

The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project Annual Report 2006

Natural Variation



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Philip Benfey philip.benfey@duke.edu
Chair

Ian Small iansmall@cyllene.uwa.edu.au
Co-chair

Thomas Altmann altmann@mpimp-golm.mpg.de
David Bouchez bouchez@versailles.inra.fr
Jorge Casal casal@ifeva.edu.ar
Bill Crosby bcrosby@uwindsor.ca
Ian Furner ijf@mole.bio.cam.ac.uk
Mary Lou Guerinot Mary.Lou.Guerinot@Dartmouth.edu
Pierre Hilson pierre.hilson@psb.ugent.be
Heribert Hirt heribert.hirt@univie.ac.at
Gerd Jürgens gerd.juergens@uni-tuebingen.de
Jaakko Kangasjärvi jaakko.kangasjarvi@helsinki.fi
Keith Lindsey keith.lindsey@durham.ac.uk
Sean May sean@arabidopsis.info
Andrew Millar Andrew.Millar@ed.ac.uk
Peter McCourt mccourt@botany.utoronto.ca
Barry Pogson barry.pogson@anu.edu.au
Ben Scheres b.scheres@bio.uu.nl
Kazuo Shinozaki sinozaki@rtc.riken.go.jp
Willem Stiekema willem.stiekema@cbsg.nl
Paola Vittorioso paola.vittorioso@uniroma1.it
Yang Weicai wcyang@genetics.ac.cn

Joanna Friesner jdfriesner@stanford.edu
Coordinator and Executive Secretary

The Multinational *Arabidopsis* Steering Committee – June 2006

Cover: A number of diverse *Arabidopsis thaliana* accessions overlay a map of the world demonstrating the wide genetic variation that exists in this reference plant. A recent analysis of twenty natural accessions resulted in the identification of over 500,000 unique single-nucleotide polymorphisms (SNPs) making *Arabidopsis* the organism with the highest SNP density relative to genome size. Studies of natural variation and comparative genomics, current areas of focus for the MASC, will be enabled by the availability of these data. *Cover image concept: Philip Benfey, Duke University. Cover image design: Detlef Weigel, Max Planck Institute.*

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Foreword to the Report

This is the 2005/2006 annual report of the Multinational *Arabidopsis* Steering Committee (MASC) on the status of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. This 10-year program, initiated in 2001 following publication of the complete *Arabidopsis thaliana* genome sequence, was described fully in the 2002 MASC report. The primary project goal is to determine the function of every *Arabidopsis* gene and thus obtain a detailed and comprehensive understanding of a flowering plant. The value of this tractable plant system is immediately apparent and the intent is that the knowledge gained on this experimental model organism will serve as the central reference and conceptual framework for all of plant biology.

The availability of the complete genome sequence was an invaluable step towards the goal of understanding the function of every *Arabidopsis* gene. Using this knowledge, researchers around the world were newly equipped to investigate numerous facets of *Arabidopsis* biology. However, as the considerable scale of the proposed project became clear, the necessity for newly developed high-throughput technologies, novel experimental tools and comprehensive collections of plant resources as well as powerful procedures for data analysis, storage and display, became apparent. In addition, it was realized that the complexity of even such a “simple” flowering plant as *Arabidopsis* requires continuous evaluation of the goals and needs of the research community in order to adeptly respond to progress and bottlenecks.

Establishing and maintaining world-wide collaboration is critical to the success of the *Arabidopsis* Functional Genomics Project. The nature and volume of the proposed work necessitates that global resources be coordinated to attain a maximum level of synergy as well as to avoid duplication of effort. Only sustained and earnest collaborations will enable the *Arabidopsis* community to achieve its ambitious goals. The Multinational *Arabidopsis* Steering Committee, supported by a full-time staff member, plays a key role in supporting this international coordination by collecting and disseminating information from the various initiatives and projects on technology development and functional analyses and by giving specific recommendations for further directions.

This report highlights the progress made over the last year by the international *Arabidopsis* functional genomics community. It also demonstrates the continued high level of cooperation that exists throughout the global community and the importance of the support by funding agencies in producing important and exciting results in plant biology. **The continuing rapid progress in *Arabidopsis* functional genomics emphasizes the central role that work on this reference plant has for furthering our understanding of all plants.**

The Multinational *Arabidopsis* Steering Committee
June 2006

Executive Summary

The publication of the *Arabidopsis thaliana* genome just over five years ago marked the release of the first complete plant sequence. As the third multicellular organism to have its entire genome sequenced, following *C. elegans* and *D. melanogaster*, *Arabidopsis thaliana* not only is the most important model system for plant biology but is also an invaluable resource for the study of other multicellular organisms. Increasingly comprehensive and sophisticated knowledge of *Arabidopsis* biology allows researchers from both inside and outside the plant community to leverage *Arabidopsis* resources and data for comparative genomics and complex systems modeling. Following the success of the international collaborative genome sequencing project the *Arabidopsis* community continues to strengthen and grow; according to The *Arabidopsis* Information Resource (TAIR) there are currently more than 15,000 *Arabidopsis* researchers in nearly 6,000 laboratories worldwide. While much has been accomplished it is clear that there is even more that can and should be done. It is only through continued widespread research funding and international collaboration, particularly through timely sharing of data, stocks, and other resources, that we will fully realize the utility of *Arabidopsis thaliana* as a reference plant and model organism.

Arabidopsis continues to play a dominant role in plant science research. In the past year alone a number of major breakthroughs were reported. While it has been known for many years that plant hormones are key regulators of a variety of processes with high agronomic importance, including growth rate and flowering time, none of the hormone receptors had previously been identified. Starting with auxin, two groups identified the receptor in *Arabidopsis* as a protein involved in targeting other proteins for degradation^{1,2}. Next, a gibberellin receptor was identified in rice, and its identity confirmed through its interactions with the DELLA proteins, first identified in *Arabidopsis* as transducers of gibberellin signaling³. Most recently, a receptor for abscisic acid was identified as a gene in *Arabidopsis* known to be directly involved in controlling flowering time⁴. Hormones also regulate the number of branches on a shoot. While it was known that auxin is partially responsible, a new family of regulators known as MAX genes was shown this year to control the flow of auxin in the shoot and thus the number of

branches⁵. Another developmental puzzle involves the timing of plant flowering which has been shown to be under the influence of a mysterious graft-transmissible substance known as "florigen." Two studies, one in *Arabidopsis*, the other in tomato, revealed the long-sought identity of florigen as the FLOWERING TIME (FT) gene. How the signal is transmitted is still controversial - in *Arabidopsis* the claim is that the FT RNA moves, while in tomato, it seems that only the protein moves^{6,7}. Finally, a report that over-expressing a yeast chromatin-remodeling protein in *Arabidopsis* dramatically increased the rate of gene targeting may point the way for precisely reshaping the genomes of plants to enhance specific traits⁸.

The specific aims of the multinational *Arabidopsis thaliana* functional genomics project comprise short-term, mid-term, and long-term goals. Many of the short-term goals have been achieved and mid-term goals initiated including:

- Improved genome annotation through the use of expressed sequences and expert knowledge and curation.
- Generation of comprehensive sets of sequence-indexed mutants that are listed in an integrated database and available as seed stocks. This highly-utilized resource efficiently allows researchers to ascertain knowledge of gene function.
- The production of genome-wide sets of gene-specific probes for expression analysis and the establishment of reference transcriptomes.
- Full-length cDNA sequence information has been determined for much of the genome and many cDNAs are systematically being cloned into expression vectors that will enable a variety of functional genomics and proteomics studies.
- Development of standardized vocabularies including Gene Ontology (GO) and Phenotype, Attribute, and Trait Ontology (PATO), and the Plant Ontology Consortium for plant structure, growth and developmental stages.
- The development of numerous combinations of Recombinant Inbred Lines (RILs) to enable analysis of natural variation.

- The identification of species for survey genomic sequencing to enable studies of comparative genomics and natural variation.
- The establishment of metabolic profiling facilities for global metabolite analysis.
- Facilitation of international collaboration through the appointment of a full-time MASC coordinator to foster information flow and monitor progress of the program.

This past year's progress included the following achievements

- The first *Arabidopsis* genome release by TAIR (The *Arabidopsis* Information Resource, November, 2005): version 6.0 includes 26,751 protein coding genes, 3818 pseudo-genes, and 838 non-coding RNAs (31,407 genes in the entire genome).
- Identification of insertion mutations for 28,607 of 31,128 (92%) nuclear-encoded genes with approximately 75% of the insertions located in exons.
- 2,729 homozygous mutant insertion lines (representing 2,227 genes) have been identified from the newly-initiated project (Ecker/Salk Institute) to identify two homozygous mutants for 25,000 *Arabidopsis* genes.
- Availability of nearly 22,000 RNAi clones targeting 19,202 genes. Completion of the AGRIKOLA project (expected mid-2006) will involve more than 25,000 clones targeting over 20,000 genes.
- Over 500,000 unique single-nucleotide polymorphisms (SNPs) were identified for 20 natural accessions making *Arabidopsis* the organism with the highest density of high quality SNPs per kilobase of genomic sequence. (D. Weigel, Max Planck Institute).
- Fully-supported release of the Affymetrix Tiling 1.0 R full genome tiling array (April, 2006).
- Isolation of full-length cDNAs for nearly 75% of the nuclear protein-coding genes (approximately 19,500 of 26,541); clones of 14,216 are currently being distributed and an additional 9,058 are targeted for cloning.
- An AT2010 Midcourse evaluation workshop to evaluate the progress made toward the specific goals of the program and to recommend directions for the next five years (Virginia, U.S., August, 2005).
- A workshop on the needs and goals for a plant cyberinfrastructure for facilitating the synthesis of new biological insights from all available functional genomics data (Virginia, U.S., October, 2005).
- BioMoby pilot project workshops on web services for data integration were held in Germany (March, 2006) and the U.S. (April, 2006). Demonstrations will be made to the wider *Arabidopsis* community at the Annual International Conference on *Arabidopsis* Research (Madison, WI, June/July, 2006).
- Establishment of a Metabolomics working group.
- Establishment of a Phenomics working group.

The MASC's (Multinational *Arabidopsis* Steering Committee) short-term plan for the next year includes

- Ensure the successful establishment of recently formed MASC subcommittees including Metabolomics, Natural Variation and Comparative Genomics, Phenomics, and Proteomics.
- Update and improve the Project's webpages at TAIR.
- Work toward completion of genetic resources projects including collections of homozygous insertion mutants (SALK) and RNAi clones (AGRIKOLA).
- Develop resources for studying protein interactions and localization, including complete cloning of full-length cDNAs into expression vectors.
- Expand data integration and interoperability efforts for optimal use of data resources.
- Facilitate and encourage submission of data and stocks into public repositories.
- Implement a Systems Biology working group.

Past success of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project can be attributed to the strength of both international collaborations and funding support within the *Arabidopsis* community. Future successes will require that we continue to share information and resources so that our efforts are synergistic, not redundant, and that we effectively convey to funding agencies, decision-makers, and the public, our progress and the importance and relevance to society of studying and understanding this reference plant. The MASC will continue to monitor the Project's progress and coordinate activities of the global *Arabidopsis* research community.

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Progress and Activities of the Multinational *Arabidopsis* Steering Committee (MASC)

MASC Activities in 2005/2006

In 2005/2006, Philip Benfey (Duke University) and Ian Small (University of Western Australia) continued as MASC chair and co-chair, respectively. Dr. Small will become the new MASC chair when Dr. Benfey steps down following the annual International Conference on *Arabidopsis* Research (ICAR) in June, 2006. At this time, Xing-Wang Deng (Yale University) will become the new MASC co-chair.

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. As the field progresses, changes in needs and priorities require reassessment of each MASC subcommittee. A major revision of the MASC subcommittee structure was initiated at the annual MASC meeting held in conjunction with the 16th ICAR in Madison, Wisconsin (U.S.) June, 2005. Two new subcommittees were proposed, two were dissolved, and the need for two initiated at the 2004 annual meeting was re-emphasized. Newly proposed groups include the Phenome subcommittee and the Natural Variation and Comparative Genomics subcommittee. The Multiparallel Tools and Forward/Reverse Genetic Stocks subcommittees were dissolved, although some responsibilities of the Genetic Stocks subcommittee will be assumed by the Natural Variation and Comparative Genomics groups. Finally, Proteomics and Metabolomics subcommittees, originally proposed in 2004, were given renewed emphasis to form and chairs recently have been identified. These four new groups will join the original Bioinformatics and ORFeome subcommittees.

In April, 2005, an NSF-funded workshop on "Data Integration" was held at TIGR, followed by a workshop at the annual *Arabidopsis* meeting in Madison in June, 2005. The goals of the workshops were to assess needs, gather community input and exchange ideas about improving data integration in the *Arabidopsis* research community. Based on these workshops, Chris Town (TIGR) and Heiko Schoof (Max Planck) submitted successfully-funded proposals to establish an integrated pilot project to NSF and DFG, respectively. The pilot program includes workshops in Germany and the U.S., held in March and April, 2006, as well as plans to have web services

in place for demonstrations at the annual *Arabidopsis* meeting in Madison in June, 2006. The Bioinformatics Subcommittee section of this report contains a more detailed description of the program.

A full-time MASC coordinator position was established in 2002, initially funded for two years by the NSF (U.S.), then for one year by the DFG (Germany), followed by another two-year grant from the NSF with current funding expiring at the end of 2006. 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 ICAR, (3) producing and editing the annual MASC progress report and other MASC documents, (4) serving as a liaison between 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 (Stanford, California) to inform the global research community about various opportunities, collaborations, large-scale activities and research progress. Isabell Witt served from 2004 to November, 2005 before returning to Germany to take up a position as Graduate Coordinator at the University of Cologne. In January 2006 the coordinator position relocated to TAIR and Joanna Friesner, a post-doctoral fellow from the University of California at Davis, became the third MASC coordinator. The position was strategically affiliated with TAIR in order to provide for continuity in coordinator location and also to facilitate the critical revision of the MASC functional genomics webpages located at TAIR. Updating and modifying the MASC webpages are among the highest priorities for the coordinator during the second half of 2006.

