | Dimitry Belostotsky, SUNY Albany |

| | | | | |
|---|---|---|---|---|
| 22 | Rachel Green | HUJI | Identification of Novel Circadian and Flowering Regulators in | Robert McClung Dartmouth |
| 23 | Robert Fluhr | WIS | The Biological function of the serpin family of proteins in plants | |
| 24 | Shaul Yalovsky | TAU | Functional analysis of small ROP-II GTP-binding proteins in *Arabidopsis* | |
| 25 | Simon Barak | BGU | Functional genomics to isolate novel clock genes in *Arabidopsis* | |
| 26 | Yuval Eshed | WIS | Design of plant organs - growth regulation in space and time | |
| 27 | Yuval Eshed | WIS | Harnessing Fine Scale Tuning of Endogenous Plant Regulatory Processes for Manipulation of Organ Growth | John Bowman, UC Davis |
| 28 | Zach Adam | HUJI | Proteomic Anaylsis of Thylakoid ftsh and degp Protease | Klaas van Wijk, Cornell |
| 29 | Zach Adam | HUJI | Degradation of integral thylakoid proteins by Rhomboid proteases | |

TAU—Tel Avuv University, HUJI—Hebrew university of Jerusalem, WIS—Weizmann Institute of Science,
BGU—Ben Gurion University of the Negev, VI—Volcani Institute

## Arabidopsis tools and resources

- Vectors for using bimolecular fluorescence complementation (BiFC) for determining protein–protein interactions in plants were constructed by the Yalovsky and Ohad labs at Tel Aviv university, and have been deposited with TAIR.

## 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
Contact: Paola Vittorioso
University of Rome "La Sapienza", Dept. Genetics and Molecular Biology, Rome
Email: paola.vittorioso@uniroma1.it

Most of the Italian groups actively engaged in *Arabidopsis* research are involved in national and international plant functional genomic network projects. In the last few years, development of a common technological platform has allowed for creation of a network among groups of the highest qualification active in Italian universities, public research institutes and the most relevant plant biotechnology companies. This national network, funded by the Italian Ministry of Research (MIUR), represents a first step towards the establishment of a National Plant Biotechnology Center. Post-genomic technologies and other existing technologies will be made available to all partners of the network. The network has developed technologies for (1) gene functional analysis (i.e., RNA interference, negative and positive dominant transformants, Tilling), (2) the analysis of interactions between genes (i.e., *Arabidopsis* macro- and micro-arrays, real-time PCR) and (3) the identification of protein partners and targets (i.e., TAP-TAG analysis, two hybrid analysis in yeast and plants, and stable antibodies phage display libraries).

## Current Research Projects

- Italy will participate in the ERA-NET program, a novel feature of the European Union's 6th Framework Program that provides support for transnational networking and coordination of national research programs.
- Two projects on *Arabidopsis* have been selected by the ERA-NET Plant Genomics program involving several Italian groups, and will be funded by the Italian Ministry of University and Scientific Research from this year. The projects are the following: "Multiple stress responses and adaptations," Italian coordinator Paolo Costantino, Italian participants Costantino and Ruberti; and "Conservation and diversity in transcriptional regulation of developmental processes in crop and model plant species," Italian coordinator G. Morelli, Italian participants Morelli, Colombo, Tonelli.
- A new collaborative project between the University of Verona (R. Bassi) and ENEA (G. Giuliano), involves *Arabidopsis* mutants lacking specific xanthophylls or xanthophyll groups.
- Another Italian group (B. Mattei), is one of the partners involved in the project "Functional Genomics for Biogenesis of the Plant Cell Wall" which is funded by the UE Marie Curie Training Network. This project will be developed using *Arabidopsis* as a model system.
- Italy (L. Colombo) is also participating in the EU FP6 Marie Curie Training Project "TRANSISTOR" (Trans-cis element regulating key switches in plant development). Moreover, several Italian groups have been funded by MIUR, through national scientific programs that are proposed as part of national scientific collaborations.

## Major funding sources for Arabidopsis functional genomics

- MIUR (www.miur.it) will support the First Call for Proposal of the ERA-NET Plant Genomics as part of its institutional activities. National Call Coordination: Dr. M. Massulli, mauro.massulli@miur.it. The Ministry has also funded many national projects (PRIN 2005-2007).
- 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 Italian Space Agency (www.asi.it)
- The European space Agency (www.esa.int/esaCP/index.html)
- The Insitut Pasteur (www.pasteur.fr/pasteur/international/Dai_en/lines.html)

# Japan

http://www.arabidopsis.org/portals/masc/countries/Japan.jsp
Contact: Kazuo Shinozaki
RIKEN Plant Science Center
Email: sinozaki@rtc.riken.go.jp

In Japan, ongoing programs for *Arabidopsis* functional genomics are mainly found at RIKEN (www.riken.go.jp/engn/index.html) and Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html). Other programs are supported by the CREST program of the Japan Science & Technology Corporation, the Program of Promotion of Basic Research Activities for Innovative Biosciences (BRAIN), the NEDO project, and Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT).

## RIKEN

- RIKEN groups involved in *Arabidopsis* functional genomics include the Plant Functional Genomics Research Group (PFGRG), the Plant Science Center (PSC) and the BioResource Center (BRC). In 2005, the PSC (Director: Kazuo Shinozaki) started a new project entitled "Understanding metabolic systems for plant productivity" to integrate metabolomics with transcriptomics. The Metabolomics Research Group (Group Director: Kazuki Saito) was established at the PSC (http://prime.psc.riken.jp/) in 2005, while the PFGRG (Group Director Minami Matsui) joined PSC in April 2006.
- PFGRG in the RIKEN PSC (http://pfgweb.gsc.riken.go.jp/index.html) PIs are Kazuo Shinozaki, Minami Matsui and Motoaki Seki; projects include: (1) A collection of full-length cDNAs, (2) A collection and phenotype analysis of *Ds*-tagged lines, Activation tagging lines, and *Arabidopsis* and rice Full-length-cDNA-overexpressing (FOX) *Arabidopsis* transgenic lines, (3) Transcriptome analysis of genes expression in response to both abiotic and biotic stress using tiling array, (4) Homozygous *Ds*-insertional lines in gene-coding regions, (5) Reverse proteomics for functional analysis of *in vitro* expressed proteins using the wheat germ cell-free protein synthesis system in collaboration with a group at Ehime University (Yaeta Endo, Principal Investigator & Motoaki Seki).
- Since 2004, PSC has contributed to AtGenExpress (Yukihisa Shimada and Shigeo Yoshida) (www.arabidopsis.org/info/expression/ATGenExpress.jsp). PSC is now collecting large-scale transcriptome and metabolome data (Yukihisa Shimada and Kazuki Saito) to develop the integrated database.
- The RIKEN BRC is supported by the National BioResource Project and distributes plant materials developed in Japan. More than 23,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines (see below for more information) have been provided to approximately 920 laboratories located in 36 countries. Homozygous seeds of Ds-tagged mutants are under preparation, and some of them are publicly available now. Masatomo Kobayashi (kobayasi@rtc.riken.jp) is in charge of distributing *Arabidopsis* resources at the BRC (www.brc.riken.jp/lab/epd/Eng/).
- The PFGRG and Genome Exploration Research Group of the RIKEN Genome Sciences Center and the Experimental Plant Division of the BRC produced the *Arabidopsis* DNABookTM containing 1,069 RIKEN *Arabidopsis* Full-Length (RAFL) cDNAs for transcription factors (http://pfgweb.gsc.riken.jp/DNA-Book/).

