

**The Multinational Coordinated
Arabidopsis thaliana
Functional Genomics Project**

Annual Report 2003

The Multinational *Arabidopsis*

Steering Committee

June 2003



Cover: In the background, sequence from *Arabidopsis thaliana* chromosome 5, determined by the Kazusa Group, Japan.

In the foreground and to the right, a drawing of an *Arabidopsis* plant from an unknown source, discovered in a print shop in East Sound, Washington, USA, by Stephen H. Howell (Director, Plant Sciences Institute, Iowa State University). According to Howell, "the print was obviously cut from an old botanical book, however, none of the citations were attached to the print nor was any additional information available from the print shop owner."



The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

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The Multinational *Arabidopsis* Steering Committee June 2003

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TABLE OF CONTENTS

FOREWORD TO THE REPORT	1
EXECUTIVE SUMMARY	3
ANALYSIS AND RECOMMENDATIONS	4
INTRODUCTION TO <i>ARABIDOPSIS</i>	7
Arabidopsis: The Model Plant	7
<i>Arabidopsis</i> versus plants of economic significance	8
A tradition of <i>Arabidopsis</i> research	8
Technological innovation and education	9
<i>Arabidopsis</i> research is the first step in an exciting future of plant improvement	9
International Cooperation	9
The Genome of Arabidopsis	10
PROGRESS OF THE PAST YEAR	11
Progress and Activities of the Multinational Arabidopsis Steering Committee	11
INITIAL REPORTS OF THE MASC SUBCOMMITTEES	14
Bioinformatics	14
cDNAs and Clone-Based Functional Proteomics (ORFeomics)	15
Multiparallel Analytical Tools & Phenotype Analyses	17
Reverse Genetic Stocks	18
Table 1: Worldwide Arabidopsis Reverse Genetic Stocks	20
THE INTERNATIONAL <i>ARABIDOPSIS</i> FUNCTIONAL GENOMICS COMMUNITY	23
Argentina	23
Australia & New Zealand	24
Austria	25
Canada	26
China	27
European Union	28
France	30
Germany	31
Italy	32
Japan	33
The Netherlands	34
Nordic Arabidopsis Network	35
United Kingdom	36
United States	37
MEMBERS OF THE MULTINATIONAL <i>ARABIDOPSIS</i> STEERING COMMITTEE	38

FOREWORD TO THE REPORT

In 2002, the Multinational *Arabidopsis* Steering Committee published a long-range plan for a new phase of the Multinational Coordinated *Arabidopsis thaliana* Genome Research Project: the Functional Genomics Project. This year, we are pleased to present to the biological research community a report summarizing progress that has been made toward achieving our goals.

The *Arabidopsis* research community has proposed an ambitious mission: to determine the function of every gene in *Arabidopsis* by 2010. Our ultimate goal is a comprehensive understanding of the biology of a flowering plant, using *Arabidopsis* as an experimental model system. The availability of the complete genome sequence of *Arabidopsis* gives us a glimpse of the information needed for a mechanistic understanding of plant biology; however, this glimpse currently provides us with only an idea about the complexity of the whole story. In this sense, the genome sequence is an outline that provides the means for highly efficient analyses, but itself gives little specific information about how this plant grows, develops, and interacts with its environment. To achieve our goals, a full-blown, in-depth coordinated research program is needed to determine how information encoded in the genome is interpreted and translated into the complex set of cellular, physiological and developmental processes manifested by flowering plants.

Sustained and expanded exploitation of the data provided by the genome sequence will continue to move *Arabidopsis* forward as the premier species for studying basic mechanisms in the physiology, biochemistry, and development of plants, and will serve as a basis for comparative studies with more economically important agricultural species. The *Arabidopsis* genome sequence was an essential frame of reference for the recently completed rice genomic sequence, and plans for the next generation of genomes to be sequenced (such as maize) suggest that *Arabidopsis* will remain as the gold standard for the best sequenced and annotated plant genome.

It is clear that a major element in global *Arabidopsis* research activities as we move forward in this new field we call ‘functional genomics’ is the evaluation and integration of new high throughput technologies. In the sequencing era, there was a high level of unanimity on the technological aspects of the project. In this initial post-sequence era, a consensus remains to be built as to which instrumentation, expression systems or software, to name just a few items, will best satisfy our needs. It is apparent that *Arabidopsis* is the place where the plant research community can ‘shake-down’ these new technologies as they arise, and provide a real-world test to see which of them will work best with a plant genome.

Overall, it is clear that *Arabidopsis* will become the essential frame of reference in plant functional genomics, as it did with whole-genome sequencing. The reasons for this are simple:

- (1) *Arabidopsis* has the best understood plant genome;
- (2) the best reverse and forward genetic tools and resources are available for research with *Arabidopsis*;
- (3) a large, active, and highly co-operative international research community uses *Arabidopsis* as a model plant; and
- (4) it is a cost-effective strategy to approach almost ANY problem in plant biology, whether applied or basic, using *Arabidopsis*.

This document will serve as an update to the *Arabidopsis* research community of the efforts being made in *Arabidopsis* functional genomics worldwide. To maintain optimal

research efficiency, it is important to keep the community current not only on the status of research but also on the funding, biological resources and services being made available around the world. It has become clear that international cooperation and communication are essential to success in an undertaking as large as the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. **The members of MASC continue to assert that we have put forth a goal of no less than the complete mechanistic understanding of the biology of higher plants, on which human existence relies, using *Arabidopsis thaliana* as a model.**

The Multinational *Arabidopsis* Steering Committee
June 2003

EXECUTIVE SUMMARY

The genome sequence of *Arabidopsis thaliana* was determined by a multinational, cooperative group of scientists and published in the year 2000. The sequence offers to the entire scientific world a vast array of information; the means to achieve full understanding of the biology of an organism is offered up for those who would pursue it. Achieving this comprehensive understanding of the organism is only possible, however, with a substantial and concentrated investment of time, energy, and monetary resources.

In addition to its vital role as a source of food for the human population, this basic research into the growth and development of higher plants may contribute a unique and new understanding of the way groups of highly complex cells communicate and coordinate their growth for the good of the organism. In a similar way, the global *Arabidopsis* research community has attempted to coordinate our own efforts.

In the two years that have transpired since the *Arabidopsis* genome sequence was published, the worldwide *Arabidopsis* research community has begun to develop and utilize an impressive toolbox of functional genomics technologies. We have seen the widespread adoption of advanced genetic, genomic, proteomic and metabolomic technologies. We have witnessed a re-emergence of the cooperative spirit so evident during the sequencing project. And most significantly, we have seen in many MASC member countries the development of new funding programs specifically designed to take advantage of the *Arabidopsis* sequence.

In order to avoid needless duplication of effort, the MASC has attempted to coordinate worldwide resources devoted to understanding the *Arabidopsis* sequence. A fulltime employee was hired as an executive coordinator for the MASC, who has made visits to and communicated extensively with the member countries in order to facilitate the flow of information and cooperation. At last year's MASC meeting in Seville, Spain, the MASC formed subcommittees charged with tracking and aiding progress in specific subdisciplines of *Arabidopsis* functional genomics. These subcommittees – **Bioinformatics, ORFeomics, Multiparallel Analytical Tools, and Reverse Genetic Stocks** – have delivered their first reports, presented in this document.