Highlights of the Past Year

Arabidopsis continues to play a dominant role in plant science research. In the past year alone a number of major breakthroughs were reported. While it has been known for many years that plant hormones are key regulators of a variety of processes with high agronomic importance, including growth rate

and flowering time, none of the hormone receptors had previously been identified. Starting with auxin, two groups identified the receptor in *Arabidopsis* as a protein involved in targeting other proteins for degradation^{1,2}. Next, a gibberellin receptor was identified in rice, and its identity confirmed through its interactions with the DELLA proteins, first identified in *Arabidopsis* as transducers of gibberellin signaling³. Most recently, a receptor for abscisic acid was identified as a gene in *Arabidopsis* known to be directly involved in controlling flowering time⁴. Hormones also regulate the number of branches on a shoot. While it was known that auxin is partially responsible, a new family of regulators known as MAX genes was shown this year to control the flow of auxin in the shoot and thus the number of branches⁵. Another developmental puzzle involves the timing of plant flowering which has been shown to be under the influence of a mysterious graft-transmissible substance known as "florigen." Two studies, one in *Arabidopsis*, the other in tomato, revealed the long-sought identity of florigen as the FLOWERING TIME (FT) gene. How the signal is transmitted is still controversial - in *Arabidopsis* the claim is that the FT RNA moves, while in tomato, it seems that only the protein moves^{6,7}. Finally, a report that over-expressing a yeast chromatin-remodeling protein in *Arabidopsis* dramatically increased the rate of gene targeting may point the way for precisely reshaping the genomes of plants to enhance specific traits⁸.

AT2010 Midcourse Evaluation

2005 marked the halfway point of the NSF-sponsored AT2010 program which has funded 86 projects in its first five years (U.S.). The program's primary goal is to determine the function of every *Arabidopsis* gene by 2010 and ultimately achieve a complete understanding of the biology of a flowering plant, using *Arabidopsis thaliana* as an experimental model system. Scientific objectives of this long-range plan include (1) development of an expanded genetic toolkit, including new technology development that enables the broad community to conduct *Arabidopsis* functional genomics, (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 for bioinformatics, (4) development of community and human resources, and (5) promotion of international cooperation. The NAASC organized a workshop in Virginia (U.S.) on Aug. 25 and 26, 2005, to evaluate the progress made toward the specific goals of the program and to recommend directions for the next five years. Workshop participants felt that the majority of the initial program goals had been met or surpassed, and that high-throughput and/or bioinformatics approaches have particularly been useful for functional analysis of biological processes. The participants developed a number of specific recommendations for the project's remaining five years and looked towards the future and a possible *Arabidopsis* 2020 project. For a more detailed description of the midterm

evaluation, please refer to the United States submission in the International *Arabidopsis* Functional Genomics Community section of this report. The full report is also available at www.nsf.gov/pubs/2006/bio0601/bio0601.pdf

Tiling Chips

Whole genome tiling chips covering the entire *Arabidopsis thaliana* genome sequence (designed by Joe Ecker and Affymetrix) were made available last year through an early access program; the fully supported array was officially released in April, 2006. The *Arabidopsis* Tiling 1.0R array is a single chip comprised of over 3.2 million probe pairs tiled through the complete non-repetitive *Arabidopsis* genome (1 probe pair PerfectMatch/MisMatch every 38 bases) and includes nuclear, chloroplast, and mitochondrial sequences. Through the early access program the array has been used in a number of currently unpublished experiments including transcript mapping and chromatin immunoprecipitation (ChIP/chip) (Ecker), analysis of DNA methylation (Ecker/ Steve Jacobsen labs), and polymorphism discovery in different *Arabidopsis* accessions (Justin Borevitz). A second public-private project, initiated by Detlef Weigel (Max Planck Institute) and Joe Ecker (Salk Institute), and funded by a grant from the Max Planck Institute, involves whole genome study of natural variation in twenty *Arabidopsis thaliana* accessions using tiling arrays with Watson and Crick strands on independent chips. In collaboration with Perlegen Sciences, Weigel recently completed the data acquisition phase, identifying over 500,000 unique single-nucleotide polymorphisms (SNPs), making *Arabidopsis* the organism with the highest density of high quality common SNPs per kilobase of genomic sequence. Seeds of the 20 accessions used in the study have been deposited with the *Arabidopsis* Biological Resource Center (ABRC, stocks CS22676-22695), and all data will be released upon publication, expected this year.

Mutant Biological Resources

A number of international projects have developed and catalogued plant lines containing insertion elements. The Salk Institute Genomic Analysis Laboratory (SIGnAL, Joe Ecker, <http://signal.salk.edu/cgi-bin/tdnaexpress>) has integrated data from many of these sources including SALK, SAIL, Wisconsin knockout facility, FLAG, RIKEN, JIC suppressor-mutator transposons, IMA Ds collection, GABI-KAT, and CSHL into an online searchable database, essentially providing "one-stop" access to almost all available information on insertions within a given locus. According to the SIGnAL website there are T-DNA and transposon mutants with insertions in nearly 92% (28,607) of the 31,128 nuclear-encoded *Arabidopsis* genes (re-annotated by TAIR in November, 2005.) Approximately 75% of these loci contain insertions within exons and about 83% contain insertions in either introns or exons. In addition, a project was initiated last year to experimentally identify two homozygous insertion mutants for 25,000 *Arabidopsis* genes (Ecker).

Project data can be found at the SIGnAL website, and seed stocks will be distributed through the ABRC (<http://signal.salk.edu/gabout.html>). Currently, there are 2,729 homozygous mutant insertion lines representing 2,227 genes, and about 60% of the lines contain insertions in exons and introns. The project was designed to produce mutant plant lines in a high-throughput manner, however, some homozygous lines are difficult to grow and mutants that require specialized growth conditions often die before producing seeds. This makes it more important than ever that the *Arabidopsis* community deposits homozygous lines for published mutants in publicly-accessible stock centers. Recently, a “Portal of Mutants and Mapping Resources” has been incorporated into the TAIR website which summarizes and provides links to and information about available *Arabidopsis* forward and reverse genetics resources. Of particular note are tables that summarize available mapped mutation lines and seed resources (www.arabidopsis.org/portals/mutants/). This useful site provides a chart of, and links to, the major international reverse genetic projects and the corresponding genome browsers in which the *Arabidopsis* sequence coordinates can be viewed. Furthermore, the site provides links to germplasm and seed stock catalogs, allows users to use BLAST, order stocks, and request EMS-induced mutations in a gene of interest through the TILLING project.

Measuring Gene Function Knowledge

At 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. In the 2004 and 2005 MASC annual reports this was illustrated by thermometers to provide a visual illustration of the progress in *Arabidopsis* functional genomics efforts. This year the thermometers are updated with data available at the middle of April 2006.

Functional categories have been defined for easier quantification

1. For protein-encoding genes
 - Protein activity/molecular function (catalytic or otherwise: e.g., kinase, chaperone, phosphatase, proteinase)
Gene and trait ontologies should be used for functional categorizations
 - Tertiary structure
 - Post-translational modification data
 - Expression pattern at cell and tissue level
 - Subcellular localization
 - Protein interaction data
 - Phenotype of genetic knockout/ other loss-of-function alleles

- Biological processes (e.g., photosynthesis, amino acid metabolism, cell wall biosynthesis, DNA repair)
2. For non protein-encoding genes
 - Activity of RNA/gene product
 - Expression pattern at cell and tissue level
 - Structure of RNA/gene product
 - Subcellular location for RNA/gene product
 - Phenotype of genetic knockout/other loss-of-function alleles
 - Interaction data

The ultimate goal for functional characterization of a gene is to have full information for each of these categories. At the opposite end of the knowledge spectrum is complete lack of characterizing features:

- Sequence has no homology to any sequence that we know the function of
- ORF has no expression
- No cDNA has been isolated, just predicted

In the next five years it should be possible to collect at least one category for every gene in the genome. As shown in the thermometers below, there are functional data for nearly one-third of *Arabidopsis* genes, full-length cDNA information is known for nearly 70%, and at least some expression information is available for more than 90% (excluding pseudogenes). Most remarkably, just over 95% of all genes (excluding pseudogenes) are reported to be currently under study, or proposed for future study. With continued funding and international collaboration we can look forward to numerous insights and discoveries from the community over the next five years, substantiating the value of *Arabidopsis* as the foremost reference plant.

For this year’s report, Eva Huala and colleagues from TAIR, and Hank Wu from TIGR provided the numbers of genes that fall into different evidence codes, genes for which there are full-length cDNAs, genes that have been detected in various expression profiling experiments, and genes for which there was experimental evidence in the literature for a function. Information regarding genes with existing and targeted ORF clones was provided by Joe Ecker (Salk Institute) and includes data from a number of projects including Salk, CESC, Wisconsin, ORPHEUS, Atome, and TIGR. Information for the thermometers was also obtained through the *Arabidopsis* community. A questionnaire was sent to 2010/AFGN researchers by the MASC coordinator about the categories listed under section 1: functional categories for protein-coding genes. Fifty-seven 2010/AFGN projects supplied data which were forwarded to TAIR and filtered for redundancy with other data. New non-redundant information was integrated into the Function thermometer and called community input (CIP).

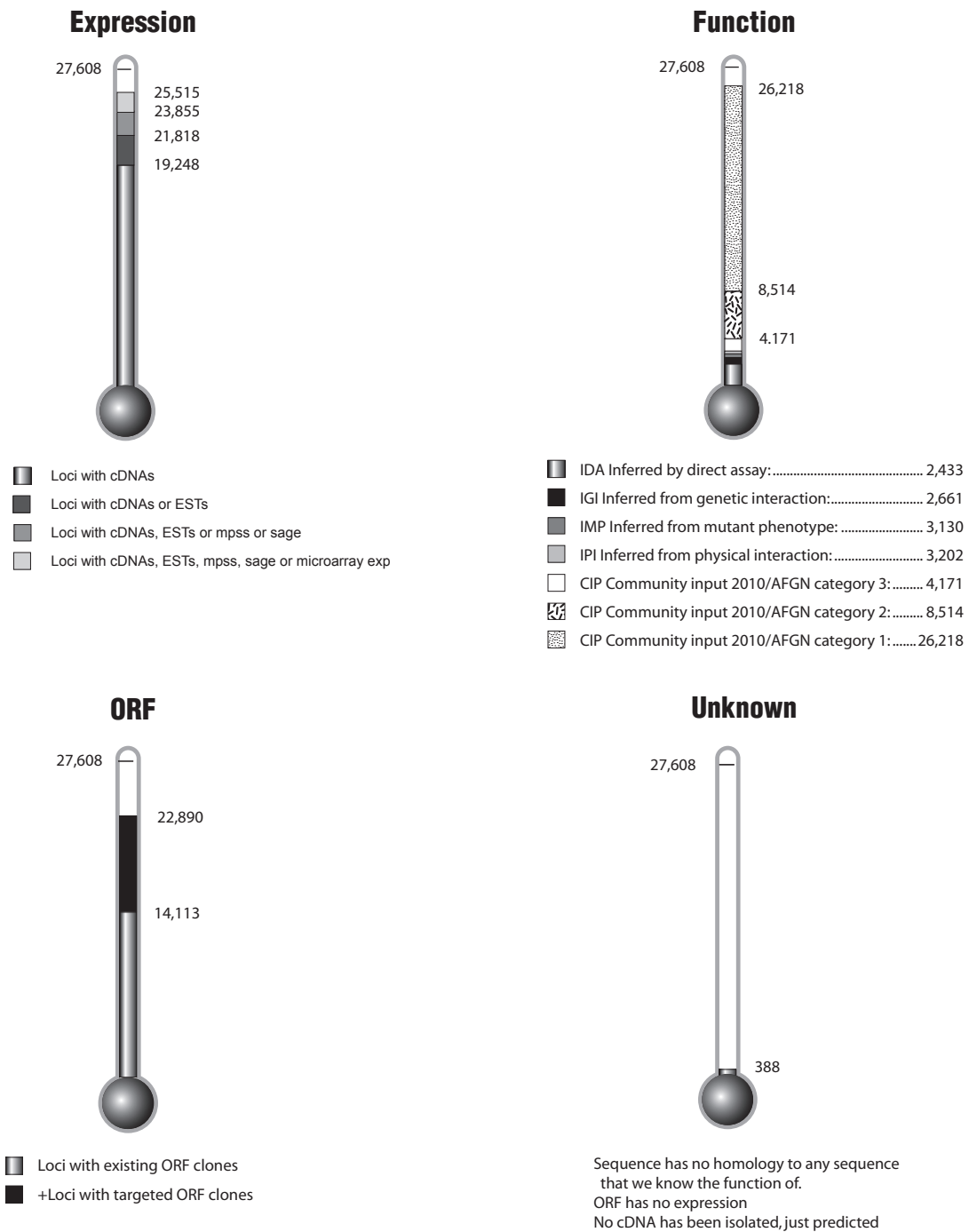


Figure 1: Measuring *Arabidopsis* Gene Function Knowledge. Each thermometer measures against the total number of genes annotated in the most recent TAIR *Arabidopsis* genome release, including organellar genes (279) and excluding pseudogenes (3,818). Exact numbers for the different categories are as follows: Gene Expression: genes with full-length cDNA (19,248), additional genes with expressed sequence tags (ESTs; 2,570), additional genes from massively parallel signature sequencing or serial analysis of gene expression (MPSS/SAGE; 2,037), additional genes from microarray data (1,660). Gene Function (includes loci annotated to Gene Ontology (GO) function, process or component with the listed evidence codes): IDA/inferred by direct assay (2,433), additional IGI/inferred by genetic interaction (228), additional IMP/inferred from mutant phenotype (469), additional IPI/inferred from physical interaction (72), CIP/community input class 3- genes for which characterization in one or more functional categories is finished, or nearly finished (969), CIP class 2- additional genes for which characterization in one or more functional categories is partly finished (4,343), CIP class 1- additional genes selected for study but have not yet been characterized (17,704). Genes with existing ORF clones (14,113), additional genes with targeted ORFs for cloning (8,777). The total number of genes where the sequence has no homology to any sequence that we know the function of, ORF has no expression, or no cDNA has been isolated, just predicted (388). Please note that gene accessions were compared for redundancies; the numbers in each thermometer refer to non-redundant gene accessions.