## Kazusa DNA Research Institute

- At the Kazusa DNA Research Institute (Satoshi Tabata) ongoing projects include a collection of T-DNA tagged lines and *Arabidopsis* and *Lotus japonicas* ESTs. A major project is the genomic sequencing of *Lotus japonicas* and tomato.
- *Arabidopsis* T87 cultured cells have been transformed with RAFL cDNAs and other cDNAs for metabolic profiling of primary and secondary metabolites (Daisuke Shibata).
- New websites include KaPPA-View: Integration of transcriptome and metabolome data in plant metabolic pathways (Dr. Toshiaki Tokimatsu), and KATANA, Kazusa Annotation Abstract: Integration of major database sites of *Arabidopsis* genome annotation (Dr. Kentaro Yano).

## Other Arabidopsis functional genomics activities

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

• Gene Regulation Reseach Group of Research Institute of Genome-based Biofactory in AIST (http://unit.aist.go.jp/rigb/gf-gre/index.html)is systematically analyzing function of transcription factors using dominant repressors (CRES-T system) (Masaru Ohme-Takagi, National Institute of Advanced Industrial Science & Technology in Tsukuba).

• Genome-wide analysis of the two-component system is performed in Nagoya University (Takeshi Mizuno).

• A database on metabolites, KNApSacK, is available from NAIST (Shigehiko Kanaya).

## *Arabidopsis* genomics tools and resources

- Plant Functional Genomics Research Group in The RIKEN PSC (PIs of the PFGRG are Minami Matsui, Kazuo Shinozaki and Motoaki Seki) (http://pfgweb.gsc.riken.go.jp/index.html)
  1. A collection of full-length cDNAs (RAFL clones: Motoaki Seki) (http://rarge.gsc.riken.go.jp/)
  2. A collection and phenotype analysis of *Ds*-tagged lines (Takashi Kuromori), (http://rarge.gsc.riken.go.jp/)
  3. A collection and phenotype analysis of activation tagging lines (Minami Matsui), (http://amber.gsc.riken.jp/act/top.php)
  4. A collection and phenotype analysis of Arabidopsis full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (Takanari Ichikawa)
  5. A collection and phenotype analysis of rice FOX Arabidopsis transgenic lines (Minami Matsui)
  6. Structural proteomics of plant regulatory proteins with novel structures in collaboration with the GSC Protein Research Group (PI: Dr. Shigeyuki Yokoyama) (http://protein.gsc.riken.go.jp/Research/index_at.html)
  7. Transcriptome analysis using tiling arrays and 454 sequencing (Motoaki Seki and Tetsuro Toyoda)
  8. Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori, Fumiyoshi Myouga) (http://pfgweb.gsc.riken.go.jp/pjAcds.html)
  9. Reverse proteomics for functional analysis of *in vitro* expressed proteins using the wheat germ cell-free protein synthesis system in collaboration with a group at Ehime University (Yaeta Endo, Principal Investigator & Motoaki Seki) (www.ehime-u.ac.jp/English/faculties/cell.html)
  10. A collection of large-scale-transcriptome data using the Affymetrix GeneChip as part of the AtGenExpress project. The data, consisting mainly of phytohormone responses, has been provided from the AtGenExpress JAPAN web site (http://pfg.psc.riken.jp/AtGenExpress/index.html) as well as from TAIR (http://www.arabidopsis.org/info/expression/ATGenExpress.jsp).
  11. Based on the data of AtGenExpress, correlations in gene expression patterns were analyzed in a genome-wide scale. A web-based system to show co-expressed genes has been provided as "Cluster Cutting" (http://prime.psc.riken.jp/?action=agetree_index).
- RIKEN Plant Science Center (www.psc.riken.go.jp/indexE.html)
- RIKEN Genome Sciences Center (www.gsc.riken.jp/indexE.html)
- Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html)
- RIKEN BioResource Center (www.brc.riken.jp/lab/epd/Eng/)
- KaPPA-View (http://kpv.kazusa.or.jp/kappa-view/)
- KATANA (Kazusa Annotation Abstract: www.kazusa.or.jp/katana/)
- 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/)

## 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
Contacts:
Ben Scheres
Department od Molecular Cell Biology, University of Utrecht
Email: b.scheres@uu.nl
Willem Stiekema
Plant Research International, Wageningen
Email: w.j.stiekema@plant.wag-r.nl

## Centre for BioSystems Genomics, the Netherlands Plant Genomics Network

Within this national plant genomics research programme the Arabidopsis research focuses on the analysis of the regulatory network of genetic, biochemical, physiological and environmental interactions that control plant performance and the complex traits involved in plant-oomycete interactions and adaptation to stresses. Fully integrated large-scale activation tag screening, gene expression, proteome and metabolite profiling is aimed for and based on the full exploration of the available genetic variation with emphasis on control of metabolic composition. Understanding the adaptive traits relevant for research in potato and tomato and the development of concepts and technologies based on the availability of the whole *Arabidopsis* genome sequence and efficiency of Arabidopsis genetics are key. Four different projects respectively focus on:

1. Arabidopsis quality: the genetic and genomics analysis of metabolic composition. Koornneef/Vreugdenhil, Wageningen University; Pereira, Plant Research International, Wageningen; Smeekens, Utrecht University.
2. The analysis of ligand-receptor interaction networks in Arabidopsis. Angenent, Plant Research International, Wageningen; Heidstra, Utrecht University; De Vries, Wageningen University.
3. The role of chromatin structure in gene expression of Arabidopsis and tomato. Bisseling/de Jong, Wageningen University.
4. Priming of defence gene expression in plant-oomycete interactions. Pieterse/van den Ackerveken, Utrecht University.

*Arabidopsis* projects funded by other sources such as first flow university funds, second flow Netherlands Organisation for Scientific Research, EU etc. and third flow contract research**:**

## Wageningen University

1. QTL express: identification of plant performance traits in Arabidopsis by combining high-throughput mapping and expression profiling (M. Koornneef, D. Vreugdenhil).
2. Heavy metal tolerance and accumulation in *Thlaspi caerulescens*, a heavy metal hyperaccumulating plant species (M. Aarts).
3. Brassica vegetable nutrigenomics (M. Aarts).
4. Do plants love heavy metals? (A. Assunção)
5. The role of tomato serine and cysteine proteases in defence signalling (R. van der Hoorn)
6. A molecular genetic approach to chemical ecology and community ecology (M. Dicke)
7. Cross-talk between signal-transduction pathways in induced defence of Arabidopsis against microbial pathogens and herbivorous insects. M. Dicke (joint projects with C. Pieterse, Utrecht University)
8. Development of a method for breeding of cucumber for improved attraction of biological control agents (M. Dicke, H. Bouwmeester)
9. From genetic code to ecological interactions: molecular, phytochemical and ecological aspects of a glucosinolate polymorphism in Barbarea vulgaris. (N. van Dam)
10. Arabidopsis: the system to study structure and function of heterochromatin (T. Bisseling)
11. Chromatin genomics: functional analysis of Arabidopsis chromatin remodeling genes in development (T. Bisseling)
12. Wageningen Phytoinformatics: the added value from plants (W. Stiekema)