In this report, the MASC offers several specific recommendations on resource allocation in the coming period. These include:

- sequencing and distribution of a complete collection of *Arabidopsis* cDNAs to the academic community without intellectual property restrictions,
- the creation of centralized mass spectrometer facilities that can be used for proteomic and metabolomic analyses,
- completion of the remaining unsequenced portions of the genome, including those within the repetitive centromeres and telomeres,
- continued pursuit of a knockout mutant in every gene and the development of strategies to delete or inactivate complete families of genes.

The committee further recommends that all functional genomic resources, such as knockout plants, DNA chip data, or cDNA expression libraries, continue to be widely available to the global academic research community without intellectual property restrictions.

ANALYSIS AND RECOMMENDATIONS

It is apparent that the efforts of the world community in unveiling the secrets of *Arabidopsis* biology are beginning to set seed. While the more economically important plants are getting their genomes sequenced, it remains clear that the extremely high quality of the *Arabidopsis* sequence, coupled with the facile genetic tools that make this model plant tractable for rapid studies in the laboratory have continued to place this small weed at the forefront as the benchmark for basic plant science. This is reflected in an ever-increasing size of the worldwide *Arabidopsis* research community. In summary, the species *Arabidopsis thaliana* continues to be the key to rapid and efficient plant biology research.

So what does the future hold for the world *Arabidopsis* community? Clearly, we have only begun to delve into the many secrets that the first plant genome sequence revealed. There remains much work to be done; but a cooperative, interactive communicative world-wide research community and application of newly emerging methods and technologies will lead the way into the future of plant science.

We now have knockouts for about three quarters of the predicted genes of *Arabidopsis*. The remaining small and tandemly duplicated genes have shown themselves to be recalcitrant to standard technologies. We need to conquer these small but critical genes, as well as make double mutants, triple mutants, quadruple mutants, and higher-order multiple loss-of-gene-function lines, so that entire families of genes can be eliminated, or genes active in alternative pathways can be shut down simultaneously. It is possible that such new combinations of knockout alleles will provide fascinating phenotypes not previously seen, which in turn will help to elucidate functions of unknown genes and allow experimental examination of the redundancy question. The genome-wide production of all possible double knockout mutants recently initiated by the yeast biological community is an example the *Arabidopsis* community may wish to replicate. The more difficult technological features of growing and crossing individual plants on a genome-wide scale will be surmountable only by the creativity and ingenuity of new generations of *Arabidopsis* scientists currently being trained in laboratories around the world. If they are successful, as in yeast, we may see a joining of genetic and biochemical approaches to determining protein interaction partners in *Arabidopsis*, in the near future.

The comprehensive analysis of the natural genetic diversity represented by the growing collection of *Arabidopsis* accessions sampled from various locations around the world has just started. These investigations hold great potential for providing insight into the molecular basis of adaptation conferred by manifestation of allelic or non-allelic genetic variation. The knowledge gained through this emerging area will strongly influence the way natural diversity in crop species will be viewed, which for many years will continue to serve as an important target for genetic improvement.

Approximately half of the genes encoded by the *Arabidopsis* genome have a primary sequence that does not look like that of any proteins we know anything about. These "pioneer proteins" continue to represent the frontier of our knowledge of plant science. Structural biologists have begun to look at this database of proteins as a possibly rich reservoir of completely new motifs and catalytic sites. It is ironic that, whereas small size is a disadvantage for insertional mutagenesis of genes, diminutive size is an advantage for structural determination because small proteins are easier to express, crystallize and also, to analyze by NMR.

As we enjoy using high throughput technologies for exploring the secrets within the genome sequence, we must not ignore the opportunities afforded by an integrated approach in understanding the organism. *Arabidopsis* is not a simple unicellular organism like yeast. *Arabidopsis* is a complicated, multicellular eukaryote and its many differentiated cells have evolved together for mutual benefit. Hence, in our enthusiasm for exploring the intricacies of plant cell biology and biochemistry, we must not lose sight of the opportunities for uncovering important, unknown mechanisms by which immobile differentiated cells within a large organism coordinate their activities.

Plant metabolism remains a relatively untapped territory for plant scientists, but one that is beginning to receive the attention it deserves. Plants have, over hundreds of millions of years of evolution, developed an amazing array of metabolic pathways for primary and secondary metabolites. The result for us is a treasure trove of metabolic processes, chemicals, and proteins that hold vast promise for our future on earth. The pressing question is this: do we have the desire and audacity to achieve an understanding, for this one organism, of all aspects of its interactive metabolic pathways and combinatorial chemistry? Our understanding of one organism will lead us to a greater understanding of similar and divergent processes in all plants.

But in the end, it remains an important task for all of us to continue communicating, in the most emphatic means, why we want to spend a large amount of money studying a plant that is so unimportant as a crop. This same problem has been faced by the medical community, and it is gratifying to see the Nobel Prize this year being awarded to scientists involved in basic research with *C. elegans*. Communication with the general public remains one of the most important activities we should all engage in, but one that most scientists fail to perform. This is important. We must be careful not to let our funding agencies become micromanaged by political forces, and stray from the logic that has served them so well in the past, i.e., using the **best** model organisms for pursuing basic knowledge.

In conclusion, it is clear that the availability of the *Arabidopsis* genome sequence has changed how we approach research within the plant sciences. The opportunities before us are amazing, and we can see the emergence of a myriad number of new questions being asked, new techniques being utilized, and new goals being put forth by the worldwide *Arabidopsis* community. As we move forward into the exciting future foretold by the secrets we are beginning to uncover, it is imperative that we do so working together.

The MASC makes the following specific recommendations for future funding in *Arabidopsis* research. It is, first of all, very important to recognize that the computer-aided interpretation of information provided in the genome sequence needs to be experimentally verified. While informatics remains an important tool for pointing experimentalists in the right direction, it is also critical that the difficult (and expensive) laboratory ‘wet’ work ahead of us not be avoided. The recommendations below focus on that theme:

- It is critical that a complete collection of sequenced cDNAs be obtained and made available to the entire academic community without intellectual property restrictions. This is absolutely essential as we seek to find the best heterologous system for expressing and purifying, in an active state, each of the *Arabidopsis* proteins. All future work with the many proteins that have no sequence homology to other proteins awaits the establishment of a comprehensive sequenced cDNA resource.
- Centralized facilities containing mass spectrometers that can be used for proteomic and metabolomic analyses must be established within the academic community.

- The remaining unsequenced parts of the genome, including those within the repetitive centromeres and telomeres, must be finished.
- It is important that efforts to obtain a knockout in every gene are continued and especially, that strategies to eliminate complete families of genes be pursued. Making these resources available to the global academic research community without intellectual property restrictions remains a worthy goal that should be continued.