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Reports of the MASC Subcommittees

Bioinformatics

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

Last year's report described the first major step towards improved data integration in the *Arabidopsis* community in the form of an NSF-funded Workshop on "Data Integration" at TIGR in April, 2005. This was followed by a workshop at the International *Arabidopsis* Meeting in Madison, Wisconsin in June 2005 at which the results of the TIGR workshop were presented to the research community. The Madison workshop was well attended and there was considerable enthusiasm for the prospects of Web Services to help solve some of the issues of data integration. Based upon this community response, both the Deutsche Forschungsgemeinschaft (DFG) and the National Science Foundation (NSF) indicated their willingness to consider a pilot project to begin to develop web services. In the Fall of 2005, proposals were submitted to DFG (by Heiko Schoof) and to NSF (by Chris Town) and both were funded (see <http://bioinfo.mpiz-koeln.mpg.de/araws>). Each proposal aims to implement web services that will provide and facilitate the integration of data that is not part of existing data warehouses like TAIR, NASC or MIPS. In addition to developer's workshops to be held both in Germany and the U.S., each group will provide a "flying geek" service to provide on-site assistance to clients with limited informatics expertise.

The goals of this integrated pilot project are twofold. The first is to educate a limited number of groups in web services technology, to define the IT requirements necessary to deploy web services at any site and to develop a set of Standard Operating Procedures that can be widely used by the *Arabidopsis* community. The second is to actually have some more web services and workflows up and running in time for demonstrations at the International *Arabidopsis* meeting in Madison in the summer of 2006. At this point, participation in the pilot project has, for logistical reasons, been limited to relatively small groups of people in the EU and U.S. However, this is not meant to be an exclusive process and we hope that these initial trials will allow us to more rapidly propagate web services throughout the *Arabidopsis* community in the months and years to come.

The first workshop was held at the Max Planck Institute (Cologne, Germany) from March 14-18, 2006 and was attended by representatives of MIPS, MPIEB-Tuebingen, MPIMP-Golm, RZPD-Berlin, University of Cologne, VIB/PSB-Ghent and Centre for Biotechnology in Turku, Finland as well as the TIGR partners. In addition to instruction and demonstration of the core elements of BioMoby web services technology, topics covered included ontologies, data standards, and types of data that might be served. Although many areas requiring a significant amount of work were identified, the group was optimistic about having new services in place by the summer. The parallel U.S. workshop took place at TIGR (Maryland, U.S.) from April 24-28, 2006 and built upon the experiences of the Cologne meeting.

In August, 2005 the NSF convened a meeting of prominent researchers from both within and outside the *Arabidopsis* community to assess the progress of the 2010 project at the mid-point of its 10-year period. Embedded in the report (www.arabidopsis.org/info/2010_projects/AT2010WorkshopFinal.pdf) are a significant number of comments and recommendations relating to perceived bioinformatics needs. Some of these had already been voiced and discussed at the TIGR workshop in April 2005. Practical steps towards accomplishing some of the goals were again discussed at the Cologne workshop and will continue to be the focus of the BioMoby pilot project. A successful outcome of this project, including the enabling of web services in the broader *Arabidopsis* community, will go a long way towards satisfying the recommendations of the mid-term report.

cdNAs and Clone-based Proteomics (ORFeomics)

Prepared by Pierre Hilson (Chair, Pierre.hilson@psb.UGent.be)

Clone-based functional genomics is gradually picking up among *Arabidopsis* scientists (reviewed in Hilson, 2006). Large-scale screens based on the systematic introduction of constructs designed for ectopic expression or silencing of *Arabidopsis*

genes are underway. The first limited yeast two-hybrid protein-protein interaction matrices have been published, and several groups have reported *in vivo* analyses of subcellular location for hundreds of proteins carrying fluorescent tags. Biochemical assays and protein arrays have been described that take advantage of ORF and cDNA clone collections. But, in comparison to other eukaryotic model species, no *Arabidopsis* genome-scale dataset has yet been published in this area of research.

The steady increase in the number of cloned gene sequences is for the most part due to large-scale initiatives, but also to a few projects focusing on the systematic analysis of particular mechanisms that have generously donated their materials to stock centers (Table 1). Importantly, the publicly available resources enable systematic approaches but are also used by scientists interested in the functional characterization of only a few genes. Material dissemination via stock centers is beneficial because it prevents duplication of efforts and promotes the use of well-documented reference materials across multiple experiments conducted by independent laboratories. Any functional genomics projects generating clone resources should be encouraged by funding bodies to donate their materials for public release or to include long term dissemination plans in their activity. Forward looking, our community must understand the need to record the results obtained with these shared clone collections using standard procedures and formats that facilitate the integration of diverse data types. When possible, these standards should be borrowed from well-established initiatives, for example, the European Bioinformatics Institute (EBI)-funded IntAct (open-source database system and analysis tools for protein interaction data.)

Arabidopsis cloning efforts have been increasingly coordinated with the publication of target sequence lists at early stages of planning. Such advance notice should be implemented whenever possible. But, there is still substantial overlap between certain collections, generally resulting from different format choice or validation policies.

Today, various entities distribute *Arabidopsis* clones (ABRC, NASC, RZPD, BRC, CNRGV and individual laboratories) and there is unfortunately no straightforward procedure to interrogate at once all relevant databases for constructs of interest. A system should be implemented to display the location(s) of available clones based on queries by sequence homology searches or by AGI code names. Several groups are currently investigating how to create a unique information system for *Arabidopsis* clones that will unite dispersed databases using webservices. Ideally, such a system should be extended beyond cDNA, ORF and silencing clones, to include repertoires with promoter and other non-protein coding sequence collections, as well as recipient plasmids (*e.g.* Gateway destination vectors) designed for particular functional assays. Interestingly, the first large sets of ORF entry clones from which the native stop codon was removed – and therefore compatible with carboxyl-

terminal fusions – as well as expression clones have been made available recently (See Table 1 on the next page.)

The *Arabidopsis* community has done an excellent job at promoting stock centers, supported by long-term funding, that curate and distribute clone collections for very low fees and with no material transfer agreements. These centers are key to the efficient use of resources and should be maintained for the benefit of all plant researchers.

Reference

Hilson, P. (2006) Cloned sequence repertoires for small- and large-scale biology. *Trends Plant Sci.* 11, 133-141.

Table 1. Publicly available *Arabidopsis* clone collections

Creator	Format	Focus	Validation	Count	URL	Stock center
ORF clones						
SSP consortium & Salk Institute	Univector pUNI51 and Gateway entry	Random	Full sequence	13,854	signal.salk.edu	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,283		ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	768	www.tigr.org/tdb/hypos/TargetGeneList.shtml	ABRC
J. Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
CESG	Gateway entry	Potential new fold	Full single pass seq.	~ 1,500	www.uwstructuralgenomics.org/cloning.htm	CESG
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	~ 1,000	www.gabi.rzpd.de/materials/	RZPD
Dinesh-Kumar et al.	Expression (from Peking-Yale JC)	TAP-tagged transcription factor		1,100		ABRC
Doonan et al.	Expression (from SSP)	GFP fusion for subcellular location		155		ABRC
ATOME 1 ATOME 2	Gateway entry Gateway entry, no stop	Random Random (from SSP)	5' and 3' end seq. 5' and 3' end seq.	~ 2,000 ~ 3,500	http://www.evry.inra.fr/public/projects/orfeome/orfeome.html	CNRGV
cDNA clones						
RIKEN	λ ZAP or λ PS	Random	Full sequence	16,913	http://www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml	BRC
RIKEN	λ ZAP or λ PS	Random	Single pass	246,640	same	BRC
MPI-MG	Gateway expression	Random	5' end seq.	4,500	www.gabi.rzpd.de/materials/	RZPD
RNAi clones						
AGRIKOLA	Gateway entry	Random	PCR sized insert	21,903	www.agrikola.org	NASC
AGRIKOLA	hp RNA expression	Random	PCR sized insert	19,640	www.agrikola.org	NASC
CFGC	ds RNA expression	Chromatin remodel.	Single pass seq.	144	www.chromdb.org	ABRC

Metabolomics

Prepared by Ian Graham (Chair, iag1@york.ac.uk)

A continuous goal and monitoring operation will be to ensure full integration of *Arabidopsis*-based Metabolomics research with the Metabolomics Standards Initiative that is currently being coordinated by the Metabolomics Society (www.metabolomicssociety.org). In this initiative five working groups have already been formed and documents are being finalized covering (a) Biological Sample Context; (b) Chemical Analysis; (c) Data Analysis; (d) Ontology and (e) Data Exchange. Several members of the MASC Metabolomics subcommittee are involved in drawing up the plant biology specific documentation for the Metabolomics society. In addition this committee will aim to establish a mechanism that allows the dissemination of metabolomics datasets to the wider *Arabidopsis* community and encourage and facilitate initiatives for the integration of metabolomic datasets with other 'omic datasets. This will involve depositing Metabolomic data in a usable format for data integration.

Natural Variation and Comparative Genomics

Prepared by Tom Mitchell-Olds (Chair, tmo1@duke.edu)

The newly-restructured subcommittee on Natural Variation and Comparative Genomics includes two working groups. The **Natural Variation Working Group** has been established to identify technological and resource issues which are needed for progress in analysis of *Arabidopsis* natural variation. In addition, conceptual opportunities for improved understanding of fundamental processes in plant biology will be considered.

The **Comparative Genomics Working Group** has been established to consider priorities for future research in *Arabidopsis* Comparative Genomics in order to identify conceptual and technical goals as well as recommend species which will optimize progress towards these research goals.

Finally, this subcommittee also inherits responsibilities of the former subcommittee on Genetic Resources which dealt with forward and reverse genetics, natural variation, and comparative genomics. Although much progress has been made by the International *Arabidopsis* 2010 Initiative on many of these issues, further consultation regarding possible future needs is ongoing. Members of each working group are in contact by e-mail and aim to produce recommendations and summary documents before the end of 2006.

Phenomics

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

The Phenome subcommittee is meant to track the progress of efforts including development and availability of biological materials for phenotyping, efforts to develop and use standardized phenotype descriptions including ontologies, and the availability of materials and data in stock centers and databases.

Biological resources for phenotyping

Insertion lines: A total of 28,607 genes (92%) have been tagged with insertions in the combined set of all insertion collections, and 23,509 (76%) of these genes contain insertions into the coding region, according to the SIGnAL website (<http://signal.salk.edu/cgi-bin/tdnaexpress>). A list of projects with brief descriptions, location of data and links can be found at TAIR: <http://arabidopsis.org/portals/mutants/worldwide.jsp>.

Homozygous mutant lines: The Salk "phenome-ready" project to produce homozygous mutant T-DNA lines is in the process of generating homozygous mutants for 24,357 *Arabidopsis* protein-coding genes. Currently (as of March 31 2006), seeds for 1989 lines (affecting 1740 genes) are available from the *Arabidopsis* Biological Resource Center (ABRC) and will also be available from NASC. The remainder of the Salk homozygous lines should be completed in 2007, and seeds will be available in quantities sufficient to allow partial or full sets of lines, or pools of lines, to be utilized by researchers for research projects and/or screening. A second large project at RIKEN is now preparing homozygous mutant transposon-tagged lines for approximately 5,000 *Arabidopsis* genes. RIKEN BRC (<http://www.brc.riken.jp/lab/epd/Eng/>) will start the distribution of homozygous seeds by the end of this year. In addition to these two large collections, 642 Salk and SAIL homozygous insertion lines from the community have been donated to ABRC as of April 2006 and are available for ordering.

RNAi lines: The AGRİKOLA project (<http://www.agrikola.org/>) has cloned 21,862 gene-specific tags into binary hairpin RNA vectors and made them available to the public through NASC. These lines target a total of 19,202 genes. The final targets to be achieved in mid-2006 will be over 25,000 tags for over 20,000 genes. In addition, 786 sets of transformed lines and 6755 individual transformed lines are currently available for ordering from NASC, out of a final target of around 3,000 sets of transformed lines. The AGRİKOLA lines are also being made available by ABRC (200 lines currently in-house).

Ontology development

Several efforts are underway to provide the controlled vocabulary needed to describe phenotypes in a standardized way.

POC: The goal of the POC (Plant Ontology Consortium, <http://www.plantontology.org/>) is to provide a standardized vocabulary to describe anatomy, morphology, and growth and developmental stages in *Arabidopsis*, maize, rice, Fabaceae and Solanaceae, with future plans to extend the vocabularies to other

plant families. This standardized vocabulary will serve as a basis for cross-species queries for phenotype and gene expression information, an essential capability that will permit researchers working with crop species to leverage *Arabidopsis* research results into agricultural advances. POC has released ontologies covering plant structure (release date July 2004, currently 753 terms) and growth and developmental stages (release date July 2005, currently 274 terms). These ontologies are now in use at TAIR and NASC as well as several other databases including Gramene, MaizeGDB, SGN, BRENDA, Genevestigator and ArrayExpress. Requests for additional terms can be made by using the Feedback button on the POC website.