## Plant Research International, Wageningen

1. Isolation and characterisation of key-genes in the formation of germination stimulants of the parasitic weeds Striga and Orobanche (H. Bouwmeester).
2. LRR receptor-like proteins and their functions in plant signaling (G. Angenent).
3. MADS box transcription factor functioning (G. Angenent)
4. Signalling Pathways Controlling Embryogenic Cell Development in Arabidopsis (K. Boutilier)
5. Signalling in the shoot apical meristem: A question of determinate or indeterminate growth (R. Immink)

## Utrecht University

1. Sugar signalling pathways in plants (J. Smeekens)
2. Trehalose-6-phosphate as a regulatory molecule in plants (H. Schlüpmann)
3. Control of plant architecture (M. Proveniers)
4. Dormancy as survival mechanism in plants (L. Bentsink)

5. Cross-talk between signal-transduction pathways in induced defence of Arabidopsis against microbial pathogens and herbivorous insects (C. Pieterse, joint projects with M. Dicke, Wageningen University)
6. Exploring the plant innate immunityimmune response (C. Pieterse)
7. A functional proteomics approach to identify phospho-proteins involved in plant innate immunity (F. Menke)
8. Priming in plant-pathogen interactions: the molecular mechanism of the alarmed state (J. Ton)
9. Kinome profiling in Arabidopsis using PepChips (T. Ritsema)
10. Signalling at the host-microbe interface: pathogen-induced modulation of the plant plant plant plasma membrane (G. van den Ackerveken)
11. Understanding host plant susceptibility and resistance by indexing and deploying obligate pathogen effectors (G. van den Ackerveken)
12. Functional analysis of Arabidopsis *DOWNY MILDEW RESISTANCE* genes and their application in generating downy mildew resistant crops (G. van den Ackerveken)
13. Genetic networks in root development: Interplay between cell polarity information, pattern formation cues, and control of cell division (B. Scheres)
14. Control of transcription factor movement and boundary establishment in roots (I. Blilou)
15. Control of oriented cell division by transcription factor networks in roots (V.Willemsen)
16. Genomics for multicellular development: Function of the quiescent center in regulation of pattern formation and differentiation within the *Arabidopsis thaliana* root meristem (R. Heidstra)
17. Analysis of the hyponastic and differential growth response of *Arabidopsis thaliana* petioles induced by submergence and low light conditions (T. Peeters, R. Voesenek)

## Leiden University

1. Characterization of a novel regulator of plant secondary metabolism (J. Memelink)
2. Effect of NHR mutations on genome stability and development in Arabidopsis (P. Hooykaas)
3. Artificial zinc finger transcription factors as regulators of plant function (E. van der Zaal)
4. ORA EST: Functional analysis of jasmonate-responsive AP2/ERF-domain transcription factors in *Arabidopsis thaliana* (J. Memelink)
5. Regulation of polar auxin transport by PINOID protein kinase signaling to the actin cytoskeleton. (R. Offringa)Plant protein kinases orienting auxin-mediated plant development; Phospho-fingerprinting plant development; The role of auxin in fruit initiation; Modeling auxin transport (R.Offringa)
6. Protein ubiquitination in auxin- and jasmonic acid-dependent plant development and defense (R.Offringa & J.Memelink)

## University of Amsterdam

1. Role of PA kinase in plant stress signalling (T. Munnik)
2. Targets for the novel lipid second messenger, phosphatidic acid (C. Testerink)
3. **SUMO-signaling in plants** (*H. van den Burg)*

## Vrije Universiteit, Amsterdam

1. Function of meristem identity in flower and inflorescence development (R. Koes)
2. Genetic control and evolution of inflorescence architecture (R. Koes)

## University of Groningen

1. Molecular biology of programmed cell death in higher plants (Dijkwel, J. Hille)

## Radboud University Nijmegen

1. Role of type 1 MADS box gene in gametophyte and seeddevelopment (G. Angenent)

## 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/

# Nordic *Arabidopsis* Network

http://www.arabidopsis.org/portals/masc/countries/Nordic.jsp
Contact: Jaakko Kangasjärvi
University of Helsinki, Finland
Email: Jaakko.kangasjarvi@helsinki.fi

## Norway

The Norwegian Plant Functional Genomics Program (NARC) started in 2003 and is fully operative. NARC is 1 of 11 genomics technology platforms forming the national functional genomics program (FUGE). The plant platform includes service activities within transcriptional profiling (full genome arrays and custom designed arrays) and bioinformatics (Atle Bones, NTNU) genotyping and clone collection (Odd-Arne Rognli, UMB), *in situ* hybridization and yeast two-hybrid screening (Reidunn Aalen, UIO). Most of the activity involves *Arabidopsis thaliana*. NARC will be extended until 2012 (first period 2003-2008). It is expected that systems biology will be a hot topic in the second period of the program. More information: www.forskningsradet.no/servlet/Satellite?cid=1088005968933&pagename=fuge%2FPage%2FHovedSideEng. In November 2006 the 5th Norwegian *Arabidopsis* meeting was held at NTNU in Trondheim by the Norwegian *Arabidopsis* Research Centre, NARC. More information: http://www.spps.kvl.dk/cgi-bin/SPPSreader.pl?Story=NARC&Vol=0612. Norway is a partner of the EU Plant Genomics network ERA-PG and hosted the Nordic *Arabidopsis* meeting 2004.

## Sweden

The Umeå Plant Science Center (UPSC (www.upsc.se/) is a center of experimental plant biology in Umeå. It was created in 1999 by moving plant groups from the Umeå University and Swedish University of Agricultural Sciences (Umeå) to the same building. 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 that have a well-conserved counterpart in *Arabidopsis*. Research topics include; plant development, flower development and hormone physiology; photosynthesis and metabolism with a special interest for stress responses (low temperature in particular); ecophysiology studying C- and N- assimilation. The research groups are supported by technical platforms in genomics, proteomics, metabolomics, production of transgenic plants, microscopy. The UPSC is also a partner in the European CATMA-project.

## Finland

The Finnish groups involved in *Arabidopsis* research are concentrating on stress-physiology and functional genomics of plant stress responses, developmental and hormone biology, and in photosynthesis. They are using genomics, proteomics, and metabolomics to determine plant defense and adaptation to biotic and abiotic stresses and the functions of the proteins in chloroplast thylakoid membranes. *Arabidopsis* genomic information is also used in functional and comparative genomics of the lower plants as a template for the eurosids. Information is stored and made available at openSputnik- the comparative genomics platform (www.opensputnik.org). The outcrossing relative *Arabidopsis lyrata* is being used in studies of population genetics of adaptation to abiotic conditions. The eight chromosomes of the species differ from the *A. thaliana* genome mainly by a small number fusions and reciprocal translocations. The Finnish Plant Functional Genomics Project Program was created in the spring of 2003 in order to increase collaboration in functional genomics between the participating groups. It is also member in the European plant functional genomics network ERA-PG.