So where are we now? The MASC has made a good start, in establishing four or five major subcommittees based on scientific disciplines. These committees will continue to meet, and publish their reports and analyses, such as presented in this year's report. The MASC as a whole needs to continue meeting and reporting to the community, and to help individual countries satisfy the needs of their scientists and funding agencies. The goal of understanding the function of all *Arabidopsis* genes by 2010 remains an audacious goal. At this point, we may have an understanding of at least some function for no more than 10-20% of the ca. 30,000 genes in the *Arabidopsis* genome.

Clearly, we are standing at the first rung of a very high ladder. There are only seven years left until 2010, and for us to glean an understanding of tens of thousands of genes in this period will require a MAJOR acceleration of global research efforts on this tiny plant.

INTRODUCTION TO *ARABIDOPSIS*

Humans depend on plants in nearly every aspect of life. We use plants for food, both directly and as secondary consumers. We use plant structural components as building materials and textiles, and plant metabolites for their nutritional and medicinal properties and as industrial raw materials. Photosynthesis provides the biological and chemical energy that fuels our world and is responsible for the oxygen and carbon dioxide cycling that makes our very existence on Earth possible. **The importance of plants in our world cannot be overemphasized.**

Although these facts have been true throughout human history, gaining knowledge about the biology of plants has never been more important than at this moment. The population of the world is expanding rapidly: at 2.5 billion in 1950, the population has more than doubled to 6.3 billion today, and is estimated to reach the 7 billion mark in just ten years (US Census Bureau). It seems clear that to feed this growing population, world food production must be increased, especially in regions of the world with the greatest population density. Because the world's arable land is already utilized almost to its limit, it will be necessary to find new ways to improve crop yields, and to perform agricultural production in the most environmentally friendly fashion.

Large strides have been made in plant research in the last several years. Research has given us insight into the natural processes of disease resistance, response to environmental stresses and plant metabolism, to name just a few. We have also begun to understand the developmental processes, biochemistry, and physiology of many species of plants.

This research has provided tantalizing clues about a future in which we can utilize our knowledge of plant biology to make positive changes in plant species of economical importance. Possibilities include enhancing resistance to disease caused by insects, bacteria, viruses and parasitic pests; increasing tolerance to abiotic stresses, such as heat, drought and soil salinity; and achieving these improvements while decreasing dependence on expensive and harmful herbicides and pesticides. The amount of an important nutrient that is present at unhealthy or low levels in a crop can be increased, other nutrients introduced, or adverse components removed to enhance nutritional value. The net result will be plants that produce more, higher quality food and many other important resources for our growing population.

These goals cannot be accomplished until we have achieved a deep and thorough understanding of plant biology. We cannot hope to be able to use rational strategies to improve a plant until we know how it functions under normal conditions, how it responds to altered conditions, and how such a response affects the physiology of the entire organism. The task of achieving a comprehensive knowledge of the biology of even one plant seems daunting, indeed. However, it must be done.

As all properties of a living organism are determined by its genetic constitution through interaction with its environment, the starting point is to discover the structure and function of each gene of a flowering plant and determine its role in the control of the metabolic and developmental processes of the plant.

Arabidopsis: The Model Plant

Arabidopsis thaliana is a small dicotyledonous species, a member of the Brassicaceae or mustard family. Although closely related to agronomically important crop plants such as turnip,

cabbage, broccoli, and canola, *Arabidopsis* is not an economically important plant. Despite this, it has been the focus of intense genetic, biochemical and physiological study for over 40 years because of several traits that make it very desirable for laboratory study. As a photosynthetic organism, *Arabidopsis* requires only light, air, water and a few minerals to complete its life cycle. It has a fast life cycle, produces numerous self-progeny, has very limited space requirements, and is easily grown in a greenhouse or indoor growth chamber. It possesses a relatively small, genetically tractable genome that can be manipulated through genetic engineering more easily and rapidly than any other plant genome.

Arabidopsis, like all flowering plants, dehydrates and stores its progeny in seeds at ambient temperature for long periods of time. This fact, together with a facile method for creating gene knockout lines, has convinced many basic biologists that *Arabidopsis* may be the best model system for basic fundamental research in the biology of multicellular eukaryotes. A complete knockout collection of *Arabidopsis* seeds can be housed in a room no larger than a closet; to create and store a similar library of knockouts for mouse, flies and worms would be much more labor and space intensive. All together, these traits make *Arabidopsis* an ideal model organism for biological research and the species of choice for a large and growing community of scientists studying the biology of complex, multicellular organisms.

***Arabidopsis* versus plants of economic significance**

Why *Arabidopsis*? Why not concentrate our research efforts and resources on the species that will actually provide food for our world or products for industrial uses? To make the strides necessary to increase crop production in a relatively short time, we have to be able to move forward quickly and spend the available human and financial resources as efficiently as possible.

This is the advantage of a model system: an organism that is easily manipulated, genetically tractable, and about which much is already known. By studying the biology of *Arabidopsis* as the model plant, we can gain comprehensive knowledge of a complete plant. In the laboratory, *Arabidopsis* offers the ability to test hypotheses quickly and efficiently. With the knowledge we gain from this model plant thus established as a reference system, we can move forward with research and rapidly initiate improvements in plants of economic and cultural importance.

A tradition of *Arabidopsis* research

Arabidopsis has been the organism of choice for many plant biochemists, physiologists, developmental biologists and geneticists for several decades. In this time span, a great deal of knowledge has been gained about the biology of this flowering plant. With the completion of the *Arabidopsis* genome sequencing project, we now have in hand the sequence of the approximately 30,000 genes in its genome. An extensive toolkit for manipulation has been developed over the last 20 years, including efficient mutagenesis, facile transformation technology, and methods for detecting and isolating nucleic acids, proteins and metabolites. The many biological reagents that have been made available to the community have greatly facilitated efficient and rapid research progress. Ongoing research within the community has already resulted in a rudimentary working knowledge of many of the biochemical, physiological, and developmental processes of *Arabidopsis*.

Technological innovation and education

The availability of a broad base of knowledge about *Arabidopsis* and the previously developed research toolkit invites scientists to establish new techniques, develop new approaches, and test new concepts in *Arabidopsis* prior to their application in other species. The novel technologies made available not only continually increase the efficiency of research done in *Arabidopsis*, but expose researchers (most importantly young scientists) to the most up-to-date methods in plant research, which they can apply to other species as they move forward in their career. Furthermore, these techniques support a transition of biological research towards discovery biology, leading to the rapid gain of entirely novel information through the systematic use of multiparallel, high throughput analytical techniques coupled with sophisticated tools for data mining and analysis.

***Arabidopsis* research is the first step in an exciting future of plant improvement**

Much work remains to be done before the goal of complete knowledge of the biology of even one plant species comes to fruition. It is essential that the work leading to the achievement of this goal be done as quickly and efficiently as possible. When we have achieved this ambitious goal, we will have the power to predict experimental results and the ability to efficiently make the meaningful improvements in crop species that will lead to increased food production, environmentally friendly agricultural practices, new uses for plants, and even totally new plant-based industries. The most efficient way to gain this understanding is by exploiting the scientific and practical advantages of the model organism *Arabidopsis thaliana*.