PATO: The Phenotype, Atttribute and Trait Ontology (PATO) is currently under development as part of the NIH-funded cBio project (<http://www.bioontology.org/>). The purpose of this ontology is to facilitate description of phenotypes using controlled vocabulary terms arranged in a syntax line referred to as the Entity, Attribute and Value (EAV) model. Entity terms describe physical entities such as body part, cell type, subcellular structure, developmental stage or biological process affected, and can be drawn from other ontologies such as PO (Plant Ontology) and GO (Gene Ontology). Attribute terms describe the trait that is altered, and Value terms describe the nature of the alteration in the mutant or natural variant (For example Entity:leaf, Attribute:color, Value:yellow could be used to describe a mutant with yellow leaves). The core participants in development of PATO include Monte Westerberfield at ZFIN (the zebrafish database), Michael Ashburner at Flybase (the *Drosophila* database) and Ida Sim of UCSF, leader of a group that will use the ontology to describe the results of human clinical trials, with Georgios Gkoutos in the UK serving as the main PATO curator. The POC organizer (Katica Ilic) has been in contact with the project organizers and there is a shared opinion that the plant community should participate more actively in PATO development to ensure that this ontology becomes more suitable for description of plant mutants and natural variants. To facilitate the development of PATO for use in plant biology, curators from plant databases are encouraged to request new PATO terms through the SourceForge website (http://sourceforge.net/tracker/?group_id=76834&atid=595654). TAIR is planning to participate in a PATO content development workshop in mid-May 2006.

Phenotyping efforts

No public domain effort to date has released data systematically describing the overall phenotype of large numbers of *Arabidopsis* gene knockouts. Rather, the emphasis has been on investigating specific traits and on describing natural variants and QTLs. Large scale phenotyping of knockouts has been carried out in the past by the private sector (for example at Paradigm genetics – see Boyes et al. 2001, *Plant Cell* 13:1499–1510). However, the phenotype data from these projects have

not been made publicly available. A group at INRA (Granier et al., *New Phytol.* 2006;169:623–35) has described a robotic setup for large scale phenotyping of general morphological traits but no large data releases to the community have resulted to date.

Examples of recent efforts aimed at phenotyping for specific traits include ion profiling of large numbers of mutants (Salt, *Plant Physiol.* 2004;136:2451–6) and searching for cell wall mutants using MALDI-TOF MS to detect structural changes in cell wall polymers (Lerouxel et al., *Plant Physiol.* 2002;130:1754–63).

Efforts to identify large numbers of natural variants include a project in Detlef Weigel's group to phenotype about 15 F2 populations from crosses among the "Nordborg 96" ecotype sets, examining 500 plants of each population for a variety of morphological traits including flowering time. Individual plants will be phenotyped and also genotyped at about 80 loci each, to produce a large number of QTL maps. It is planned to store the phenotypes in a genotype-phenotype database, as a prototype for the future integration of phenotyping data sets from many different sources.

Phenotyping at the level of individual genes or small sets is ongoing, and this information is primarily captured in the literature. Phenotype descriptions have been published for approximately 3000 loci, estimated from the number of loci at TAIR that are associated to published papers containing the word "mutant" in the abstract. TAIR is working to extract this information from the literature.

Storage and display of phenotype data

NASC currently displays PO and PATO controlled vocabulary phenotype annotations for 1,897 mutant lines and natural variants, and will continue to add additional annotations in the future.

POC currently displays NASC's PO annotations for 1,897 mutant and natural variant lines. The consortium is working on displaying plant phenotype descriptions on the POC website as a combination of controlled vocabulary terms and free text (using PO terms to describing the affected part (entity), and using free text for attribute and value).

TAIR contains phenotype descriptions for mutants in approximately 1100 AGI loci, collected from the literature and from ABRC stock data. TAIR is currently working to separate free text phenotype descriptions from other descriptive information relating to germplasm and add search and display capabilities specific to phenotype. In the next 12 months TAIR expects to begin adding PO and PATO controlled vocabulary phenotype annotations through literature curation and community submissions.

(Additional report contributors: Ian Small, Randy Scholl, Detlef Weigel, Minami Matsui and Katica Ilic)

Proteomics

Prepared by Wolfram Weckwerth (Chair, weckwerth@mpimp-golm.mpg.de)

Proteomics using *Arabidopsis thaliana* as a model system has made great progress in recent years. The throughput and accuracy of protein identification techniques such as shotgun proteomics based on liquid chromatography coupled to mass spectrometry (LC/MS) or two-dimensional gel-electrophoresis (2DE) relies strongly on the availability of whole genome sequences. The availability of both a complete genome sequence and high quality genome annotation makes *Arabidopsis thaliana* an ideal system to develop new technologies and identify candidate genes. Furthermore, *Arabidopsis thaliana* proteomics research will give direction to future plant proteomics developments and can serve as a unique database resource, especially when coordinated with the metabolomics and bioinformatics initiatives. However, in light of 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. Therefore, it is a very opportune moment to establish a working group devoted to *Arabidopsis* proteomics, and combine the efforts of different research groups to develop programs which will consolidate databases, technique standards and experimentally validated candidate genes and functions.

Subcommittee goals and priorities

- Organization of a common webpage including standards for different proteomic techniques, databases, procedures, meetings, proteome labs, etc.
- Meet at *Arabidopsis* International Conference each year.
- 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 experiments, data analysis and call of identifications. These activities will be coordinated with the MASC metabolomics subcommittee chaired by Ian Graham, the subcommittee for bioinformatics and the Proteomics Standard Initiative (PSI).
- Hold a workshop each year at the International *Arabidopsis* Conference on the methods/practice of proteomics to inform the community, make new contacts, and to develop initiatives for proposals.

- Develop a master list of the *Arabidopsis* gene loci that have been identified at the proteomic level by mass spectrometry.
- Work towards a central international database of MS/MS spectra derived from *Arabidopsis* samples.
- Collaborate with TAIR and other interested parties on *Arabidopsis* proteomic data storage.

Analysis and Recommendations

The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project has now completed its fifth year. In 2005/2006 there was a continued increase in publicly accessible data and resources including SNPs, MPSS, microarray, full length-cDNA information as well as full-length cDNA clones, ORF clones, RNAi clones and insertion mutants. Intensive international efforts have made a large number of biological resources available to the *Arabidopsis* community and the ease of access to these materials is particularly noteworthy. While there is still much to discover in the *Arabidopsis* genome and transcriptome particularly using systems approaches, new frontiers include proteomics and metabolomics. In addition, information gathering *between* genomes, *i.e.* comparative genomics and natural variation, is increasingly enabled by genome resequencing and reannotation, and the development of more sophisticated genome surveying tools and bioinformatics and data integration approaches. Subcommittees focusing on Systems Biology, Metabolomics, Proteomics, and Natural Variation and Comparative Genomics recently formed to evaluate current knowledge, identify needs and bottlenecks, and establish appropriate courses of action. International cooperation by motivated researchers, a high level of coordination, and sufficient funding remain critical to the success of this ambitious project.

Current status of the program

Strong international collaboration within the *Arabidopsis* community has contributed to the attainment of many of the short-term goals of the Functional Genomics Project, as well as the initiation of mid- and long-range goals. In the first five years the major accomplishments included:

1. The release of improved whole genome annotations, the most recent versions supported by full-length cDNA sequences and expert input. In 2004, TAIR took over the task of maintaining and improving genome annotation; their first release (version 6.0) took place in November, 2005. This release contains 26,751 protein coding genes, 3818 pseudogenes, and 838 non-coding RNAs (31,407 in all.) These data are integrated into the TAIR database and are available from NCBI.
2. Generation of comprehensive sets of sequence-indexed mutants listed in an integrated database and made available as seed stocks. Currently the mutant collection includes insertions in nearly 92% of the 31,128 nuclear-encoded *Arabidopsis* genes with approximately 75% of all loci containing insertions within exons. Recently, a "Portal of Mutants and Mapping Resources" has been incorporated into the TAIR website which summarizes and provides links to and information about available *Arabidopsis* forward and reverse genetics resources. Of particular note are tables that summarize available mapped mutation lines and seed resources (www.arabidopsis.org/portals/mutants/). Joe Ecker's lab at the Salk Institute began a project last year to isolate two homozygous insertion mutants for each of 25,000 *Arabidopsis* genes (<http://signal.salk.edu/gabout.html>). Currently there are 2,729 homozygous mutant insertion lines representing 2,227 genes, and about 60% of the lines contain insertions in exons and introns. As of March, 2006, 1,000 confirmed homozygous mutants from Joe Ecker and 600 confirmed lines from additional laboratories have been deposited with the ABRC. It is expected that 50,000 confirmed lines, searchable in the TAIR germplasm resource, will be deposited within the next two years. In addition, the EU-funded AGRICOLA project has produced nearly 22,000 RNAi Gateway clones, targeting 19,202 genes, for the creation of 'knock-down' lines. The final targets (expected to be achieved in mid-2006) will be over 25,000 clones for more than 20,000 genes. The development of artificial microRNAs (miRNAs) as a new 'knock-out' tool shows particular promise for closely related genes (Weigel lab, Schwab *et al*, The Plant Cell, 2006).
3. Steady progress in characterizing *Arabidopsis* gene function. Currently there are functional data for nearly one-third of *Arabidopsis* genes. Most remarkably, just over 95% of all genes are reported to be currently under study, or proposed for future study (excluding pseudogenes.) For

a more detailed summary of gene function knowledge, see 'Measuring Gene Function Knowledge' in the Progress and Activities of the MASC section of this report.

4. Development of new tools for comparative genomics. Data acquisition in a whole genome study of natural variation in twenty *Arabidopsis* accessions was recently completed. Over 500,000 unique single-nucleotide polymorphisms (SNPs) were identified making *Arabidopsis* the organism with the highest density of high quality common SNPs per kilobase of genomic sequence (Detlef Weigel). The decision last year by the Department of Energy (DOE) Joint Genome Initiative (JGI) to sequence the closely related species *Arabidopsis lyrata* and the more distantly related *Capsella rubella* will contribute to comparative genomics efforts; sequencing of *A. lyrata* is underway while *C. rubella* sequencing is expected to begin shortly. Another JGI project involving sequencing of the lycophyte *Selaginella moellendorffii*, which represents an intermediate between nonvascular and vascular plants, will provide a reference genome for bridging large-scale genome comparisons and contribute to defining evolutionary relationships. Portions of the *S. moellendorffii* genome sequence have been submitted to the GenBank Trace Archives.
5. The production of genome-wide sets of gene-specific probes for expression analysis and the establishment of reference transcriptomes. The amount of freely available genome-wide transcriptome data continues to increase through a number of initiatives: AtGenExpress, an international project initiated in 2004, generated a gene expression profiling database; NASCArrays, the array facility and expression profile repository of the GARNet program, allows free access to microarray data; AREXdb is a tissue-specific expression database focusing on the root (Philip Benfey lab). All three projects use the Affymetrix ATH1 full genome chip. In addition, there are a number of web-based tools and programs designed to analyze microarray data; TAIR has summarized and provided links to many of these (<http://arabidopsis.org/info/expression>). An Affymetrix tiling chip covering the entire *Arabidopsis* genome sequence became available last year via an early access program; the fully supported array was officially released in April, 2006. The *Arabidopsis* Tiling 1.0R array is a single chip comprised of over 3.2 million probe pairs tiled through the complete non-repetitive *Arabidopsis* genome.
6. Isolation of full-length cDNAs for nearly 75% of the nuclear protein coding genes. Collectively, there is full-length (fl) cDNA sequence information for about 19,498 of the 26,541 nuclear protein-encoding *Arabidopsis* genes, and fl-cDNA clones of 14,216 genes are being distributed, with an additional 9,058 ORFs targeted for cloning. Last summer, the Ecker lab, in collaboration with Invitrogen, began creating a parallel set of Gateway vector ORF clones to complement the existing pUNI vector system. As of February, 2006, 3,329 SSP/SALK pUNI ORF clones have been transferred to Gateway vectors, and will be deposited into the ABRC upon completion of sequence validation (estimated to occur in summer, 2006). This set, when combined with previously deposited ORFs, will bring the total number of fully sequenced and error free SSP/SALK/Invitrogen clones to 5,126.
7. Development and investment in tools for standardized vocabulary. Several efforts are underway to provide controlled vocabularies for genes, gene products, and phenotypes. The goal of the National Human Genome Research Institute (NHGRI)-funded Gene Ontology Consortium is to produce dynamic controlled vocabularies that can be used to describe the roles of genes and gene products in all organisms. There are currently more than 100,000 GO annotations searchable in TAIR (provided by TAIR and TIGR.) The goal of the NSF-funded Plant Ontology Consortium (POC) is to provide standardized vocabulary to describe anatomy, morphology, and growth and developmental stages of *Arabidopsis* and other plants. This vocabulary will provide a resource for researchers working with crop species to leverage *Arabidopsis* research results into agricultural advances. Phenotype, Attribute and Trait Ontology (PATO), funded by the National Institutes of Health (NIH), is currently under development. The purpose of this ontology is to facilitate description of phenotypes using controlled vocabulary terms arranged in a standard syntax, and while researchers studying zebrafish, drosophila and humans are the core organizers, the plant community is becoming involved via the POC.
8. Initiation of working groups to establish multinational consortia for target *Arabidopsis* research areas including natural variation and comparative genomics, proteomics, phenomics, systems biology, database interoperability, and metabolomics.
9. Appointment of a full-time MASC coordinator to foster information exchange, international collaboration and coordination and to monitor progress of the program.

Areas that lag behind initial plans or are currently underrepresented

1. As the *Arabidopsis* community generates an increasing amount of data and develops more resources and tools, the improvement of database integration is critical. Last year Chris Town (TIGR) and Heiko Schoof (DFG) submitted proposals for "BioMoby" pilot projects

to begin to develop web services for data integration. Workshops funded by the pilot projects were held in March and April, 2006, and a Bioinformatics workshop to demonstrate the project to the broader community will take place at the 2006 annual *Arabidopsis* meeting (Madison, WI). It is hoped that success in these pilot programs will translate into more broad-reaching data integration efforts throughout the *Arabidopsis* community.