## Denmark

In Denmark, a number of groups at The Veterinary and Agricultural University (beginning January 2007: renamed Faculty of Life Sciences, University of Copenhagen), University of Copenhagen (Faculty of Natural Sciences), Risø National Laboratory, Danish Institute of Agricultural Sciences (beginning January 2007: renamed Faculty of Agricultural Sciences, 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). Denmark hosted the Nordic Arabidopsis meeting in 2005.

## 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 (http://www.imbv.uio.no/mol/groups/narc/)

- UMB: *Arabidospsis* transformation, T-DNA genotyping, seed collection: (www.umb.no/?viewID=2552)

### Finland

- openSputnik: A comparative genomics platform (www.opensputnik.org)

## Arabidopsis Funding Sources

### Norway

- Research Council of Norway (www.forskningsradet.no): Functional Genomics in Norway (FUGE)- Funding

### Sweden

- Wallenberg Consortium North (WCN)- Funding (www.wcn.se/)

### Finland

- The Finnish Project Program on Plant Genomics- Funding (www.honeybee.helsinki.fi/esgemo/pg/eng_index.htm)
- The Academy of Finland- Funding (www.aka.fi/index.asp?id=eb9a8e15a46244d989ac56c132e8d13a)

# United Kingdom

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

Contacts
Sean May
University of Nottingham
Email: sean@arabidopsis.info
Ruth Bastow (GARNet Coordinator)
University of Bristol
Email: ruth@arabidopsis.info

## GARNet

GARNet, the **G**enomic **A**rabidopsis **R**esource **Net**work was established in 2000 to provide public functional genomics resources, which now operate through "user pays" cost recovery. Coordination activities are funded for 2005-2010, 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.

## Current Foci of UK Funding of Arabidopsis Research

The Biotechnology and Biological Science Research Council, BBSRC, is the major funding agency for *Arabidopsis* Research. BBSRC encourages applications that build upon functional genomics to develop integrative and predictive understanding, in line with Systems Biology. Recent initiatives include: Six new Centres for Integrative Systems Biology (£30M in 2005 and 2006; http://www.bbsrc.ac.uk/media/pressreleases/06_04_20_sysbio.html). The Centre for Plant Integrative Biology (CPIB, Nottingham; http://www.cpib.info/) aims to create a virtual Arabidopsis root as an exemplar of Systems Biology in multi-cellular systems. The Centre for Systems Biology at Edinburgh (CSBE; http://csbe.bio.ed.ac.uk/) aims to streamline the modelling of dynamic intracellular processes including the plant circadian clock. The independently-funded Warwick Systems Biology centre (http://www2.warwick.ac.uk/fac/sci/systemsbiology/ ) also includes *Arabidopsis* researchers. Systems Approaches to Biological Research (http://www.bbsrc.ac.uk/science/initiatives/sabr.html) in 2007 will fund £30M of projects across systems biology. Two new UK initiatives (BBR and TRDF) fund infrastructure development and maintenance.

## Future Outlook

Basic plant science, much of it in *Arabidopsis*, is being encouraged to translate into applications that address agronomic problems or deliver economic and environmental benefits, such as Bioenergy. Long-term funding, coordination, standards and data policies are understood to be needed, nationally and internationally, to underpin comprehensive *Arabidopsis* biology *in silico*. To underpin this, a BBSRC Data Sharing Policy was agreed in 2006. Other areas such as Synthetic Biology provide new interdisciplinary approaches.

## Other UK funding bodies supporting *Arabidopsis* research include

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

## International Genomics Collaborations

The first call from ERA-PG (European Research Area in Plant Genomics; http://www.erapg.org/) funded 15 projects across Europe, of which 13 had UK partners.

- The FP6 plant project AGRON-OMICS (http://www.agron-omics.eu/ which includes two UK partners) focuses on integrative biology for leaf growth.
- BBSRC supported part of the *Brassica rapa* sequencing consortium (www.brassica.info); it also supports international collaborations via partnering schemes with China, India and Japan (http://www.bbsrc.ac.uk/international); and has a joint scheme with the Department for International Development (DFID) to promote Sustainable Agriculture Research (http://www.bbsrc.ac.uk/science/initiatives/sus_ag_dfid.html).

## UK *Arabidopsis* Meetings

- GARNet hosts an annual meeting for plant scientists across the UK and Europe to disseminate information about new technologies and resources. GARNet 2007 will be held at the John Innes Centre, Norwich, 11-12th September (http://garnet.arabidopsis.info/garnet_meeting.htm).
- The Genetics Society hosts an annual one-day meeting on *Arabidopsis*, which in 2007 was held at Durham University on May 12th (http://www.genetics.org.uk).

## *Arabidopsis* genomics tools and resources

Resources initiated by GARNet include transcriptomics, proteomics and metabolomics, insert clone libraries and

insertional mutagenesis populations. Data from GARNet-funded projects are available at NASC (http://arabidopsis.info), and Rothamsted http://www.metabolomics.bbsrc.ac.uk/. The CPIB and CSBE centre will develop new biological resources, software and modeling standards over 5 years.

## European Stock Centre

NASC (http://arabidopsis.info) has acted as the European stock centre for germplasm (seed, DNA, clones and data) since 1991 and is twinned with the ABRC (U.S). In addition it provides an integrated genome browser (AtEnsembl) and acts as the primary repository for Affymetrix data within the community through NASCarrays. All data held by NASC is open and disseminated to meta-repositories such as TAIR, GenevestigATor, MapMan, BBC, GEO and ArrayExpress.en-mass and by web-services such as SOAP-labs / BioMOBY.

- Phenotype data is held according to both plant ontology (PO) and Phenotype (PATO) standards (http://arabidopsis.info/bioinformatics/Ontology_details.html).
- The NASC genome browser (http://atensembl.arabidopsis.info) brings together MIPS and TIGR annotation; germplasm; Affymetrix GeneChip data; comprehensive insertion line coverage; and RNA-i knockdown clone resources.
- NASC provides a not-for-profit international GeneChip hybridization service and database and currently holds data from 3,000 GeneChips (http://affy.arabidopsis.info).
- NASCarrays: (http://affymetrix.arabidopsis.info/narrays/experimentbrowse.pl)

# United States

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

Contacts
Philip Benfey
Duke University
Email: philip.benfey@duke.edu
Xing Wang Deng
Yale University
Email: xingwang.deng@yale.edu

## AT2010 Project

The National Science Foundation (NSF)-sponsored 2010 project, established in 2000, aims to determine a function for all genes in *Arabidopsis thaliana* by the year 2010. 119 awards have been granted between 2001 and 2006 (www.nsf.gov/bio/pubs/awards/2010awards.htm). In 2007, proposals submitted to the NSF will be reviewed jointly with proposals submitted to the *Arabidopsis* Functional Genomics Network Program (AFGN) that is supported by the German agency Deutsche Forschungsgemeinschaft (DFG). The program focus for 2007 remained unchanged from 2006 and includes: (1) projects that include genome-wide analyses for benchmarking the function of all genes in the genome; (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) research on exemplary networks that use high throughput methods and integrate modeling with experimental data to understand the gene circuitry underlying basic plant processes (www.nsf.gov/pubs/2006/nsf06612/nsf06612.htm). 2005 marked the midpoint of the program and the North American *Arabidopsis* Steering Committee (NAASC) organized a two-day workshop in August 2005, to evaluate the progress made and provide guidance for the second half of the program. The final report is available in its entirety at www.nsf.gov/pubs/2006/bio0601/bio0601.pdf.