International Cooperation

The Genome Project provided a platform for a whole new way of approaching scientific problems. It acknowledged from the outset that members of *Arabidopsis* research community are all working toward the same goal; it is therefore to the advantage of all to work in a cooperative manner. By setting forth a goal of international coordination and providing for this coordination by the creation of a multinational committee (the Multinational *Arabidopsis* Steering Committee), the Genome Project started and developed with a degree of international cooperation that had rarely been seen in the past. Indeed, the *Arabidopsis* genome sequencing project (*Arabidopsis* Genome Initiative - AGI) is widely regarded as a positive example of the progress that can be made when a research community works together to achieve a goal.

Looking back on the project thus far, it is clear that it is this spirit of cooperation that has allowed its success. As genome research enters the next phase of functional genomic research, we must take with us the lessons of the first ten years: international cooperation, coordination of efforts, and communication among the groups involved are essential. By minimizing duplication of efforts, removing obstacles for sharing of data and biological resources, and emphasizing the clear realization that all groups are working toward the same goal, we can foster a spirit of cooperation that will well serve the community, and eventually the world.

The Genome of Arabidopsis

In December of 2000, the *Arabidopsis* research community announced a major accomplishment: the completion of the genome sequence of a flowering plant. For the first time, we have in hand the sequence of all of the genes necessary for a plant to function, knowledge unprecedented in the history of science. Additionally, this sequence is freely available to every member of the scientific community.

Analysis of the sequence of the *Arabidopsis* genome tells us that the genome of a higher plant is similar in several important ways to the genome of other sequenced multicellular organisms. It also points out several important differences, which may not be too surprising, considering that plants differ in many important ways from animals whose genomes have been analyzed. Plants are autotrophic: they require only light, water, air and minerals to survive. They can therefore be expected to have genes that animals do not have, encoding the proteins and enzymes involved in plant-specific processes, including, but not limited to, the complex process of photosynthesis.

These two facts - that the genome of *Arabidopsis* is both highly similar and quite divergent from the genome of other sequenced, complex eukaryotes - highlight the value of *Arabidopsis* research, and especially functional genomics research using *Arabidopsis* as a model.

The extensive similarities between the sequence of *Arabidopsis* and that of other complex organisms means *Arabidopsis* research has the potential to lead to a greater understanding of broad biological questions. *Arabidopsis* has proven to be a fertile ground for answers to questions relating to development in complex, multicellular organisms; basic cellular processes, chromosome biology, and metabolism, and answers found here can be transferred to other species.

On the other hand, the differences between the genome of *Arabidopsis* and that of other organisms will prove valuable for investigations into plant-specific processes such as photosynthesis, plant-pathogen interactions, plant cell biology, and the adaptations necessary for sessile existence for a complex organism. Understanding of these and other questions will lead to the important advances in our understanding of and methods for improvement of crop plants so important to our future on this planet.

Finally, comparative genomics enabled by knowledge of the genome sequence of *Arabidopsis* will allow for elucidation of the evolutionary history of *Arabidopsis* and other plants. The sequence also gives us a basis for the discovery of key differences between *Arabidopsis* and other plant species, leading to a broader understanding of plant biology and to important pharmaceutical and biochemical discoveries.

PROGRESS OF THE PAST YEAR

In 2002, the international *Arabidopsis* research community set out goals for the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics project, and identified as its mission the determination of the function of every gene of a reference species in its cellular, organismal, and evolutionary context by the year 2010. The ultimate goal of the project was identified as a comprehensive understanding of the biology of a flowering plant, using *Arabidopsis* as an experimental model system.

The objectives identified for the scientific community over the course of the project were:

1. Development of an expanded genetic toolkit, including new technology development that enables individual scientists to conduct functional genomics research in *Arabidopsis*.
2. Whole-systems identification of gene function, including global analyses of gene expression, the plant proteome, metabolite dynamics, molecular interactions and comparative genomics.
3. Expansion of the role for bioinformatics.
4. Development of community and human resources.
5. Promotion of international cooperation.

Active participation in *Arabidopsis* functional genomics research by the community in the last year has led to progress in each of these priority areas. Reports addressing some of the areas of active work and progress can be found below.

The worldwide *Arabidopsis* community continues to grow. The number of registered users at TAIR, The *Arabidopsis* Information Resource (<http://arabidopsis.org>), has reached nearly 12,000 people affiliated with over 4,000 laboratories around the world. Clearly, this tiny weed has propagated itself into a favorite creature for scientists satisfying their intellectual curiosity all over the world.

Progress and Activities of the Multinational Arabidopsis Steering Committee

In 2002, the Multinational *Arabidopsis* Steering Committee (MASC) was active in the areas of establishment and maintenance of communication within the *Arabidopsis* functional genomics community; communication with and information availability to the *Arabidopsis* research community and the biological research community at large; and coordination of *Arabidopsis* functional genomics activities around the world.

Specifically, the MASC has met all of the short term goals identified at the outset of the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project, with positive results for the community.

A full-time coordinator was hired in 2002 with financial support from several MASC member countries. The role of the Coordinator has been to maintain communication and

coordination of effort both within the MASC and between the MASC and the *Arabidopsis* research community. The coordinator supervised the publication of a long-range plan for the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project in 2002 and established an internet homepage for MASC at the website of The *Arabidopsis* Information Resource (TAIR).

The MASC internet site established in 2002, available at URL http://www.arabidopsis.org/info/2010_projects/, contains project and resource information for scientists actively engaged in *Arabidopsis* functional genomics research as well as information for those seeking to learn about the progress of the Functional Genomics Project, the MASC, and the *Arabidopsis* research community in general. Users of the MASC homepage can search for genes being investigated by individual functional genomics projects, or for the projects themselves by name, PI, or gene. The expert staff at TAIR maintains the search capability and has been actively involved in getting the MASC site launched.

One of the many positive results of MASC's work in 2002 for the *Arabidopsis* research community was a growth in the communication within and throughout the community. The establishment of the website and the publication of our stated long-range goals for the functional genomics community increased the awareness level among *Arabidopsis* researchers and other biologists not only of the activities of the *Arabidopsis* functional genomics community, but also of the multinational and inclusive nature of the MASC and its efforts. There was increased interest from scientists around the world for participation in the MASC and in the establishment of *Arabidopsis* functional genomics research in countries not currently actively involved in this field. New contributors to the MASC include representatives from Argentina and Brazil, Austria, and the Nordic *Arabidopsis* Network. New interest in *Arabidopsis* research has come from Poland, other formerly Eastern European countries, and South Africa.

Despite the many new forms of electronic communication, we are all aware of the many social, cultural and political forces at work that strive to divide and separate us. *Arabidopsis* has provided a nice means for unifying plant scientists all over the world, and continues to provide an important motivation for helping to ensure the free exchange of information and materials over any border. The potential of a cooperative, communicative scientific community for breaking down international social and political barriers should not be underestimated.