2. Proteomics, metabolomics and natural variation and comparative genomics are all areas that need more emphasis. Working groups for each of these areas have been established in the last few months and in 2005, the NSF funded two AT2010 proposals involving metabolomics, and a third to design an *Arabidopsis* proteome chip. Ara-Cyc, a database containing biochemical pathways of *Arabidopsis*, was developed at TAIR to represent *Arabidopsis* metabolism as completely as possible with a user-friendly Web-based interface. Proteomics resources, including production of antibodies against, or epitope tags on all deduced proteins are needed, as well as proteomic profiling.
3. Tools for *Arabidopsis* functional research such as methods for inactivating redundant genes, homologous recombination, methods for analyzing posttranslational modifications, protein profiling, analyzing protein-small molecule interactions, subcellular localization, transcription factor binding and epigenetic phenomena.
4. Development of networks and systems biology is needed. The long-range *Arabidopsis* research plan, developed in 2000, had the overall goal of determining the function of every *Arabidopsis* gene. It is becoming increasingly clear that many genes have more than one function and many genes work together in biological processes making an understanding of genes in the context of networks critical.
5. Temporal and spatial gene expression data are still needed under varied conditions, in specific tissues, and in different genotypes. Expression profiles of single cell or populations of sorted cells are needed.
6. Analysis of non-protein coding genes is still lagging. There is increasing understanding of the importance of non-protein coding RNAs such as miRNAs, siRNAs, stRNAs, and snoRNAs, however, the genes encoding these RNAs have been underrepresented in expression analysis, functional research, and annotation.

Recommendations for the coming year

There are a number of goals remaining for the Multinational Coordinated Project including completion of resource collections (homozygous insertion lines, RNAi lines, conditional mutants, full-length cDNA and ORF clones for expressed genes, recombination inbred lines or RILs,) and devel-

opment of tools for functional genomics (antibody production against *Arabidopsis* proteins, assays to rapidly detect, quantify and determine the activities of large numbers of metabolites, high throughput sequencing to enable evaluation of natural variation and discovery of low-abundance transcripts, and improved *in vitro* and *in vivo* approaches for macromolecular interactions.) Intensive efforts should continue to determine a basic set of characteristics about all *Arabidopsis* genes including (1) temporal and spatial gene expression data under different environmental conditions and in specified accessions, and (2) for protein-coding genes, identification of interacting protein partners via comprehensive and cost effective high-throughput protein-protein interaction studies. Importantly, we must capitalize on previous efforts and encourage the international *Arabidopsis* community to submit datasets and resources to publicly-accessible repositories and stock centers.

It is critical that we improve database integration and develop new modeling and computational tools. Synchronization of data syntax and semantics within different *Arabidopsis* derived data types and also with formats from other model organisms is urgently needed. An acutely needed resource is a straightforward way to query all relevant databases at once for clones, constructs, mutants, and other resources. It is important to improve genome annotation and tool development for visualization, annotation and curation. The frequency of whole genome annotation updates should increase and should consist of both semi-automated and manual curation and use controlled syntax consistent with efforts of other model organisms. Priorities include development of standardized protocols and tools to allow for submission of common data types for genome annotation and development or adoption of visualization tools for viewing and linking the sequence annotations, in addition to new means of data integration.

We must build on the knowledge gained from completing the *Arabidopsis* genome and apply our resources to other '-omics' areas; we must establish a reference proteome and metabolome, and support metabolomics and ionomics through studies of the production, regulation and function(s) of small molecules such as metabolites as well as the transport and activities of ions. We must also further the mapping of the 'interactome' network by systematically obtaining information on where (in what cells or tissues) and when (at what stage(s) of development and/or under what conditions) large numbers of genes are expressed, and where and when their products are localized at the subcellular level.

In order to leverage the vast amount of genetic information available for *Arabidopsis thaliana* and apply these data to crops and other useful plants we need to improve natural variation and comparative genomics studies within and between informative ecotypes and develop tools for whole-genome population biology. Informative sets of RILs and ecotypes need to be developed and made easily accessible to the community for functional studies, and genome sequencing within and between

appropriately chosen ecotypes or natural populations is needed for population studies and SNP development.

As a community, we need to effectively communicate our successes as well as our needs, and convey the value of *Arabidopsis* research. We must engage the broader community by providing resources and tools and develop cyberinfrastructure for the dispersed network of resources. The *Arabidopsis* community is encouraged to reach out to all educational levels and the general public, and in particular, to policy decision-making arenas and underrepresented groups. Finally, we must enhance international collaboration. A major reason for success in the establishment of *Arabidopsis* as the reference plant is the strong international collaboration that has developed over the last decade. International collaboration is particularly important in genomics research as this scientific revolution requires costly efforts to generate resources and tools for genome-wide analyses. Mechanisms should be sought to avoid unnecessary duplication of work and collaboration should be further stimulated so that researchers share resources. These should be maintained in public stock centers making *Arabidopsis* research readily accessible to the worldwide community. Equally important is the need for international collaboration on the development of a common database or a confederated database system, which stores and makes accessible the vast array of genomic and phenotypic data on *Arabidopsis*.

Based on the analysis above as well as through feedback by the community and the MASC subcommittees, and from recommendations described in the AT2010 midterm evaluation, the MASC makes the following recommendations for the next year:

- Ensure the successful establishment of recently formed MASC subcommittees including Metabolomics, Natural Variation and Comparative Genomics, Phenomics, and Proteomics.
- Update and improve the Project's webpages at TAIR.
- Work toward completion of genetic resources projects including the collection of homozygous insertion mutants (SALK) and RNAi clones (AGRIKOLA).
- Develop resources for studying protein interactions and localization, including complete cloning of full-length cDNAs into expression vectors.
- Expand data integration and interoperability efforts for optimal use of data resources.
- Facilitate and encourage submission of data and stocks into public repositories.
- Implement a Systems Biology working group.

The International *Arabidopsis* Functional Genomics Community Argentina

http://www.Arabidopsis.org/info/2010_projects/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@dqf.fcq.unc.edu.ar
CIQUIBIC-CONICET, Facultad Ciencias Químicas, Universidad Nacional de Córdoba. 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@fbc.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 Biotecnológicas, Universidad Nacional de San Martín. Province of Buenos Aires
- Regulatory genes involved in the control of transcription of genes of the photosynthetic antenna. 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 Bioquímicas y Farmacéuticas, 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 Biotecnológicas, Universidad Nacional de San Martín, 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 to a consortium integrated mainly by research groups listed above. The equipment has been installed at IFEVA.

Major Funding Sources for *Arabidopsis*

Functional Genomics

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

Australia & New Zealand

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

Contact: Barry Pogson

The Australian National University, Canberra

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 involved *Arabidopsis* as a model system. Major areas of *Arabidopsis* research and functional genomics are Canberra, Melbourne and Perth. Major sites of plant science with foci on crops such as grains, grapes and legumes include Queensland, Tasmania, South Australia and New South Wales.

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.
- CSIRO Plant Industry (www.pi.csiro.au). Liz Dennis leads a major Program on Genomics and Plant Development. This program investigates several aspects of plant function and, importantly, is developing major facilities for *Arabidopsis* functional genomics work. Gene Discovery by Functional Genomics (Peter Waterhouse) has a 10,000-plus non-redundant cDNA microarray facility (Iain Wilson) and activation tagging (Chris Helliwell). These facilities are being used intensively in CSIRO's subprograms in reproductive development (Abed Chaudhury), floral initiation (Jean Finnegan), Genetic Engineering for Plant Improvement (Jeff Ellis), and Hormonal Control of Gene Expression (Frank Gubler).

Genomics Companies

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

Examples of Australian Universities with substantial research on *Arabidopsis*

- 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/)

Examples of Research Projects Using Functional Genomics Approaches

- Aluminum and manganese stress tolerance- Peter Ryan
- Arabinogalactan proteins - Carolyn Schultz and Tony Bacic
- Boron tolerance- Robert Reid
- CesA- related genes and cellulose synthesis- Richard Williamson
- Chloroplast development and function, oxidative stress and photoprotection - Barry Pogson
- Dehydrin genes - Roger W. Parish
- Fimbrin gene family - David McCurdy
- Flowering time control - Alan Neale and John Hamill
- Heterotrimeric G-proteins - Jimmy Botello
- Mechanical impedance in roots - Josette Masle
- Microtubule associated proteins - Geoffrey Wasteney
- Mitochondria - Jim Whelan David Day, Harvey Millar
- Myb gene function - Roger W. Parish
- Nodulation related control mechanisms - Peter Gresshoff
- Phosphorus-use efficiency - Peter Ryan
- Photosynthetic capacity regulation - Murray Badger
- Plant Natriuretic Peptide immunoanalogues (PNPs) - Helen R. Irving and David Cahill
- Plasmodesmata functional proteomics - Robyn Overall
- Respiration: non-phosphorylating pathways of associated with the mitochondrial electron transport chain - Kathleen Soole
- Sodium efflux systems in the plasma membrane - Ian A. Newman
- Defense gene expression - Karam Singh

Major Funding Sources For *Arabidopsis* Functional Genomics

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.
- The Genome-Phenome Link is one of 4 Priority Area Research Programs for ARC funding in 2003. Under the direction of the Minister responsible for the ARC, these program areas are to receive no less than 33% of the total funds allocated under the National Competitive Grants Scheme in the 2003 funding round.

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.

New Zealand

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).

Major Funding Sources for *Arabidopsis* Functional Genomics

- 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/)

Major Locations involved in Functional Genomics of *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/)

Austria

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

Contact: Heribert Hirt

University of Vienna

Email: Heribert.hirt@univie.ac.at

Current Research Projects

Three consortia are presently performing active genome research on *Arabidopsis* in Austria:

1. **APAR** (Austrian Platform of *Arabidopsis* Research) is funded by the *Austrian Science Fund FWF*:

The APAR consortium is a research platform that coordinates and promotes science on *Arabidopsis* in Austria. It currently consists of the following members:

- Marie-Theres Hauser

Functional characterization of gene families involved in root morphogenesis

Institute for Applied Genetics and Cell Biology (IAGZ), University of Natural Resources and Applied Life Science (BOKU), Vienna (www.boku.ac.at/zag/AG_hauser.htm)

- Heribert Hirt

Stress signal transduction

Department of Plant Molecular Biology, Max F. Perutz Laboratories (MFPL), University of Vienna (www.heribert-hirt.at)

- Claudia Jonak

Analysis of glycogen synthase kinase/shaggy-like kinases

Gregor-Mendel Institute of Molecular Plant Biology (GMI) Vienna (www.gmi.oeaw.ac.at/cjonak.htm)

- Irute Meskiene

Specificity and functional analysis of a PP2C protein phosphatase gene subfamily

Department of Plant Molecular Biology, MFPL Vienna (www.mfpl.ac.at/index.php?cid=53)

- Karel Riha

Functional study of the Ku complex at Arabidopsis telomeres

GMI Vienna (www.gmi.oeaw.ac.at/rkriha.htm)

- Markus Teige

Calcium-dependent protein kinases in Arabidopsis signal transduction

Department of Biochemistry, MFPL Vienna (www.mfpl.ac.at/index.php?cid=55)

2. **Lasting effects of abiotic stress in plant genomes and their potential for breeding strategies**, funded through the *Austrian Genome Research Program GEN-AU*: Plants are especially required to withstand external stress conditions due to their sessile life-style. The project addresses mechanisms by which plants overcome unfavourable environmental conditions on long terms. In a systematic approach, combining the expertise of seven Austrian research groups, the genetic and epigenetic plasticity of plants is going to be explored under well-defined stress conditions. Using *Arabidopsis* as a model organism, the effect of stress on genomic variability and its potential use for plant breeding is elucidated.

Consortium members

- Werner Aufsatz, GMI Vienna
Role of histone deacetylation in gene silencing and gene regulation (www.gmi.oeaw.ac.at/waufsatz.htm)
- Marie-Theres Hauser, IAGZ Vienna
- Heribert Hirt, MFPL Vienna
- Claudia Jonak, GMI Vienna
- Christian Luschnig, IAGZ Vienna, Coordinator
- Ortrun Mittelsten Scheid, GMI Vienna
Epigenetic changes in polyploid plants (www.gmi.oeaw.ac.at/oms.htm)
- Karel Riha, GMI Vienna

3. **Integrative analysis of stress response mechanisms to improve plant performance, funded by the Vienna Science and Technology Fund WWTF**:

The network combines expertise in the fields of protein kinases, viral-interacting host factors and micro RNAs to elucidate their roles in response to abiotic and biotic stresses. The research specifically focuses on integrative responses when plants are challenged with a combination of 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, Department of Medical Biochemistry, MFPL, Medical University of Vienna
Modes of interaction of SR splicing factors in Arabidopsis (www.mfpl.ac.at/index.php?cid=68)
- Heribert Hirt, MFPL, University of Vienna

- Claudia Jonak, GMI Vienna
- Elisabeth Waigmann, Department of Medical Biochemistry, MFPL, Medical University of Vienna

Plant viruses as a model system for intra- and intercellular spread (www.mfpl.ac.at/index.php?cid=57)

Other activities on an individual basis

- Thomas Greb, GMI Vienna

Development of vascular tissue
(www.gmi.oeaw.ac.at/tgreb.htm)

- Fritz Kragler, Department of Biochemistry, MFPL Vienna

Nature and function of systemic non-coding RNAs
(www.mfpl.ac.at/index.php?cid=52)

- Peter Schlögelhofer, Department of Chromosome Biology, MFPL Vienna

Analysis of meiotic recombination
(www.mfpl.ac.at/index.php?cid=54)

- Gerhard Adam, IAGZ, BOKU Vienna

Detoxification of Fusarium mycotoxins
(www.dapp.boku.ac.at/5499.html?&&L=1)

- Marjorie and Antonius Matzke, GMI Vienna

Epigenetics
(www.gmi.oeaw.ac.at/amatzke.htm)

Major Funding Sources for *Arabidopsis* Functional Genomics

- Basic research only: FWF (Fonds zur Förderung der wissenschaftlichen Forschung) (www.fwf.ac.at)
- Vienna region: WWTF (Wiener Wissenschafts-, Forschungs- und Technologiefonds) www.wwtf.at
- Specific programs: Bundesministerium für Wissenschaft, Bildung und Kultur, (www.bmbwk.gv.at/start.asp?bereich=5)
- Austrian Research Promotion Agency, Ltd. (FFG) (www.fff.co.at)

Belgium

http://www.Arabidopsis.org/info/2010_projects/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, the Flanders Interuniversity Institute for Biotechnology provides significant support to the Department of Plant Systems Biology (PSB) (about 5 million Euro per year) in which the Functional Genomics Division (P. Hilson) mainly carries out *Arabidopsis* research. Finally, the Flanders government participates in the European ERA-Plant Genomics initiative and has earmarked funding specifically supporting research in that framework. Furthermore, 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). Finally, PSB participates in efforts to confederate database systems and aims at providing information about clone resources and phenotypes via integrated web-services.