## Plant Science Cyberinfrastructure Collaborative (PSCIC)

In November 2006, acting on the recommendations produced from an NSF-sponsored workshop held to discuss the establishment of a Plant Cyberinfrastructure Center (complete workshop findings and recommendations can be found at www.arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp), the NSF initiated a new program whose goal is to create a cyberinfrastructure collaborative for plant science that will enable new conceptual advances through integrative, computational thinking. The collaborative will be fluid and dynamic, utilizing new computer, computational science and cyberinfrastructure solutions to address an evolving array of grand challenge questions in plant science. The collaborative will be community-driven, involving plant biologists, computer and information scientists and experts from other disciplines working in integrated teams. Final proposals to establish the PSCIC were accepted in April, 2007, and exploratory visits to potential sites are scheduled for June, 2007 (further information at www.nsf.gov/pubs/2006/nsf06594/nsf06594.htm).

## The 17th International Conference on *Arabidopsis* Research

In 1992 the North American *Arabidopsis* Steering Committee was established to provide North American representation to the MASC and to serve as the main organizing and fundraising body for the International Conference on *Arabidopsis* Research (ICAR) held roughly 2 out of every 3 years in the United States since it became an annual meeting in 1995. Historically, the NAASC is composed primarily of U.S. researchers which represent *Arabidopsis* researchers in the United States, Canada and Mexico (NAASC, www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp). The U.S. site for the annual meeting has traditionally been the University of Madison in Wisconsin and the 17$^{th}$ ICAR held June 27$^{th}$-July 2$^{nd}$, 2006 was no exception. Approximately 622 people attended the meeting which was the eighth ICAR held in Madison in the last 12 years. In 2005 the NAASC decided to change the format of the North American meetings by including additional North American sites to alternate with Madison. In 2008, the 19$^{th}$ ICAR will be held in Montreal, Canada from July 23-27.

## U.S./Germany Young Researcher Exchange Program

In late 2005 a program was established to allow graduate students and post-doctoral fellows from NSF-supported U.S. 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 U.S. labs. Since its inception, the U.S. program has funded research visits to Germany by 1 post-doctoral fellow and 8 graduate students. The program is expected to continue until mid-2008. For more information on the U.S. program including eligibility guidelines and application instructions, please see: www.arabidopsis.org/portals/masc/NSF_Arabidopsis_research_program.pdf

- Grant information: www.nsf.gov/awardsearch/showAward.do?AwardNumber=0529918
- For more information on the German program, please see: www.uni-tuebingen.de/plantphys/AFGN/yrep.htm

## Arabidopsis genomics tools and resources

- TAIR (The *Arabidopsis* Information Resource, www.arabidopsis.org) collects information and maintains a database of genetic and molecular biology data for *Arabidopsis thaliana*. TAIR collaborates with the *Arabidopsis* Biological Resource Center (ABRC) to allow researchers to search and order stocks via TAIR. More information on TAIR can be found in the 'Progress and Updates of Multinational *Arabidopsis* Functional Genomics Projects' section of this report.
- ABRC (The Arabidopsis Biological Resource Center, www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm) distributes, collects and preserves seed and DNA resources of *Arabidopsis* and related species. More information on the ABRC can be found in the 'Progress and Updates of Multinational *Arabidopsis* Functional Genomics Projects' section of this report.

## Major funding sources for Arabidopsis functional genomics

- NSF: National Science Foundation (www.nsf.gov/)
- USDA: U.S.Department of Agriculture (www.usda.gov/wps/portal/usdahome)
- DOE: U.S. Department of Energy (www.energy.gov/)
- NIH: National Institutes of Health (www.nih.gov/)

# Tables of Major Arabidopsis Resources

**Table of Major International *Arabidopsis* Stock Centers**
*(adapted from TAIR:http://www.arabidopsis.org/portals/mutants/stockcenters.jsp)*

| ***Arabidopsis* Stock Centers** | **Websites** |
|---|---|
| **Arabidopsis Biological Resource Center (ABRC, United States)** | http://www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm |
| Arabidopsis seed and DNA stock catalogs | http://arabidopsis.org/servlets/Order?state=catalog |
| **Nottingham Arabidopsis Stock Center (NASC, United Kingdom)** | http://arabidopsis.info |
| Arabidopsis seed stock catalogs | http://arabidopsis.info/BrowsePage |
| Arabidopsis genomic resources | http://atensembl.arabidopsis.info |
| **RIKEN Bioresource Center (BRC)/ SENDAI Arabidopsis Seed Stock Center (SASSC, Japan)** | http://www.brc.riken.jp/inf/en |
| Arabidopsis seed stock catalogs | http://www.brc.riken.jp/lab/epd/Eng/catalog/seed.shtml |
| Arabidopsis DNA resources | http://www.brc.riken.jp/lab/epd/Eng/catalog/pDNA.shtml |
| **INRA-Versailles Genomic Resource Center (France)** | http://www-ijpb.versailles.inra.fr/en/sgap/equipes/variabilite/crg/index.htm |
| Arabidopsis seed stock catalog | http://dbsgap.versailles.inra.fr/publiclines |
| **Lehle Seeds (Private company selling seeds and growing systems, United States)** | http://www.arabidopsis.com/main/cat/!ct_seat.html |

**Table of Worldwide Genetic Seed Stock Resources**
*(adapted from TAIR: http://www.arabidopsis.org/portals/mutants/worldwide.jsp)*