As identified in the 2002 planning document, the on-going goals for the MASC within the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project include continuing to foster international collaboration and coordination of the Project; continuing to monitor the progress of the project toward its goals and actively reassessing both the project and its goals as needed; and the publication of periodic progress reports. The MASC has been actively involved in fulfilling these goals by holding annual meetings in conjunction with the International *Arabidopsis* Conference, and in 2002, by sponsoring a workshop during the Conference examining *Arabidopsis* functional genomics efforts around the world. Additionally, the practice of publishing annual progress reports, established during the Multinational Coordinated *Arabidopsis thaliana* Genome Research Project, has been reestablished.

In the summer of 2002, the 13th International Conference on *Arabidopsis* Research was held in Seville, Spain. The MASC annual meeting was held in conjunction with this Conference. During the meeting, it was decided that as a next step in coordination of International *Arabidopsis* research, and especially the ongoing worldwide functional genomics projects, the MASC would institute a system of **subcommittees**, each of which will track progress toward the goals outlined for the Functional Genomics community in the 2002 planning document. These

subcommittees are composed of members of the *Arabidopsis* community with expertise in each of five areas. Subsequently, because of overlap, two of the subcommittees merged their activities (Multiparallel Analytical Tools and Phenotype Analysis) and a single report is presented.

1. **Bioinformatics** – including genome annotation and pioneer proteins
2. **ORFeomics** – cDNAs and Clone-based Functional Proteomics
3. **Multiparallel Analytical Tools** – including whole-genome markers, microarrays, and phenotype analyses.
4. **Reverse Genetic Stocks**

Representatives to each of the subcommittees are encouraged to be in frequent contact with *Arabidopsis* colleagues in their country or region who are contributing to research in their field. In turn, each member of the *Arabidopsis* community is encouraged to be in contact with his or her MASC representative or subcommittee representative to communicate where his or her research fits into our community efforts and where he or she sees needs or new opportunities.

It was further decided during the MASC meeting that a letter should be sent to every member of the *Arabidopsis* research community, explaining the purpose of the MASC and inviting everyone to make use of the resources being made available for *Arabidopsis* research. Accordingly, such a letter was prepared by the Coordinator and distributed to every registered user of TAIR.

INITIAL REPORTS OF THE MASC SUBCOMMITTEES

Bioinformatics

Prepared by Chris Town, Chair, MASC Bioinformatics Subcommittee and Rebecca Joy, Coordinator for MASC

The MASC Bioinformatics subcommittee met in November of 2002. The main thrust of the discussion was a re-evaluation of goals for the *Arabidopsis* bioinformatics community, and an assessment of ways in which major bioinformatics outlets can benefit from and be a service to the functional genomics community.

Issues identified for the Bioinformatics community include the need for a centralized information source: what is the scope of the activities and datasets at the major centers and how should disparate pieces of functional genomics information be gathered into a "one-stop" resource for community? Secondly, criteria for assignment of gene function should be mutually agreed upon and clearly articulated. Wherever possible, ambiguous and/or overlapping terms such as "unknown protein," "hypothetical protein," and "putative protein" that are in use at different bioinformatics outlets should be replaced by more informative and uniform nomenclature. Gene ontology assignments will form part of this process. Thirdly, individual functional genomics projects are now creating "expert" databases – extensive data collections on a specific topic; should these be incorporated into "backbone" genomics databases, and if so, how? Finally, the bioinformatics community needs a mechanism for discovering the types of bioinformatics capacity and tools needed by the community, while at the same time, the bioinformatics community would like to learn what tools and capacity are being developed by the functional genomics projects.

In response to these issues, a new set of goals was identified for the *Arabidopsis* bioinformatics community. These goals center on the idea of communication - both between the various bioinformatics outlets and between the outlets and the people they serve, the world-wide community of *Arabidopsis* scientists.

On-going goals for the *Arabidopsis* Bioinformatics community:

- Establish and maintain connectivity between the major databases.
- Survey and compile a comprehensive list of functional genomic resources that is web-accessible, searchable and extensively hyperlinked.
- Define "unknown function;" establish parameters for assigning a function to a gene.
- Establish parameters for minimal data content for submission of expert data sets into backbone databases.
- Creation of "exit strategies" for functional genomics projects to plan for successful integration of expert database contents into backbone databases.
- Make community and funding agencies aware of need for exit strategy; encourage funding agencies to require an explicit exit strategy.
- Backbone genomics sites serve as a repository for output by projects.

- Keep *Arabidopsis* community at large informed about activities of Bioinformatics community.

Bioinformatics resources specifically serving the *Arabidopsis* research community:

- AGR at UK Cropnet (<http://ukcrop.net/agr/>)
- GABI-Info and GABI-Primary Database (links from <http://www.gabi.de>)
- Genoplante-Info (<http://genoplante-info.infobiogen.fr/>)
- Kazusa Dept of Plant Gene Research (<http://www.kazusa.or.jp/en/plant/>) (plus ESTs)
- MAtDB at MIPS (<http://mips.gsf.de/proj/thal/db/index.html>)
- NCBI (http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/map_search?chr=arabid.inf)
- RIKEN Genomic Sciences Center (<http://pfgweb.gsc.riken.go.jp/>) RIKEN Arabidopsis Genome Encyclopedia (RARGE) (<http://rarge.gsc.riken.go.jp/>)
- TAIR (<http://arabidopsis.org>)
- TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>)

cDNAs and Clone-Based Functional Proteomics (ORFeomics)

Prepared by Pierre Hilson, Chair, MASC cDNAs and Clone-Based Functional Proteomics (ORFeomics) Subcommittee

The following groups are focusing on the large-scale analysis of *Arabidopsis* cDNAs and/or their functional characterization.

RIKEN Genomic Sciences Center (Motoaki Seki, Kazuo Shinozaki)

Isolation and characterization of full-length cDNA sequences. Full-length cDNA sequencing. RIKEN clones are named RAFL clones or R clones. Most of the U clones of SSP are originally recloned RAFL cDNA inserts placed into pUNI vector. RAFL clones are now available from RIKEN Bioresource Center (BRC) for the entire community. (Seki M et al. (2002). Functional annotation of a full-length *Arabidopsis* cDNA collection. *Science* **296**:141-5)

<http://pfgweb.gsc.riken.go.jp/projects/raflcdna.html>; <http://rarge.gsc.riken.go.jp/>

SSP consortium (Joe Ecker, Ron Davis, Sakis Theologis)

Full-length cDNA clone sequencing, ORF cloning, transcript unit mapping with genome tiling arrays. As a result of the work of this consortium, thousands of cDNA clones have been deposited at ABRC and are immediately available to the entire community.

<http://signal.salk.edu/SSP/>

CERES and TIGR

Isolation and characterization of full-length cDNA sequences. (Haas BJ et al (2002). Full-length messenger RNA sequences greatly improve genome annotation. *Genome Biology* **3**: research0029.1-0029.12.)