Current Research Projects

- A Belgian national research project (IAP) focuses on the study of the molecular mechanisms regulating the development of plant roots and the interaction of roots with their environment.
- 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), abiotic stress (F. Van Breusegem), genome annotation and evolution (Y. Van de Peer, P. Rouzé), computational biology (M. Kuiper), proteomics (G. De Jaegher), transcriptional networks and heterosis (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 Interuniversity 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

- Gateway-compatible destination vectors (www.psb.ugent.be/gateway)
- Large generic ongoing programs include:
 1. CATMA (www.catma.org; database hosted at PSB) maintaining a repertoire of >30,000 gene-specific sequence tags for transcription profiling and RNAi, available from NASC;
 2. AGRIKOLA (www.agrikola.org; database hosted at PSB) creating and exploiting genome-scale resources for targeted hairpin RNA gene silencing, available from NASC; in collaboration with the Belgian Coordinated Collections of Microorganisms (BCCM/LMBP), PSB is also setting up a service for the sequence validation and dissemination of AGRIKOLA resources (<http://www.belspo.be/belspo/fedra/proj.asp?l=en&COD=C3/020>)
 3. SAP (www.psb.ugent.be/SAP) creating and exploiting a genome-scale promoter amplicon collection for the analysis of transcriptional networks.

Canada

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

Contact: W.L. Crosby

University of Windsor, Ontario, Canada

Email: bcrosby@uwindsor.ca

In March of 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 repair (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.
- 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.
- Robert Hill – University of Manitoba (Rob_Hill@umanitoba.ca)
The focus of the research in the Hill laboratory is on ABA receptors and their mechanism of interaction with other signaling components.
- Kenton Ko – Queens University (kok@biology.queensu.ca)

The Ko lab uses *Arabidopsis* as a model for studying the relationship between plastid protein delivery, adaptation, and organelle biogenesis.

- Igor Kovalchuk – University of Lethbridge (igor.kovalchuk@uleth.ca)
The Kovalchuk lab uses *Arabidopsis* to study genetic and epigenetic aspects of plant genome stability and plant stress response.
- 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 subcellular 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.
- Sharon Regan – Queens University (regans@biology.queensu.ca)

The Regan lab investigates the role of ethylene in regulating developmental processes such as seed dormancy, flowering time, trichome development, and secondary growth.

- 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 (schroed3@cc.umanitoba.ca)
The Schroeder group works on the regulation of light signaling and DNA repair by DET1, DDB1A, and DDB2 in *Arabidopsis*.
- Elizabeth Schultz – University of Lethbridge (schultz@uleth.ca)
The Schultz lab studies the regulation of leaf vein pattern and its relation to leaf shape.
- Geoffrey Wasteney – University of British Columbia in Vancouver (geoffwas@interchange.ubc.ca) His laboratory uses *Arabidopsis thaliana* as a model system to understand how microtubule function is regulated in eukaryotic cells.
- Randall Weselake – University of Alberta (randall.weselake@afhe.ualberta.ca)
The Weselake group is (1) assessing the functionality (in this case the ability to impart tolerance to abiotic stress) of a number of oilseed rape genes using *Arabidopsis*, and (2) researching novel methods for modifying the fatty acid composition of seed oils.
- Tamara Western – McGill University (tamara.western@mcgill.ca)

The Western lab uses a combination of forward genetics screens for mutants affected in mucilage production and reverse genetics identification of knockouts in genes predicted to act in cell wall synthesis and modification.

- 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*.
- Jitao Zou – NRC Plant Biotechnology Institute (jitao.zou@nrc-cnrc.gc.ca)

The Zou lab is primarily interested in lipid and carbon metabolism. They study enzymatic components of the lipid metabolic network and are also interested in exploring natural variation in wild type accessions to dissect regulatory components of seed oil deposition.

Arabidopsis Genomics Tools and Resources

- Canadian reverse genetic TILLING facility, CAN-TILL (<http://www.botany.ubc.ca/can-till/>).
- Botany Array Resource (<http://bbc.botany.utoronto.ca>): Contains more than 1000 gene expression data sets consisting of more than 24.6 million data points. Tools available for the exploration of these data include: [1] an Expression Browser for performing electronic Northernblots [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 gene of interest in a specified data set, and [4] Promoter 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).

China

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

Contact: Wei-Cai Yang

Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

Email: wcyang@genetics.ac.cn

Arabidopsis research takes place mainly in the Beijing and Shanghai areas, including Peking University, China Agricultural University, Tsinghua University, and Chinese Academy of Sciences (CAS). 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. A new Center for Signal Transduction & Metabolomics (C-STM) using model plants was established at the Institute of Botany, CAS in 2005. This center will focus on hormone and peptide signaling, secondary metabolites, and plant toxins. On November 30, 2005, more than 300 participants attended the annual Workshop on *Arabidopsis* Research, held at Peking University.

Current Research Projects

- In 2005, NSFC funded Dr. De Ye at China Agricultural University and Dr. Zhong-Nan Yang at Shanghai Normal University to support two key projects on sexual plant reproduction focusing on male sterility in *Arabidopsis*.
- To facilitate international collaboration on research in epigenetics, the Chinese Academy of Sciences (CAS) funded a team project headed by Dr. Xiao-Feng Cao at the Institute of Genetics and Developmental Biology, Beijing.

A special issue of the Journal of Integrative Plant Biology dedicated to *Arabidopsis* research in China was published in January 2006. Significant progress achieved by Chinese *Arabidopsis* researchers in broad aspects of plant sciences was reviewed by Prof. Zhihong Xu of Peking University. Areas include:

- the epigenetic control in leaf development by Dr. Hai Huang's group on *RDR6* gene and in root development by Dr. Xiaoya Chen's and Dr. Huishan Guo's group on miRNA160 and miRNA164 respectively, and by Dr. Shunong Bai and coworkers on histone modification;
- the role of hormone signaling in leaf development by Dr. Lijia Qu's group on the functional study of *LAMT1* gene and *MSBP1* by Dr. Hong-Wei Xue's group;

- the genetic control on pollen tube growth by Dr. De Ye's group on *VGD1* and *TPD1* genes and gametogenesis by Dr. Wei-Cai Yang's group on *SWA1* gene function; and
- the role of blue light receptor in stomata opening by Dr. Hong-Quan Yang's group.
- In addition, progress has been made in understanding plant responses to stresses, includes functional studies on *AtNAC2* by Shou-Yi Chen's group, *LOS4* by Dr. Zhi-Zhong Gong's group, *AtERF7* by Dr. Chun-Peng Song's group, and *NHO1* by Dr. Jianmin Zhou's group.
- Finally, large scale whole genome profiling on 18 different organs and/or tissues was performed using 70mer oligomer microarrays by Dr. Xing-Wang Deng and coworkers at the Peking-Yale Joint Center for Plant Molecular Genetics and Agro-biotechnology

Major Funding Sources for *Arabidopsis* Functional Genomics

National Science Foundation of China: (www.nsf.gov.cn/)
83 Shuangqing Road, Haidian District, Beijing

France

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

Contact: David Bouchez

Institut Jean-Pierre Bourgin, SGAP-INRA Centre de Versailles, Versailles

Email: bouchez@versailles.inra.fr

The major source of funding in France for *Arabidopsis* functional genomics projects is Génoplante, 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. Over a hundred projects have been funded by the ministries of research and agriculture.

A new 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 planned to be around 12 million Euros per year. Although a large part is devoted to crop plants, several *Arabidopsis* projects are funded through the "Functional Analysis" and "New Tools" committees. The ANR also contributes to funding *Arabidopsis* research through its "white programs" for fundamental research.

Examples of Newly Funded Research Projects (2005)

([http://www.genoplante.com/doc/File/pdf/Projets 2005.pdf](http://www.genoplante.com/doc/File/pdf/Projets%202005.pdf))

(<http://www.agence-nationale-recherche.fr/documents/aap/2005/finances/financeBLANCSAE2005.pdf>)

- Improving homologous recombination and gene targeting, a three species confrontation. PI : Marie-Pascale Doutriaux, Gif
- Repair mechanisms of oxidized proteins in chloroplast of *Arabidopsis thaliana*, PI : Pascal Rey, Cadarache
- *Arabidopsis* functions involved in disease susceptibility, PI : Bruno Favery, Antibes
- The role of abscisic acid and reversible protein phosphorylation in drought adaptive responses. PI: Annie Marion-Poll, Versailles
- Characterization and control of meiotic recombination in plants. PI: Mathilde Grelon, Versailles
- Structural and functional study of oil and protein storage bodies in *A. thaliana* and in *B. napus*: towards environmentally friendly oil and protein extraction process? PI: Thierry Chardot, (Grignon)
- Dissection of redox interactions and their role in stress responses using insertion mutants and metabolomics. PI: Graham Noctor (Orsay)
- Functional and structural characterization of the *Arabidopsis* APC/cyclosome. PI: Pascal Genschik (Strasbourg).
- Identification of plant components involved in the perception by *Arabidopsis* of *Ralstonia solanacearum*, a bacterial pathogen. PI: Yves Marco (Toulouse)

Ongoing Research Projects

- A short description of ongoing Génoplante projects can be found at: ([www.genoplante.com/doc/File/pdf/Projets en cours.pdf](http://www.genoplante.com/doc/File/pdf/Projets%20en%20cours.pdf))
Arabidopsis Génoplante projects funded in 2004 included efforts on biotic stress (D Roby, I Jupin, P Saindrenan, L Jouanin), epigenetics (V Colot, O Vionnet), seed development and eQTLs (M Caboche, L Lepiniec) and new methods for purifying TAP-tagged protein complexes (H Mireau).
- 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](http://www.genoplante.com/doc/File/pdf/Projets%20collaboratifs.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.

Major Funding Sources for *Arabidopsis*

Functional Genomics

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

Arabidopsis Genomics Tools and Resources

The Plant Genomics Unit (URGV, Evry), runs large generic programs on *Arabidopsis* functional genomics (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: A complete *Arabidopsis thaliana* microarray containing more than 24000 gene-specific tags. This program involves several EU countries. (www.catma.org)
- CAGE: A reference expression database using the CATMA microarray chip. Involves a consortium of European researchers. (www.cagecompendium.org/objectives.htm)

- 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. (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/equipements/variabilite/crg) which distributes insertion lines and several populations of recombinant inbred lines and contains:

- 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 recently created "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/info/2010_projects/Germany.jsp

Contacts:

- 1) MASC, German representative: Thomas Altmann; University of Potsdam; E-Mail: taltmann@rz.uni-potsdam.de
- 2) AFGN (*Arabidopsis* Functional Genomics Network, DFG funded): Klaus Harter; University of Tuebingen; E-Mail: klaus.harter@uni-tuebingen.de
- 3) GABI (Genome Analysis of the Plant Biological System, BMBF funded): Bernd Weisshaar; Bielefeld University; E-Mail: bernd.weisshaar@uni-bielefeld.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 (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 DFG-supported AFGN was founded by a bottom-up approach of the German *Arabidopsis* research community in 2001 as a basic research program. AFGN currently funds 25 projects in Germany and has, almost from the start, been organized in close coordination with the 2010 Project of the United States National Science Foundation (NSF). Together with many other research programs throughout the world, these programs aim to elucidate the function of all *Arabidopsis* genes by the year 2010. A coordinated and unique reviewing process of the jointly submitted proposals from US and German research groups was organized for the first time for the projects currently running between the 2010 Project and the AFGN.

AFGN Current Research Projects

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. From the methodical point of view, the AFGN members utilize many techniques and methods of the functional genomics approach.

In 2003, AFGN initiated the largest international *Arabidopsis* transcriptome project entitled AtGenExpress. It consists of 497 data sets almost all of which cover duplicate or triplicate experiments. The AFGN part of the project includes 310 data sets for *Arabidopsis* development and responses to the biotic and abiotic environment (photomorphogenic light, different stresses, pathogens) and for several natural accessions. Further major contributions to AtGenExpress were provided by colleagues from RIKEN (mainly hormone and inhibitor responses), from the 2010 Project (responses to pathogens) and from ETH Zürich (cell cycle). The overall database, which is open to the scientific public, provides the experimental base for many open access bioinformatics tools such as Geneinvestigator and MapMan.