| Resource name | Resource URL | Resource Type | Ecotype | Vector Info | Vector URL | View Mutation on Genome | Available From |
|---|---|---|---|---|---|---|---|
| AGRIKOLA | http://www.agrikola.org/ | RNAi knockout (individual lines) | Col | pAGRIKOLA pDONR207 | | n/a | ABRC NASC |
| Alonso, Crosby and Ecker | http://arabidopsis.org/abrc/alonso.jsp | Simple insert (sets of pools and individual lines) | Col-0 | pROK2 | http://signal.salk.edu/tdna_protocols.html | n/a | ABRC NASC |
| Biological Research Center (Hungary) * | http://www.szbk.u-szeged.hu/~arabidop/mappingoftdnalines.htm | Promoter trap and activation tag (individual lines) | Col | multiple T-DNA vectors | http://www.szbk.u-szeged.hu/~arabidop/mappingoftdnalines.htm | PW | contact authors |
| Bressan, Yokoi and Koiwa | http://arabidopsis.org/abrc/bressan.jsp | Activation tag (sets of pools) | C24 | pSKI15 | http://www.weigelworld.org/resources/plasmids/activationtagging/pski015 | n/a | ABRC NASC |
| CSHL | http://genetrap.cshl.org/ | Gene trap and enhancer trap (individual lines) | Ler | Ac, DsG and DsE T-DNAs | http://genetrap.cshl.org/traps.html | AE, AIDB, SV, SIG | ABRC NASC |
| EXOTIC/ JIC Gene Trap | http://www.jic.bbsrc.ac.uk/science/cdb/exotic/index.htm | Gene trap transposon (individual lines) | Ler | Ds-GT and Tpase | http://www.jic.bbsrc.ac.uk/science/cdb/exotic/index.htm | AE, AIDB, SIG | ABRC NASC |
| Feldmann | http://arabidopsis.org/abrc/feldmann.jsp | Simple insert (sets of pools and individual lines) | Ws-2 | 3850:1003 Ti | http://www.arabidopsis.org/servlets/TairObject?type=vector&id=500300068 | n/a | ABRC NASC |
| GABI-Kat * | http://www.gabi-kat.de/ | T-DNA insertion (individual lines) | Col | pAC161 | http://www.gabi-kat.de/General_Information/GABI-Kat-pAC161T-DNAmapPr.html | AE, AIDB, SV, SIG | ABRC NASC |
| GARNet - JIC SM | http://garnet.arabidopsis.org.uk/transposons_for_functional_genomics.htm | Single insert Ds-Spm (insertion lines) | Col-0 | SLJ8313 SLJ8337 SLJ8353 | http://jicgenomelab.co.uk/fileadmin/Download/Documents/pdf/Tissier_PC_1999.pdf | AE, AIDB, SIG | ABRC NASC |
| Haseloff/U. Cambridge | http://www.plantsci.cam.ac.uk/Haseloff/geneControl/catalogFrame.html | Enhancer trap (individual lines) | C24 | pBIN m-gfp5-ER | http://www.arabidopsis.org/servlets/TairObject?type=vector&id=500400069 | n/a | ABRC NASC |
| IMA * | http://www.arabidopsis.org/abrc/ima.jsp | Ds insertion (individual lines) | Ler | Ds element (kanamycin resistance, GUS reporter) | http://www.plantcell.org/cgi/content/full/11/12/2263 | SV, SIG | ABRC NASC |
| INRA-Versailles FLAG_FST * | http://urgv.evry.inra.fr/projects/FLAGdb++/HTML/index.shtml | Promoter trap (individual lines) | Ws | pGKB5 | http://www-ijpb.versailles.inra.fr/fr/sgap/equipes/cyto/ressources/pGKB5.html | AE, AIDB, SV, SIG | INRA |

**Table of Worldwide Genetic Seed Stock Resources** (continued)

*(adapted from TAIR: http://www.arabidopsis.org/portals/mutants/worldwide.jsp)*

| Resource name | Resource URL | Resource Type | Ecotype | Vector Info | Vector URL | View Mutation on Genome | Available From |
|---|---|---|---|---|---|---|---|
| INRA | http://arabidopsis.org/abrc/inra.jsp | Promoter trap (set of pools) | Ws-4 | pGKB5 | http://www-ijpb.versailles.inra.fr/fr/sgap/equipes/cyto/ressources/pGKB5.html | n/a | ABRC NASC |
| JIC Activate | http://arabidopsis.info/CollectionInfo?id=29 | Activation trap (individual lines) | Ler | Tn113 (Ds starter line) X Tn25 (Ac transposase lines) | | AE, AIDB | ABRC NASC |
| Jack | http://arabidopsis.org/abrc/jack.jsp | Enhancer trap (set of pools) | Col-6 (gl1) | pD991 | http://www.dartmouth.edu/~tjack/ | n/a | ABRC NASC |
| Poethig/U. Penn | http://enhancertraps.bio.upenn.edu/ | Enhancer trap (individual lines) | Col | pBIN m-gfp5-ER | http://www.arabidopsis.org/servlets/TairObject?type=vector&id=500400069 | PW | ABRC NASC |
| RIKEN * | http://rarge.gsc.riken.jp/dsmutant/index.pl | Ds transposon insertion (individual lines) | No-O | series of Ds constructs | http://rarge.gsc.riken.jp/dsmutant/index.pl | AE, RAR, SIG | RIKEN BRC |
| RIKEN * | http://amber.gsc.riken.jp/act/top.php | Activation trap (individual lines) | Col | pPCVICEn4HPT (hygromycin resistance, 4x 35CaMV enhancer) | | AE, RAR, SIG | RIKEN BRC |
| SAIL (formerly GARLIC/TMRI) | http://www.arabidopsis.org/abrc/sail.jsp | T-DNA insertion (individual lines) | Col | pCSA110 pDAP101 | | AE, AIDB, SV, SIG | ABRC NASC |
| SALK | http://signal.salk.edu/tabout.html | T-DNA insertion (individual lines) | Col | pROK2 | http://signal.salk.edu/tdna_protocols.html | AE, AIDB, SV, SIG | ABRC NASC |
| Confirmed SALK insertion lines | http://signal.salk.edu/gabout.html | T-DNA insertion (PCR-validated homozygous or heterozygous individual lines) | Col | pROK2 | http://signal.salk.edu/tdna_protocols.html | SV, SIG | ABRC NASC |
| Scheible and Somerville | http://arabidopsis.org/abrc/Scheible.jsp | Activation tag (set of pools) | Col-2 | pSKI15 | http://www.weigelworld.org/resources/plasmids/activationtagging/pski015 | n/a | ABRC NASC |
| Sussman and Amasino | http://arabidopsis.org/abrc/sussman_fwd.jsp | Simple insert (set of pools) | Ws-2 | pD991-AP3 | http://www.biotech.wisc.edu/NewServicesAndResearch/Arabidopsis/pD991-AP3_finalseq.html | n/a | ABRC NASC |
| TAMARA | http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=16087178 | Tn mediated activation tag (individual lines) | Col-0 | TAMARA | http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=16087178 | contact authors | NASC |
| TILLING | http://tilling.fhcrc.org:9366/ | EMS mutagenized (individual lines) | Col er-105 | n/a | | SV | ABRC NASC |
| Weigel | http://arabidopsis.org/abrc/weigel.jsp | Activation tag (set of pools) | Col-7 | pSKI15 | http://www.weigelworld.org/resources/plasmids/activationtagging/pski015 | n/a | ABRC NASC |
| Wisconsin Ds-Lox | http://www.hort.wisc.edu/krysan/Ds-Lox/ | Ds-Lox insertion (individual lines) | Col | pDS-Lox | http://www.hort.wisc.edu/krysan/Ds-Lox/ | AE, AIDB, SV, SIG | ABRC NASC |
| Wisconsin KO | http://www.arabidopsis.org/abrc/akf.jsp | T-DNA insertion (set of pools) | Ws | pD991-AP3 | http://www.biotech.wisc.edu/NewServicesAndResearch/Arabidopsis/pD991-AP3_finalseq.html | n/a | ABRC NASC |