Génoscope, Unité de Recherche en Génomique Végétale (URGV) and Invitrogen (Marcel Salanoubat)

A novel collection of full-length cDNA clones has been characterized and will be released shortly. This collection matches at least partially 11,500 genes. It provides information about roughly an additional 2,000 genes covered by new full-length cDNA sequences, 60% confirming pre-existing gene models and 40% correcting them. In addition, 165 genomic regions not previously annotated were detected with this novel cDNA collection.

Atome URGV (Claire Lurin, Ian Small)

ORF cloning based on the Génoscope collection

<http://www.evry.inra.fr/public/projects/Atome/index.html>

AtORFEUS (coordinator: Pierre Hilson)

ORF cloning coordinated between multiple European laboratories

<http://www.orfeome.org/orfweb/>

CESG (directors: John Markley, George Phillips)

Large-scale, genome-wide study of protein structure, especially those proteins with unknown function (X-ray crystallography and NMR spectroscopy).

<http://www.uwstructuralgenomics.org/goals.htm>

REGIA (coordinator: Javier Paz-Ares)

Transcription factor ORF collection, primarily used for yeast two-hybrid protein-protein interaction mapping (Paz-Ares et al (2002). REGIA, an EU project on functional genomics of transcription factors from *Arabidopsis thaliana*. *Comparative and Functional Genomics* **3**: 102-108)

As of today (Spring 2003), the community has full-length cDNA sequence information for approximately 15,000 unique *Arabidopsis* genes. Due to the effort of RIKEN GSC, over 13,000 RAFL cDNAs are now available from the RIKEN Bioresource Center.. Via the effort of the SSP consortium, over 10,000 ORFs will soon be available thru the ABRC, in vectors compatible with recombinational cloning, the majority of them in pUNI derivatives, others in Gateway(tm)-compatible plasmids. All SSP ORFs are in the closed configuration (with stop codon). Additional consortia have joined in similar efforts in the last year. For example, European laboratories, lead by the URGV group and coordinating their efforts in the framework of AtORFEUS, are building an ORF collection in the open configuration (no stop) in a Gateway(tm) entry vector. Other projects, such as REGIA and CESG, have chosen alternative formats dictated by the specific application in which the ORFs are generated and utilized in the project. Coordination between these major consortia remains a major goal for the future efforts of the MASC.

Multiparallel Analytical Tools & Phenotype Analyses

Prepared by Mike Beale, Chair, MASC Multiparallel Analytical Tools Subcommittee and Mary Lou Guerinot, Chair, MASC Functional Proteomics, Metabolomics, and Phenotype Analysis Subcommittee

One of the requirements to advance post-genomic biology is the development of multiparallel analytical tools to a level where whole system analysis of gene expression can be integrated with similar measurement of the proteome and metabolome.

Massive, high-throughput analysis of gene expression using DNA microarrays is now developing into a routine technique in many laboratories and the establishment of service facilities in several countries provides access to the technology for most *Arabidopsis* researchers. Considerable effort is being put into refining the technology to provide arrays that are fully representative of the *Arabidopsis* transcriptome or contain oligonucleotides specific for each gene in the genome. In Japan, the RIKEN GSC, a plant functional genomics group (<http://pfgweb.gsc.riken.go.jp/projects/>) is collecting more than 15,000 full-length cDNAs (RAFL clones) and sequencing more than 4,000 RAFL clones. In the USA, the SSP group (<http://signal.salk.edu/SSP/index.html>) in conjunction with the RIKEN plant functional genomics group (<http://pfgweb.gsc.riken.go.jp/projects/index.html>) are sequencing and verifying ORFs for 8,000 genes. The EU funded CATMA project (<http://www.catma.org>) has produced gene sequence tags representing about 70% coverage of the *Arabidopsis* genome. A new EU project CAGE (Compendium of *Arabidopsis* Gene Expression, <http://www.psb.rug.ac.be/CAGE/>) will develop the bioinformatics and experimental methodology, using the CATMA arrays in a large-scale standardized screen of gene expression in *Arabidopsis*. Finally, a large collaborative project, AtGenExpress, has been proposed by the German DFG's AFGN (<http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/AFGNHome.html>) project, the US NSF, RIKEN, GARNet, and several smaller groups that will combine resources to use microarray technology to profile gene expression patterns across developmental time and in response to hormones and stress. RIKEN GSC opens the RAFL cDNA microarray data from RARGE (<http://rarge.gsc.riken.go.jp/>). These projects and the recent commercial release of more extensive *Arabidopsis* genome microarrays are moving *Arabidopsis* genomics towards the mid-term goal, set out in June 2002, to be able to determine all mRNA expression profiles at the organ, cellular and subcellular levels. It is critical that scientists carrying out microarray experiments make their datasets available to the community in a timely fashion to allow comparisons across experiments.

The tools for global analysis of proteins rely on separation of proteins prior to identification by mass spectrometry of peptides derived from them by proteolytic digestion. A variety of large-scale and service projects have been initiated, e.g., GARNet (<http://www.york.ac.uk/res/garnet/garnet.htm>) and GABI-LAPP (<http://www.gabi.de>) projects. Tools for the cataloguing of proteins in plant or organ extracts are based on two-dimensional SDS-PAGE, capillary electrophoretic or HPLC separation before mass spectrometry. The technology is not able to quantitate all of the proteins in an organism, and research has concentrated on proteomics of organelles or comparative proteomics using labeling techniques such as Isotope-Coded Affinity Tags (ICAT) or Cy3.Cy5 dyes to focus only on differences in proteins/peptides in two samples. Systematic heterologous expression of all proteins and study of protein-protein interactions using two hybrid techniques are in their infancy. The goal of being able to routinely catalogue protein profiles has not yet been achieved although new angles

on the technology such as Multidimensional Protein Identification Technology (MudPIT) (see Koller et al. (2002). PNAS 99 (18):11969-74) have proven to be very rewarding when applied to organisms with full genome sequences. Despite these advances, we have only begun to chip away at the tip of the proteome iceberg.

Amongst the 'omics' technologies the ability to simultaneously quantify all of the metabolites at the cell, organ or plant level is the goal that may prove to be the most difficult to achieve. Traditional analytical techniques based on chromatographic separation of metabolites and subsequent identification such as GC-MS and LC-MS have played an important role in the opening developments in this area. However application of 'fingerprinting' to unchromatographed extracts by NMR and direct injection ESI-MS or FT-ICR-MS are promising methods that will play a role in mass screening of mutants and natural variants, highlighting areas of metabolism for more detailed analysis by targeted and high resolution techniques. Much *Arabidopsis* metabolomics is being pursued in the private sector. Service and large-scale activities in publicly funded *Arabidopsis* metabolomics are less prevalent than the other 'omics'. Nevertheless, the UK GARNet project contains an *Arabidopsis* metabolomics service, and activities in *Arabidopsis* metabolomics are beginning to emerge in the Netherlands (<http://www.biosystemsgenomics.nl/>) and in Sweden (<http://wcn.ntech.se/platforms/Metabolomics.htm>).