AFGN Programs and Funding

- In collaboration with the 2010 Project, AFGN founded the Young Researcher Exchange Program. This program financially supports short term research visits (up to three months) of young German scientists in cooperating US laboratories and vice versa.
- Together with colleagues from Austria and Switzerland, AFGN initiated an international conference on *Arabidopsis* functional genomics which is recognized and attended by many European and US scientists.
- The second funding period of the AFGN will end in the fall of 2007. Discussions about the structure and the main goals for future funding periods are presently underway. In any event, AFGN will maintain the basic character of its research and will continue to concentrate on the reference plant *Arabidopsis*. The future direction of the research in AFGN will aim to get in-depth predictions of how certain plant processes and pathways take place under given endogenous or environmental conditions. This approach requires the analysis of gene networks and a strongly integrated view of gene functions.

GABI Funding and 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.

Major Funding Sources for *Arabidopsis* Functional Genomics

- AFGN: (www.uni-tuebingen.de/plantphys/AFGN/) 2 million €/year budget from the German Research Foundation (DFG) (www.dfg.de)
- 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)

Arabidopsis Genomics Tools and Resources

- AtGenExpress: (web.uni-frankfurt.de/fb15/botanik/mcb/AFGN/atgenex.htm)
- 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/agfluec/HOME/projects/GABI_rkunze/index.html)
- GABI-TILLING: (www.gabi-till.de/index.de.html)

Italy

http://www.Arabidopsis.org/info/2010_projects/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 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.
- The Italian Ministry of Research has funded several collaborations between *Arabidopsis* groups from two different countries. One such collaboration involving Italy (P. Costantino) and Spain (R. Solano) aims to contribute to transcriptional regulation analysis of two important processes of higher plants: seed germination and the responses to necrotrophic fungi, respectively. This project is based on the joint exploitation of complementary technologies for the identification of TF targets available in the two proposing laboratories: (1) TAP-TAG and ChIP technologies, being developed in Rome for *Arabidopsis* (MIUR funded), and (2) microarray analysis, with technology fully established in Madrid.

- Another Italian group (B. Mattei) is one of the partners involved in the project "Functional Genomics for Biogenesis of the Plant Cell Wall" using *Arabidopsis* as a model system, and funded by the UE Marie Curie Training Network.
- Italy (L. Colombo) is also participating in the EU FP6 Marie Curie Training Project "TRANSISTOR" (Trans-cis element regulating key switches in plant development).

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 Institut Pasteur (www.pasteur.fr/pasteur/international/Dai_en/lines.html)

Japan

http://www.Arabidopsis.org/info/2010_projects/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). A joint meeting on *Arabidopsis* and rice research was held on July 6th and 7th, 2005 in Nara; more than 300 attendants discussed systematic analyses of gene functions and networks.

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 in April, 2006.
- Since 2004, PSC has contributed to AtGenExpress (Yukihisa Shimada and Shigeo Yoshida) (www.arabidopsis.org/info/expression/ATGenExpress.jsp).
- The BRC is supported by the National Bio-Resource Project and distributes plant materials developed in Japan. More than 18,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines (see below for more information) have been provided to approximately 730 laboratories located in 38 countries. Homozygous seeds of *Ds*-tagged mutants are under preparation, and some of them will be publicly available this year. 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* DNABook™ 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.

- The Plant Gene Function Research Team of AIST (<http://unit.aist.go.jp/gfrc/pgrt/>) is systematically analyzing various functions of transcription factors using repressor domain (CRES-T system) (Masaru Ohme-Takagi, Agency of 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).

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 (<http://brain.naro.affrc.go.jp/index-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)

Arabidopsis Genomics Tools and Resources

- Plant Functional Genomics Research Group in The RIKEN PSC (PIs of the PFGRG are Minami Matsui and Kazuo Shinozaki) (<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 (Miki Nakazawa), (<http://amber.gsc.riken.jp/act/top.php>)
 4. Full-length-cDNA-overexpressing (FOX) transgenic lines (Takanari Ichikawa)
 5. 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)
- 6. Transcriptome analysis of genes expression in response to both abiotic and biotic stress using RAFL full-length cDNA microarray analysis (Motoaki Seki) (<http://pfgweb.gsc.riken.go.jp/pjCdma.html>)
- 7. Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori, Fumiyoshi Myouga) (<http://pfgweb.gsc.riken.go.jp/pjAcds.html>)
- 8. 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)
 - 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)
 - 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/>)
 - The Metabolomics database at the PSC (<http://prime.psc.riken.jp/>)

The Netherlands

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

Contacts: Willem Stiekema,

Centre for BioSystems Genomics, Wageningen

Email: willem.stiekema@cbsg.nl

Ben Scheres

Department of Molecular Cell Biology, University of Utrecht

Email: b.scheres@bio.uu.nl

Center for BioSystems Genomics, the Netherlands Plant Genomics Network

Arabidopsis research within this national plant genomics research program 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. The Center strives for fully integrated large-scale activation tag screening, gene expression, proteome and metabolite profiling based on the full exploration of the available genetic variation with emphasis on control of metabolic composition. Additional projects involve understanding the adaptive traits relevant for research in potato and tomato and the development of concepts and technologies based on *Arabidopsis* genetics and genomics. Four current projects funded through 2008 focus on:

- *Arabidopsis* quality: the genetic and genomic analysis of metabolic composition (Koornneef/Vreugdenhil, Wageningen University; Pereira, Plant Research International, Wageningen; Smeekens, Utrecht University)
- The analysis of ligand-receptor interaction networks in *Arabidopsis* (Liu, Plant Research International, Wageningen; Heidstra, Utrecht University; De Vries, Wageningen University)
- The role of chromatin structure in gene expression of *Arabidopsis* and tomato (Bisseling/de Jong, Wageningen University)
- Priming of defense gene expression in plant-oomycete interactions (Pieterse/van Ackervecken, Utrecht University)

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

Wageningen University–Current Projects

- QTL express: identification of plant performance traits in *Arabidopsis* by combining high-throughput mapping and expression profiling (funded to 2008; M. Koornneef, D. Vreugdenhil).
- Controlling phytate and micronutrients as determinants of food quality (funded to 2007; Jianjun Zhao, M. Koornneef, G. Bonnema, D. Vreugdenhil)
- Heavy metal tolerance and accumulation in *Thlaspi caerulescens*, a heavy metal hyper-accumulating plant species (M. Aarts, J. van de Mortel, S. Talukdar; 2002-2007).
- Do plants love heavy metals? (A. Assunção, M. Aarts; 2005-2008)
- Functional genomics of secondary metabolite biosynthesis: the *Arabidopsis* glucosinolate model (W. van Leeuwen, M. Aarts; 2004-2006)
- Natural variation for *Arabidopsis* mineral content (A. Ghandilyan, M. Aarts; 2003-2007)
- Brassica vegetable nutrigenomics (G. Bonnema, M. Aarts; 2005-2010)
- The role of tomato serine and cysteine proteases in defense signaling (R. van der Hoorn)
- A molecular genetic approach to chemical ecology and community ecology (M. Dicke)
- Cross-talk between signal-transduction pathways in induced defense of *Arabidopsis* against microbial pathogens and herbivorous insects. M. Dicke (joint projects with C. Pieterse, Utrecht University)
- Development of a method for breeding of cucumber for improved attraction of biological control agents (M. Dicke, H. Bouwmeester)
- From genetic code to ecological interactions: molecular, phytochemical and ecological aspects of a glucosinolate polymorphism in *Barbarea vulgaris* (N. van Dam)
- *Arabidopsis*: the system to study structure and function of heterochromatin (T. Bisseling)
- Chromatin genomics: functional analysis of *Arabidopsis* chromatin remodeling genes in development (T. Bisseling)
- Wageningen Phytoinformatics: the added value from plants (funded to 2008; W. Stiekema)

Plant Research International, Wageningen– Current Projects

- Identification and characterization of genes for drought tolerance (2006; A. Pereira)
- Identification of plant genes for abiotic stress resistance (2006; A. Pereira)
- Isolation and characterization of key-genes in the formation of germination stimulants of the parasitic weeds Striga and Orobanche (H. Bouwmeester)
- LRR receptor-like proteins and their functions in plant signaling (2004–2008; G.C. Angenent)
- MADS box transcription factor functioning, their signaling and protein interaction (2004–2008; G. Angenent)
- Cis-Trans regulation in floral organogenesis (G. Angenent; 2005–2008)
- Signaling pathways controlling embryogenic cell development in *Arabidopsis* (funded to 2008; K. Boutilier)
- Signaling in the shoot apical meristem: A question of determinate or indeterminate growth (funded to 2007; R. Immink)

Utrecht University–Current Projects

- Sugar signaling pathways in plants (funded to 2010; J. Smeekens)
- Trehalose-6-phosphate as a regulatory molecule in plants (funded to 2010; H. Schlüpmann)
- Control of plant architecture (funded to 2010; M. Prove-niers)
- Dormancy as survival mechanism in plants (funded to 2010; L. Bentsink)
- Induced disease resistance signaling in *Arabidopsis* (funded to 2010; C. Pieterse)
- Cross-talk between signal-transduction pathways in induced defense of *Arabidopsis* against microbial pathogens and herbivorous insects (funded to 2006; C. Pieterse, joint projects with M. Dicke, Wageningen University)
- Plant innate immunity: cross-talk between signaling pathways to fine tune defense (funded to 2009; C. Pieterse)
- Controlled regulation of broad spectrum pathogen resistance in plants (C. Pieterse; 2004–2008)
- A functional proteomics approach to identify phospho-proteins involved in plant innate immunity; the relation between innate immunity signal transduction and plant development. (F. Menke)
- Priming in plant-pathogen interactions: the molecular mechanism of the alarmed state (2005–2008; J. Ton)
- Signaling at the host-microbe interface: pathogen-induced modulation of the plant plasma membrane (A. van den Ackerveken)
- Genetic networks in root development: Interplay between cell polarity information, pattern formation cues, and

control of cell division; Chromatin dynamics; Ubiquitination and cell cycle control; dissection of retinoblastoma-mediated control of cell differentiation; in silico modeling of developmental pathways, with an emphasis on emergent properties of feedback loops between auxin transport, cell polarity and transcription factor networks (B. Scheres)

- Genomics for multicellular development: Function of the quiescent center in regulation of pattern formation and differentiation within the *Arabidopsis thaliana* root meristem (R. Heidstra)
- Analysis of the hyponastic and differential growth response of *Arabidopsis thaliana* petioles induced by submergence and low light conditions (funded to 2010; T. Peeters, R. Voese-nek)

Leiden University–Current Projects

- Auxin-mediated orientation of plant development directed by plant protein kinases (R. Offringa)
- The role of ubiquitination in auxin and jasmonic acid signaling (funded to 2008; R. Offringa; J. Memelink)
- Characterization of a novel regulator of plant secondary metabolism (funded to 2008; J. Memelink)
- Regulation of jasmonate-responsive gene expression in *Arabidopsis* (funded to 2007; J. Memelink)
- Novel approach for dissection of jasmonate signaling in *Arabidopsis* (funded to 2006; J. Memelink)
- T-DNA activation tagging: an approach to isolate components in jasmonate-dependent defense responses in *Arabidopsis* (funded to 2009; J. Memelink)
- Plant stress resistance: jasmonate-responsive defense signalling (funded to 2008; J. Memelink)
- Analysis of the ORA47 transcription factor involved in jasmonic acid signal transduction in *Arabidopsis thaliana* (funded to 2008; J. Memelink)
- Analysis of the transcription factor ORA59, which plays a crucial role in the jasmonate- and ethylene-mediated defense response in *Arabidopsis* (funded to 2010; J. Memelink)
- Jasmonate-mediated changes in the modification and protein interaction status of AP2/ERF-domain transcription factors in *Arabidopsis* (funded to 2006; J. Memelink)
- How do plants discriminate between specialist and generalist insects (funded to 2010; H. Linthorst, P. Klinkhamer, R. Verpoorte)
- Changes in the *Arabidopsis* metabolome after stress, using NMR-metabolomics and targeted analyses of secondary metabolites (R. Verpoorte, H. Linthorst, P. Klinkhamer, C. van den Hondel)
- Effect of Non-homologous recombination mutations on genome stability and development in *Arabidopsis* (P. Hooykaas)

- Targeted transgene integration in plants (funded to 2009; S. de Pater, P.Hooykaas)
- Cre-lox mediated cassette exchange in the *Arabidopsis* genome (funded to 2007; J. Louwerse, P.Hooykaas)
- Development of artificial zinc finger transcription factors as regulators of plant function (funded to 2009; E. van der Zaal, P.Hooykaas)
- Phospho-fingerprinting *Arabidopsis* development (R.Offringa)
- The role of auxin in fruit initiation (funded to 2009; A.Vivian-Smith, R.Offringa)

University of Amsterdam–Current Projects

- Role of PA kinase in plant stress signaling (funded to 2007, B. van Schooten, T. Munnik)
- Sensing the lipid second messenger, phosphatidic acid (funded to 2011, T. Munnik)
- Targets for the novel lipid second messenger, phosphatidic acid (funded to 2006; C. Testerink, T. Munnik)
- Role of phospholipase C signaling in plant defense (funded to 2007; S. van Wees, Munnik)
- SUMO-signaling in plants (H. van den Burg)

Vrije Universiteit, Amsterdam–Current Projects

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

University of Groningen–Current Projects

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

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)

Nordic *Arabidopsis* Network

http://www.Arabidopsis.org/info/2010_projects/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*. Norway is a partner of the EU Plant Genomics network ERA-PG and hosted the Nordic *Arabidopsis* meeting 2004.

Arabidopsis Resources and Funding

- 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: *Arabidopsis* transformation, T-DNA genotyping, seed collection: (www.umb.no/?viewID=2552)
- Research Council of Norway (www.forskningradet.no): Functional Genomics in Norway (FUGE)- Funding

Sweden

The Umeå Plant Science Center (UPSC) 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.

Arabidopsis Resources and Funding

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

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. 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.

Arabidopsis Resources and Funding

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

Denmark

In Denmark, a number of groups at The Veterinary and Agricultural University, Copenhagen University, Risø National Laboratory, Danish Institute of Agricultural Sciences 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).