*** MTA needs to be signed and/or IP restrictions**

**AE** (AtEnsembl) **AIDB** (A. thaliana Integrated Database) **PW** (Project Website) **SV** (SeqViewer) **SIG** (SIGnAL)
**RAR** (RARGE) **ABRC** (Arabidopsis Biological Resource Center) **NASC** (Nottingham Arabidopsis Stock Centre)

# Tables of Major Arabidopsis Resources

## (continued)

**Table of Major Reverse Genetic Projects and Browsers Where Collections can be Viewed**

*Note: If a set of lines is not visible in any of the browsers, the flanking sequence, RNAi construct used and/or locus assignments are available at the project website. (adapted from TAIR: http://www.arabidopsis.org/portals/mutants/findmutants.jsp)*

| | **Browsers:** | **AtEnsembl** | **AtIDB** | **SeqViewer** | **SIGnAL** | **RARGE** |
|---|---|---|---|---|---|---|
| | | http://atensembl.arabidopsis.info | http://atidb.org/cgi-perl/gbrowse/atibrowse | http://www.arabidopsis.org/servlets/sv | http://signal.salk.edu/cgi-bin/tdnaexpress | http://rarge.gsc.riken.jp/genomemap/genomemap.pl |
| **Reverse Genetics Project** | **Project URLS** | | | | | |
| AGRIKOLA | http://www.agrikola.org/index.php?o=/agrikola/html/database | | | | | |
| Biological Research Center(Hungary) | http://www.szbk.u-szeged.hu/~arabidop/mappingoftdnalines.htm | | | | | |
| CSHL | http://genetrap.cshl.org/ | x | x | x | x | |
| EXOTIC/JIC Gene Trap | http://www.jic.bbsrc.ac.uk/science/cdb/exotic/index.htm | x | x | | x | |
| GABI-Kat | http://www.gabi-kat.de/ | x | x | x | x | |
| GARNet- JIC SM | http://garnet.arabidopsis.org.uk/transposons_for_functional_genomics.htm | x | x | | x | |
| IMA | http://www.arabidopsis.org/abrc/ima.jsp | | | x | x | |
| INRA-Versailles FST | http://urgv.evry.inra.fr/projects/FLAGdb++/HTML/index.shtml | x | x | x | x | |
| JIC Activate | http://arabidopsis.info/CollectionInfo?id=29 | x | x | | | |
| Poethig/U. Penn | http://enhancertraps.bio.upenn.edu/default.html (click 'search) | | | | | |
| RIKEN Transposon Insertion | http://rarge.gsc.riken.jp/dsmutant/index.pl | x | | | x | x |
| RIKEN Activation Trap | http://amber.gsc.riken.jp/act/top.php | x | | | x | x |
| SAIL (formerly GARLIC/TMRI) | http://www.arabidopsis.org/abrc/sail.jsp | x | x | x | x | |
| SALK | http://signal.salk.edu/tabout.html | x | x | x | x | |
| TILLING | http://tilling.fhcrc.org:9366/ | | | x | | |
| Wisconsin Ds-Lox | http://www.hort.wisc.edu/krysan/Ds-Lox/ | x | x | x | x | |

**Table of Full-Length cDNA and ORF Clone Large Collections**

*(adapted from TAIR: http://www.arabidopsis.org/portals/clones_DNA/clones.jsp)*

| Source | Source URL | Type | Vector(s) | Summary |
|---|---|---|---|---|
| Gabi Expression Clones | http://gabi.rzpd.de/materials/expressionClonesArabidopsis.shtml | cDNA | pQE-30NAST-attB | About 4,500 cDNA expression clones, comprising a Unigene set of about 1500 clones. Coding sequences are predicted to be in frame with the N-terminal His-tag. |
| Gabi Full Length ORF Clones | http://gabi.rzpd.de/materials/fullORFArabidopsis.shtml | cDNA (full length) | pDONR201, pENTR3c | About 1000 full-length ORF clones encoding transcription factors. For more information see Paz-Ares: The REGIA Consortium (2002). |
| Genoscope/LifeTechnologies (GSLT) | http://www.genome.org/cgi/content/full/14/3/406 | cDNA | pCMV-Sport6 | Single pass sequenced cDNAs available from Genoscope. Gateway™ compatible vector. |
| ATOME (Arabidopsis thaliana orfeOME) 1 | http://www.evry.inra.fr/public/projects/orfeome/orfeome.html | ORF | pDONR221 | PCR amplified, sequence verified ORFs from GSLT full length cDNA clones in a Gateway ™ compatible vector. |
| ATOME2 | http://www.evry.inra.fr/public/projects/orfeome/orfeome.html | ORF | pDONR207 | PCR amplified, sequence verified ORFs from SSP ORF collection lacking short (10-50 bp) 3' UTR sequences. Cloned into Gateway ™ compatible vector. Clones available from ABRC |
| Peking/Yale Consortium Transcriptome | http://www.pubmedcentral.gov/articlerender.fcgi?tool=pubmed&pubmedid=15208423 | ORF | pENTR/DTOPO | 1282 transcription factor ORFs cloned into Gateway ™ vectors. Nomenclature is PY+locus name (e.g.PYAT1G03790).Clones available from ABRC. |
| Riken FlcDNA (RAFL) clones | http://www.brc.riken.jp/lab/epd/Eng/QA/RAFL.shtml | cDNA (full length) | RAFL 2-3;RAFL4-6; RAFL 7-11,26; RAFL 12-25 | cDNA clones derived from a variety of phagemid libraries.All clones subjected to single pass sequence. NOTE: These clones are only available from Riken. |
| SSP Consortium | http://signal.salk.edu/SSP/ | ORF/fl-cDNA | pUNI (most) some pENTR | PCR-amplified, sequence verified ORF (U) and fl-cDNA (S) clones derived from FlcDNA (Riken clones), EST and GSLT clones. Includes over 10,000 full length ORF clones available from ABRC. |
| TIGR Hypothetical Gene Clones | http://www.tigr.org/tdb/hypos/ | ORF | pENTR221 | PCR generated ORF clones amplified from genomic DNA representing a subset of predicted genes of unknown function which lacked cDNA/EST support.Clones available from ABRC. |

# Members of the Multinational *Arabidopsis* Steering Committee


**Ian Small, Chair**
Representing Australia
iansmall@cyllene.uwa.edu.au
University of Western Australia
Perth, Australia

**Xing Wang Deng, Co-chair**
Representing the United States of America
Xingwang.deng@yale.edu
Yale University
New Haven, Connecticut, USA

**Thomas Altmann**
Representing Germany
Altmann@mpimp-golm.mpg.de
Universitaet Potsdam
Golm, Germany

**Ruth Bastow**
Representing the United Kingdom/ GARNet
ruth@arabidopsis.info
University of Bristol
Bristol, United Kingdom

**Philip Benfey**
Representing the United States of America
philip.benfey@duke.edu
Duke University
Durham, NC, USA

**David Bouchez**
Representing France
bouchez@versailles.inra.fr
INRA Centre de Versailles
Versailles, Cedex, France

**Jorge Casal**
Representing Argentina
casal@ifeva.edu.ar
University of Buenos Aires
Buenos Aires, Argentina

**Danny Chamovitz**
Representing Israel
dannyc@ex.tau.ac.il
Tel Aviv University
Tel Aviv, Israel

**Bill Crosby**
Representing Canada
bcrosby@uwindsor.ca
University of Windsor
Ontario, Canada

**Klaus Harter**
Representing Germany
klaus.harter@zmbp.uni-tuebingen.de
University of Tübingen
Tübingen, Germany

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

**Pierre Hilson**
Representing Belgium
Pierre.hilson@psb.UGent.be
Ghent University
Ghent, Belgium

**Jaakko Kangasjärvi**
Representing the Nordic *Arabidopsis* Network
jaakko.kangasjarvi@helsinki.fi
University of Helsinki
Helsinki, Finland

**Sean May**
Representing the United Kingdom/ NASC
sean@arabidopsis.info
Nottingham *Arabidopsis* Stock Center
Loughborough, U.K.