Reverse Genetic Stocks

Prepared by Bernd Weisshaar (bernd.weisshaar@uni-bielefeld.de) Chair, MASC Reverse Genetic Stocks Subcommittee

Fast and reliable access to mutants in selected genes is crucial for systematic reverse genetic approaches. The MASC Reverse Genetic Stocks subcommittee, which addresses issues of coordination and communication among the existing projects in this field, met at the Cold Spring Harbor meeting on Comparative Plant Genomics. The current status of existing resources was discussed, and a summary table collecting the existing (known) resources has been put together (see Table 1). With regard to access to the primary sequence information from flanking sequence tag (FST)-based projects, all providers of FST collections were encouraged to allow access to their sequence data on their web sites. In addition, the discussion demonstrated that a unification of the definitions of, for example, what constitutes a "potential FST gene hit" is required. Analysis of the current resources showed that coverage of the *A. thaliana* gene inventory with KO mutations is already impressive, but it also showed that the number of really useful FSTs, namely those that are likely to be a null mutation, is still not sufficient.

Recently, some progress has been made to allow users of reverse genetic resources a "one-stop" access to information on T-DNA insertions in a given gene. The Salk Institute Genomic Analysis Laboratory (SIGnAL) has integrated GABI-Kat and FLAGdb T-DNA insertion sequences into their T-DNA express database. As a result, a quite comprehensive collection of sequence-indexed T-DNA insertion mutants can be searched at a single location on the basis of FST sequence information.

To complement the efforts to saturate the *A. thaliana* genome with addressable mutations, other projects are under way to systematically set up collections of RNAi lines that cover the

genome. Also, projects based on TILLING are underway to allow access additional mutations, including change-of-function alleles of a given gene. Finally, the combination of all existing resources significantly increases our chance to obtain plants containing the mutation(s) and alleles we need to find answers to the biological questions that interest us.

Table 1: Worldwide Arabidopsis Reverse Genetic Stocks

Project	Ecotype	Project Goal
AGRIKOLA – RNAi http://www.agrikola.org/	Col	1. Hairpin constructs for 20-25,000 genes in constitutive and inducible promoters (2 collections) 2. 5,000 of these used to make transgenic RNAi lines
Amasino-Sussman 2010 Project	Col	50,000 Launchpad lines with cre/lox for deletions, Ds for attacking tandem genes
CSHL http://atidb.cshl.org/	Ler	30,000 Ds gene/enhancer trap lines
Ecker 2010 Project http://signal.salk.edu/about.html	Col	120,000 TDNA lines with flanking sequence
FST (INRA-Versailles and URGV-Evry) http://flagdb-genoplante-info.infobiogen.fr/projects/fst/	WS	35,000 FSTs
GABI-Kat http://www.mpiz-koeln.mpg.de/GABI-Kat/	Col	78,000 lines (70K T-DNA, 8K ZIGIA)
GARNet Project/ EU-EXOTIC http://atidb.cshl.org/	Col	27,000 Ds/Spm lines, expecting 5,000 KOs
GARNet Project/ EU-EXOTIC http://atidb.cshl.org/	Ler	30,000 Ds Gene-trap lines
RIKEN http://pfgweb.gsc.riken.go.jp/ , http://rarge.gsc.riken.go.jp/	No-0	15,000 Transposon (Ac/Ds) lines
RIKEN http://pfgweb.gsc.riken.go.jp/	Col	60,000 Activation trap lines
TMRI SAIL lines (formerly GARLIC lines) http://www.tmri.org	Col	100,000 TDNA
UK- Transposon lines http://atidb.cshl.org/	Ler	5,000 Activation trap lines
Wisconsin Knock-Out Project http://www.biotech.wisc.edu/Arabidopsis/	WS	130,000 TDNA lines

^AMTA for liability and responsibility for the care of the transgenic material

^BMTA allows distribution to third parties but not sale of material

^CCDSi = Coding Sequence including introns

Current Status	Available	Restrictions
Begun 11/2002	none yet; plasmids will go to ABRC; seeds to NASC	MTA through Invitrogen; no restrictions for academic use
50,000 lines created, not sequenced	none yet	none
~15,000 sequenced	all through CSHL	MTA; disclaimer, no IP restrictions
120,276 done	All sequences online, seeds at ABRC	None
30,000	12,300 from INRA Versailles	MTA signed at each order; no IP strings ^A , 200 Euro/line
78,000 lines	31,734 with genome hits, 7,599 gene hits (in CDSi ^C)	MTA signed at each order; no IP strings ^{A,B} , 500 Euro/confirmed line
25,000 sequenced	15,000 through NASC, require bulking	None
30,000 made, 5,500 sequenced	4,000 through NASC, require bulking	None; some lines will remain inside a Euro consortium until the end of the project, 9/2003
10,000 collected, 10,000 sequenced	1,000 deposited to RIKEN BRC (5,000 more in 2003)	MTA; includes IP restrictions
50,000 collected, 1,000 seq	none yet	MTA; includes IP restrictions
100,000 collected, ~53,000 sequenced	all through Syngenta	MTA; no 3rd party transfer
500 sequenced	500 through NASC, require bulking	None
130,000 lines	130,000 lines (no flanking sequence), seeds at ABRC	None; charge for screening (\$500 for 2 rounds)

THE INTERNATIONAL *ARABIDOPSIS* FUNCTIONAL GENOMICS COMMUNITY

Argentina

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

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Several university-associated groups are actively engaged in *Arabidopsis* research in Argentina. Funding for *Arabidopsis* research is available from the organizations listed below.

- Analysis of transcriptome in plant-pathogen interactions: plant genes required for susceptibility to fungal infection.
Malena Alvarez (malena@dqb.fcq.unc.edu.ar)
URL: <http://www.fcq.unc.edu.ar/ciquibic>
- The genetic network involved in plant responses to the light environment, analysis of transcriptome in phytochrome and cryptochrome mutants.
Jorge J. Casal (casal@ifeva.edu.ar)
URL: <http://www.ifeva.edu.ar/staff/perpages/casal.htm>
- Cytochrome c, cytochrome oxidase subunit 5b and other genes involved in respiration
Daniel H. Gonzalez (dhgonza@fcb.unl.edu.ar)
- Role of senescence associated genes in the formation of lytic vacuoles during senescence.
Juan José Guiamet (jguiamet@museo.fcym.unlp.edu.ar)
- Genes involved in Potassium and Sodium transport
Guillermo E. Santa-Maria (gsantama@pop.unsam.edu.ar)
- Regulatory genes involved in the control of transcription of genes of the photosynthetic antenna
Roberto J. Staneloni (RStaneloni@Leloir.org.ar)
- Identification of new components of the antioxidant response in higher plants by transcriptomic and functional analyses of oxidative stress-regulated genes in *Arabidopsis*
Estela M. Valle (evalle@arnet.com.ar)

The main sources of financial support for *Arabidopsis* research are:

- 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/>
- Fundacion Antorchas (Argentina) <http://www.fundantorchas.retina.ar/>

Australia & New Zealand

Australia has a strong tradition in plant scientific research. Many institutions, including the Plant Industry Division of the Commonwealth Scientific and Industrial Research Organisation (CSIRO), the major Universities and private enterprise are engaged in *Arabidopsis* Functional Genomics work ranging from individual projects to international collaborations through to major resource development. Funding is mainly available through the Australian Research Council's (ARC's) Discovery and Linkage Grant Schemes and the Grains Research and Development Corporation of Australia (GRDC).