United Kingdom

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

Contacts: Andrew Millar (Coordinator)

University of Edinburgh

Email: andrew.millar@ed.ac.uk

Ruth Bastow (Administrator)

University of Bristol

Email: ruth@arabidopsis.info

If *Arabidopsis* researchers are to make the best possible progress as we move into the 21st century they will need to understand the contemporary questions in crop science in order to facilitate the translation of basic plant science into practical outcomes. Long-term funding, coordination and coherent data policies will also need to be developed at both national and international levels to provide the informatics, mathematical models and data required for a comprehensive framework of *Arabidopsis* biology *in silico*.

GARNet

GARNet, the **Genomic *Arabidopsis* Resource Network** was established in 2000 to provide publicly available functional genomics resources for *Arabidopsis* research. Funding was extended to move the services provided by GARNet to self-sustaining cost recovery. Coordination activities are funded 2005-2010, to provide an information resource (<http://garnet.arabidopsis.info/>, newsletter, annual meeting) and point of contact for other UK plant communities and international plant genomics programs. Plant systems biology and translational research are now important parts of GARNet's activities.

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 2006, "Plant Networks – How to integrate data" will be held at the University of Bristol 11-12th September (http://garnet.arabidopsis.info/garnet_meeting.htm).
- The Genetical Society hosts an annual one-day meeting on *Arabidopsis*, which in 2006 will be held at Cambridge on May 20th (<http://www.genetics.org.uk>).
- GARNet is also involved in the organization of Plant-GEMS 2006, 11-14 October, Venice (<http://www.plant-gems.org/>)

Major Funding Sources for *Arabidopsis* Functional Genomics

The Biotechnology and Biological Science Research Council, BBSRC (<http://www.bbsrc.ac.uk/>) is the major funding agency for *Arabidopsis* functional genomics. BBSRC encourages applications that use genomic technologies and has launched several initiatives to stimulate research in this area, (www.bbsrc.ac.uk/science/initiatives/) including:

- Centers for Integrative and Systems Biology (www.bbsrc.ac.uk/science/initiatives/cisb_phase2.html)
- The Crop Science Initiative; exploitation of *Arabidopsis* Research for crop science (www.bbsrc.ac.uk/science/initiatives/crop_science.html)
- Tools and Resources; (<http://www.bbsrc.ac.uk/science/initiatives/trdf.html>)
- E-science (www.bbsrc.ac.uk/science/initiatives/escience/Welcome.html)

Other UK funding bodies supporting *Arabidopsis* research include

- NERC (Natural Environment 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 Funding

The BBSRC is one of 17 funding bodies involved in ERA-PG (European Research Area in Plant Genomics), allowing UK researchers to participate in the funding initiative; 'Structuring Plant Genomic Research in Europe' <http://www.erapg.org/>.

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 Affymetrix and proteomics projects are available at NASC, and metabolomics results at Rothamsted <http://www.metabolomics.bbsrc.ac.uk/>. Many leading universities and institutes in the UK have established their own functional genomics centers and resources including METRO and ProtLocDB.

European Stock Centre

NASC (<http://arabidopsis.info/>) is an international resource for seed, DNA amplicons, clones and data. The UK BBSRC government funding body currently subsidizes all of NASC services.

- 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>).
- NASC's resources are available as BioMOBY web services (70+) for automated data-mining engines and desktop workflow GRID applications such as Taverna.

United States

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

Contacts: Philip Benfey

Duke University

Email: philip.benfey@duke.edu

Mary Lou Guerinot

Dartmouth College

Email: Mary.Lou.Guerinot@dartmouth.edu

AT2010 Midterm Progress

A major event in the U.S. *Arabidopsis* functional genomics community was the marking of the midpoint in the National Science Foundation *Arabidopsis* 2010 program (www.nsf.gov/bio/pubs/awards/2010awards.htm.) 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. Workshop participants came from the U.S., Pacific Rim and Europe and represented a wide range of subspecialties within the *Arabidopsis* genomics community. The final report is available in its entirety at www.nsf.gov/pubs/2006/bio0601/bio0601.pdf. Prior to the workshop, a web-based survey was conducted to solicit input from the broader community. In addition, data were collected on the impact of the 86 funded projects to date, including publications, stocks deposited and database submissions. The overall assessment was that most of the initial goals set in 2000 for the first five years had been met or surpassed. Of particular note was the utility of genome-wide resources such as insertion lines. In assessing the funded projects, the panel came to the conclusion that those that used high throughput and/or computational approaches to understanding biological processes had the highest impact. For the upcoming five years of the program, the panel recommended focusing on these 11 areas:

1. Benchmarking gene function
2. Developing genome-wide tools and reagents for analyzing gene function and regulation
3. Improving genome annotation and tools for visualization, annotation and curation
4. Improving database integration and developing new modeling and computational tools
5. Exploring exemplary networks and systems
6. Analyzing non-protein coding genes
7. Leveraging natural variation to understand gene function in *Arabidopsis thaliana*

8. Localizing gene products at the cellular and subcellular level

9. Facilitating metabolomics and ionomics

10. Engaging the broader community

11. Enhancing international collaboration

Looking beyond 2010, the panel foresaw a program that "enables the international community of plant biologists to analyze, understand, and manipulate the full spectrum of biological processes required to make a plant that functions effectively and predictably under both standardized laboratory conditions and complex natural environments."

Plant Cyberinfrastructure Center Workshop

Recent progress in plant science has resulted in the development of a wide range of new tools and resources for research and education. Optimal use of these resources requires combining the information represented among them in innovative ways to achieve a better understanding of fundamental principles in plant biology; and it also requires that individuals from multiple fields and disciplines be able to find, understand and effectively employ these resources in novel ways.

To discuss the means by which to achieve such a synthesis of resources, and to design the appropriate cyberinfrastructure for their best utilization, a workshop for a Plant Cyberinfrastructure Center was held at the National Science Foundation on October 17 and 18, 2005 (complete report at www.arabidopsis.org/info/2010_projects/index.jsp.) Participants represented the widest possible range of plant and computational biologists, with experts in plant genomics, development, metabolism, ecology, and evolutionary biology, ecoinformatics and experts in computational modeling, databases, computer infrastructure, software, and mathematics. The participants achieved consensus on the need for a center to provide the cyberinfrastructure for facilitating interdisciplinary research in plant science and for generating a new kind of plant biologist, and made a number of recommendations and suggestions outlining their vision for such a center.

Workshop recommendations

1. There is a strong need to create a plant cyberinfrastructure center to promote the integration of diverse and large-scale genomics and other data to address a few fundamental problems in plant biology using multi-disciplinary approaches.

2. A core mission should be to train a new generation of scientists who can combine multi-disciplinary approaches and utilize data in public repositories maximally.
3. The center should be composed of an entity that is connected to a number of adjunct institutions with different types of scientific expertise and facilities.
4. The core infrastructure and staffing should follow the successful models of NCEAS (National Center for Ecological Analysis and Synthesis) and NESCent (National Evolutionary Synthesis Center) and designate enough core staff to facilitate the activities of the center efficiently.
5. The center should provide an umbrella infrastructure to coordinate disparate outreach activities and train students and faculty in achieving a comfort level in interacting with the public about plant science and its importance.
6. The center should maximally leverage existing databases and standards to promote international integration of data.

Young Researcher Exchange Program

In collaboration with the German *Arabidopsis* Functional Genomics program, AFGN, an NSF-funded Young Researcher Exchange Program was started. This program provides stipends and travel expenses for short-term research visits (up to three months) for graduate students (and postdoctoral fellows in the U.S.) to work in German laboratories and for German students to work in U.S. labs. For more information please see (www.arabidopsis.org/news/job_postings/friesner022806.doc) and (www.uni-tuebingen.de/plantphys/AFGN/yrep.htm).

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/)

Arabidopsis Genomics Tools and Resources

- TAIR (The *Arabidopsis* Information Resource, <http://arabidopsis.org>) collects information and maintains a database of genetic and molecular biology data for *Arabidopsis thaliana*, a widely used model plant. TAIR is produced by the Carnegie Institution of Washington Department of Plant Biology, Stanford, California, and the National Center for Genome Resources (NCGR), Santa Fe, New Mexico. Funding is provided by the National Science Foundation, (Grant No. DBI-9978564) and DBI-0417062. TAIR collaborates with the *Arabidopsis* Biological Resource Center (ABRC) to provide researchers with the ability to search and order stocks. The data in TAIR can be searched, analyzed, downloaded, and

viewed using the interactive SeqViewer tool. In addition, pages on news, information on the *Arabidopsis* Genome Initiative (AGI), *Arabidopsis* lab protocols, and useful links are provided.

TAIR's first genome release, version 6.0, has been integrated into the TAIR database, SeqViewer, MapViewer and sequence analysis datasets, and is also available from NCBI. The TAIR6 release contains 26,751 protein coding genes, 3818 pseudogenes and 838 non-coding RNA genes (31,407 genes in all). A total of 437 new genes were added and nine genes were made obsolete. Updates were made to 973 genes including 831 updates to coding sequences, 14 gene splits and 7 gene merges and the addition of 1200 new splice variants. A total of 3159 *Arabidopsis* genes (10%) now have annotated splice variants. No changes were made to the chromosome sequences for this release. Access to the fully annotated chromosome sequences in TIGR xml format as well as FASTA files of cDNA, coding, genomic and protein sequences and lists of added, deleted and changed genes are available at the TAIR website. FASTA formatted files for all sequence analysis datasets including sets of intron, intergenic, UTR, upstream and downstream sequences are also available. Access the new release using TAIR's genome browser (<http://arabidopsis.org/servlets/sv>).

- ABRC (The *Arabidopsis* Biological Resource Center, www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrhome.htm) distributes and is actively collecting stocks that are associated with genomics and phenomics. The NSF grant which supports the Center was recently renewed for a five-year period, through March 2011. Relevant seed stocks include insertion lines (200,000+ from many major contributors as well as smaller sets of purified lines from individual researchers), the lines of the *Arabidopsis* TILLING service, 800+ distinct natural accessions, 9 recombinant inbred populations, related species and RNAi lines including the AGRİKOLA lines. In addition, 1,900 of the ca. 50,000 "Confirmed" (genetically purified) T-DNA lines being produced by the J. Ecker laboratory have been received, and the remainder will be arriving during the next two years. These will be made available as they arrive, and distribution of these as large sets and sub-sets for phenotypic experimentation, etc, is planned. On the DNA side, ABRC presently houses full-length ORF and cDNA clones for 15,000+ genes, BACs covering the entire genome, BACS of four related species, the AGRİKOLA RNAi clones and various sets of Expression and Destination clones. The extensive Expression ORF collection from S. P. Dinesh Kumar is being received, with 1,100 of these currently in-house. 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 continues to exceed 90,000 in total volume.

Members of the Multinational *Arabidopsis* Steering Committee

Thomas Altmann

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

Philip Benfey, Chair

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

Bill Crosby

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

Ian Furner

Representing the United Kingdom
ijf@mole.bio.cam.ac.uk
University of Cambridge
Cambridge, United Kingdom

Mary Lou Guerinot

Representing the United States
Mary.Lou.Guerinot@Dartmouth.edu
Dartmouth College
Hanover, New Hampshire, USA

Pierre Hilson

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

Heribert Hirt

Representing Austria
Heribert.hirt@univie.ac.at
University of Vienna
Vienna, Austria

Gerd Jürgens

Representing Germany
gerd.juergens@uni-tuebingen.de
University of Tübingen
Tübingen, Germany

Jaakko Kangasjärvi

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

Keith Lindsey

Representing the United Kingdom
keith.lindsey@durham.ac.uk
University of Durham
Durham, United Kingdom

Sean May

Representing the United Kingdom
sean@arabidopsis.info
Nottingham *Arabidopsis* Stock
Center
Loughborough, United Kingdom

Peter McCourt

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

Andrew Millar

Representing the United Kingdom
Andrew.millar@ed.ac.uk
University of Edinburgh
Edinburgh, United Kingdom

Lutz Nover

Representing Germany
nover@cellbiology.uni-frankfurt.de
Biozentrum
Universitaet Frankfurt
Frankfurt, Germany

Javier Paz-Ares

Representing Spain
jpazares@cnb.uam.es
Centro Nacional de Biotechnologia
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@bio.uu.nl
University of Utrecht
Utrecht, The Netherlands

Kazuo Shinozaki

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

Randy Scholl

Representing the United States
ex officio
scholl.1@osu.edu
Arabidopsis Biological Resource
Center
Columbus, Ohio, USA

Ian Small, Co-chair

Representing Australia
iansmall@cyllene.uwa.edu.au
University of Western Australia
Perth, Australia

Willem Stiekema

Representing The Netherlands
willem.stiekema@cbsg.nl
Center for BioSystems Genomics
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
Beijing, China

Joanna Friesner

Coordinator and Executive
Secretary
jdfriesner@stanford.edu
The Carnegie Institution
Stanford, CA, USA

Members of the MASC Subcommittees

Bioinformatics

Chris Town (chair)

cdtown@tigr.org

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

Heiko Schoof

schoof@mpiz-koeln.mpg.de

cDNAs and Clone- Based Functional Proteomics (ORFeomics)

Pierre Hilson (chair)

pihil@psb.UGent.be

Kazuo Shinozaki

sinozaki@rtc.riken.go.jp

Ian Small

iansmall@cyllene.uwa.edu.au

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

ofiehn@ucdavis.edu

Alisdair Fernie

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@warwick.ac.uk

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

Martin Lysak
m.lysak@rbgkew.org.uk

Chris Pires
piresjc@missouri.edu

Ming Ray
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

Katica Ilic
katica@acoma.stanford.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

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

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

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

Sigrun Reumann
sreuman@gwdg.de

Michel Rossignol
rossign@ensam.inra.fr

Klaas van Wijk
kv35@cornell.edu

Julian Whitelegge
jpw@chem.ucla.edu