**Peter McCourt**
Representing Canada
mccourt@botany.utoronto.ca
University of Toronto
Toronto, Ontario, Canada

**Ortrun Mittelsten-Scheid**
Representing Austria
ortrun.mittelsten_scheid@gmi.oeaw.ac.at
GMI, Austrian Academy of Sciences
Vienna, Austria

**Javier Paz-Ares**
Representing Spain
jpazares@cnb.uam.es
Centro National de Biotechnoligia
Madrid, Spain

**Barry Pogson**
Representing Australia and New Zealand
barry.pogson@anu.edu.au
Australian National University
Canberra, Australia

**Ben Scheres**
Representing the Netherlands
b.scheres@uu.nl
University of Utrecht
The Netherlands

**Randy Scholl**
Representing the United States of America/ABRC *Ex officio*
Scholl.1@osu.edu
ABRC
Columbus, OH, USA

**Kazuo Shinozaki**
Representing Japan
sinozaki@rtc.riken.go.jp
RIKEN Genomic Sciences Center
Tsukuba, Ibaraki, Japan

**Willem Stiekema**
Representing The Netherlands
Center for BioSystems Genomics
willem.stiekema@cbsg.nl
Wageningen, The Netherlands

**Paola Vittorioso**
Representing Italy
paola.vittorioso@uniroma1.it
University of Rome
Rome, Italy

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

**Joanna Friesner**
Coordinator and Executive Secretary
jdfriesner@ucdavis.edu
University of California, Davis
Davis, CA, USA

# Members of the MASC Subcommittees

## Bioinformatics

**Chris Town (co-chair)**
cdtown@tigr.org

**Heiko Schoof (co-chair)**
schoof@mpiz-koeln.mpg.de

**Fabrice Legeai**
flegeai@infobiogen.fr

**Sean May**
sean@arabidopsis.info

**Klaus Mayer**
Kmayer@gsf.de

**Yasukazu Nakamura**
yn@kazusa.or.jp

**Yves van de Peer**
yvdp@psb.UGent.be

## Clone-Based Functional Genomics Resources (ORFeomics)

**Pierre Hilson (chair)**
pierre.hilson@psb.ugent.be

**Kazuo Shinozaki**
sinozaki@rtc.riken.go.jp

**Ian Small**
iansmall@cyllene.uwa.edu.au

**Chris Town**
cdtown@tigr.org

## Metabolomics

**Ian Graham (co-chair)**
iag1@york.ac.uk

**Basil Nikolau (co-chair)**
dimmas@iastate.edu

**Mike Beale**
mike.beale@bbsrc.ac.uk

**Oliver Fiehn**
ofeihn@ucdavis.edu

**Alisdair Firnie**
Fernie@mpimp-golm.mpg.de

**Tony Larson**
trl1@york.ac.uk

**Rob Last**
lastr@msu.edu

**Kazuki Saito**
ksaito@faculty.chiba-u.jp

**Steven Smith**
ssmith@cyllene.uwa.edu.au

**Wolfram Weckwerth**
weckwerth@mpimp-golm.mpg.de

## Natural Variation and Comparative Genomics

*Natural Variation*

**Tom Mitchell-Olds (chair)**
tmo1@duke.edu

**Carlos Alonso-Blanco**
calonso@cnb.uam.es

**Thomas Altmann**
altmann@mpimp-golm.mpg.de

**Ian Bancroft**
ian.bancroft@bbsrc.ac.uk

**Joy Bergelson**
jbergels@uchicago.edu

**Justin Borevitz**
borevitz@uchicago.edu

**Kathleen Donohue**
kdonohue@fas.harvard.edu

**Matthias Hoffmann**
matthias.hoffmann@botanik.uni-halle.de

**Olivier Loudet**
loudet@versailles.inra.fr

**Julin Maloof**
jnmaloof@ucdavis.edu

**Annie Schmitt**
Johanna_Schmitt@brown.edu

# Members of the MASC Subcommittees (continued)

## Natural Variation and Comparative Genomics

*Comparative Genomics*

**Tom Mitchell-Olds (chair)**
tmo1@duke.edu

**David Baum**
dbaum@wisc.edu

**Hans Bohnert**
bohnerth@life.uiuc.edu

**Sean Cutler**
cutler@botany.utoronto.ca

**Graham King**
Graham.King@bbsrc.ac.uk

**Marcus Koch**
marcus.koch@urz.uni-heidelberg.de

**Martin Lysak**
lysak@sci-muni.cz

**Chris Pires**
piresjc@missouri.edu

**Ray Ming**
rming@life.uiuc.edu

**Detlef Weigel**
weigel@tuebingen.mpg.de

## Phenomics

**Eva Huala (co-chair)**
huala@acoma.stanford.edu

**Sean May (co-chair)**
sean@arabidopsis.info

**Joe Ecker**
ecker@salk.edu

**Minami Matsui**
minami@postman.riken.go.jp

**Randy Scholl**
scholl.1@osu.edu

**Detlef Weigel**
weigel@tuebingen.mpg.de

## Proteomics

**Wolfram Weckwerth (chair)**
Weckwerth@mpimp-golm.mpg.de

**Sacha Baginsky (co-chair)**
sacha.baginsky@ipw.biol.ethz.ch

**Harvey Millar (co-chair)**
hmillar@cyllene.uwa.edu.au

**Klaas van Wijk (co-chair)**
kv35@cornell.edu

**Hans-Peter Braun**
braun@genetik.uni-hannover.de

**Joshua Heazlewood**
joshua.heazlewood@uwa.edu.au

**Kathryn S. Lilley**
k.s.lilley@bioc.cam.ac.uk

**Hans-Peter Mock**
mock@ipk-gatersleben.de

**Loïc Rajjou**
loic.rajjou@gmail.com

**Sigrun Reumann**
sreuman@gwdg.de

**Michel Rossignol**
rossign@ensam.inra.fr

**Jay Thelen**
thelenj@missouri.edu

**Julian Whitelegge**
jpw@chem.ucla.edu

## Systems Biology

**Philip Benfey (chair)**
philip.benfey@duke.edu

**Wilhelm Gruissem**
wgruissem@ethz.ch

**Rodrigo Gutierrez**
rodrigo.gutierrez@gmail.com

**Andrew Millar**
andrew.millar@ed.ac.uk

**Eve Syrkin Wurtele**
mash@iastate.edu