Researchers in all Australian States and the Capital Territory now use *Arabidopsis* functional genomics approaches. Projects are generally highly focused, but increasingly involve international collaborators. Canberra, Australia's capital city, remains a major node for *Arabidopsis* research activity. Together, CSIRO's Division of Plant Industry, the Australian National University (ANU), and CAMBIA, is a formidable unit of fundamental, industrial and application-driven research.

The Australian Centre for Plant Functional Genomics is a major initiative announced in 2001, and now underway at the University of Adelaide. Established jointly by the ARC and the GRDC, the Centre's objective is to contribute to ensuring that Australia remains internationally competitive in plant science research. Its current focus, however, is on major crop plants, with little emphasis on *Arabidopsis*.

New Zealand has a small population but is nevertheless home to several *Arabidopsis* research programs. Increasing numbers of New Zealand plant scientists are incorporating *Arabidopsis thaliana* into their research, and at least six groups 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. Geographically, *Arabidopsis* research seems to be concentrated in three regions: in the North Island cities of Auckland and Palmerston North and at the University of Otago in Dunedin, on the South Island. In addition to the Universities, research programs are carried out at the Government-owned Crown Research Institutes, including Horticulture and Food Research Institute of New Zealand (HortResearch) and the New Zealand Institute for Crop & Food Research Limited (Crop & Food Research).

The horticultural industry is a big part of the New Zealand economy and, reflecting this, much of the *Arabidopsis* research impinges on reproductive development and fruiting. Other functional genomics programs include work on a magnesium transporter gene family and a recently initiated study on the role and function of carboxylesterases.

Austria

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Recent years have seen major changes in the development of molecular biology research facilities in Austria. One of the hot spots of constant change is the Vienna BioCenter, a newly established science campus close to the city center. In addition to several smaller biomedical companies, the Vienna BioCenter has become home of several research institutes of the University of Vienna, the Academy of Sciences and the pharmaceutical company Böhringer-Ingelheim. These developments spurred the government, the local authorities and the University of Vienna to concentrate the plant molecular research groups of the Inst. of Botany, Inst. of Microbiology and Genetics, Inst. of Biochemistry and Mol. Cell Biology, and the Inst. of Medical Biochemistry at the PMZ (Pflanzen Molekularbiologie Zentrum). The PMZ is presently built and expected to open in early 2004. Directly adjacent to the PMZ, the Austrian Academy of Sciences is establishing two new institutes: the Gregor-Mendel-Institute of Molecular Plant Sciences (GMI) and the Institute of Molecular Biotechnology (IMBA). Whereas the IMBA will concentrate on generating knowledge with the aim to ultimately cure major human diseases, the role of the GMI is a basic understanding of how plants work. Building of both institutes has just begun and their opening is scheduled for 2005. These new developments considerably add value to the research potential of Austria and provide the necessary critical mass for starting a coordinated thematic program on *Arabidopsis* biology.

It is the intention of the Austrian Platform of *Arabidopsis* Research (APAR) consortium to function as a Research Platform for coordinating and promoting science on *Arabidopsis* in Austria. The activities of APAR are tightly linked to several programmes of the European Union and the world-wide coordination efforts by MASC. Additional Austrian project partners will be incorporated into APAR in the future.

APAR currently comprises projects concerning molecular regulation of cytokinesis during plant development; molecular analysis of MAPK-mediated ethylene signaling in *Arabidopsis thaliana*; analysis of glycogen synthase kinase/shaggy-like kinases; novel aspects of salt stress signaling in plants; specificity and functional analysis of a PP2C protein phosphatase gene subfamily; calcium-dependent protein kinases in *Arabidopsis* signal transduction; and the functional study of the Ku complex at *Arabidopsis* telomeres.

Additional activities on *Arabidopsis* research in Austria include projects examining structure-function relationships of ribonucleoproteins; signal transduction and cell cycle regulation; auxin and cytokinin; transport and cell differentiation; epigenetics; chromosome biology; genes involved in the reprogramming of microspores; and MAP kinase signal transduction in plants.

Funding for *Arabidopsis* research in Austria is available from FWF (basic research only) (<http://www.fwf.ac.at>), WWTF (Vienna region) (<http://www.wwtf.at>), BMBWK (<http://www.bmbwk.gv.at/>), and FFF (applied research) (<http://www.fff.at/>).

Canada

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Arabidopsis functional genomics efforts are ongoing at several major institutions in Canada.

The *Arabidopsis* Research Group (ARG) at the University of Toronto, which includes eight research groups housed out of the Department of Botany, was originally established to provide resources and expertise for the *Arabidopsis* community in Canada. These programs are jointly funded through the Ontario Genomics Initiative (OGI), Genome Canada, the National Science and Engineering Research Council (NSERC) and by private industry. All resources and data will be made publicly available through various databases and international stock centers. Contacts for each program are listed or the ARG program director Dr. John Coleman can be reached directly at coleman@botany.utoronto.ca.

The functional genomics program at the UBC includes participants from the Biotechnology Laboratory, Department of Botany and the Department of Plant Science, along others. The program has recently received diverse funding input in support of its programs, including CFI, NSERC, OTIP, FRBC, HFSP, Genome BC and Genome Canada. Select program elements include the exploitation of *Arabidopsis* as a model system for studying development, and the development of TILLing resources.

The recently implemented University of Saskatchewan program derives from activity initiated in late 1999, under the auspices of the NRC 'Genomics in Health and Agriculture Initiative' (GHI). The program was additionally funded by Genome Canada, the Saskatchewan-Canada Agri-Food Innovation Fund and, more recently, has linked to an NSF 2010 project concerned with the functional genomics of the Ubiquitin-Protein Ligase (E3) families in *Arabidopsis*. In addition, the US ask has supported a new Bioinformatics group that includes a research emphasis involving plant genomics and Systems Biology.

The ongoing program at the NRC Plant Biotechnology Institute continues to explore the interface between *Arabidopsis* functional genomics for its implication to *Brassica* crop improvement, with a new emphasis on food quality and secondary metabolism.

The Saskatoon Research Center of Agriculture Canada is conducting an active program designed to exploit *Arabidopsis* model system in support of genomics approaches to *Brassica* crop development. The program is funded by the Agriculture Canada Genomics Program, and is supplemented by recent support from Genome Canada. Program elements include genetic, physical and bioinformatics approaches to defining the relationship between the *Arabidopsis* and *Brassica* genomes and the development of an *Arabidopsis* activation-tagged T-DNA insert population.

China

http://www.arabidopsis.org/info/2010_projects/China.html

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This report briefly summarizes the research efforts made by the Chinese *Arabidopsis* community during 2002 as well as biological resources and funding currently available to *Arabidopsis* researchers in China.

In October 2002, an *Arabidopsis* Research Workshop, organized by Prof. Zhihong Xu, the President of Peking University and Vice President of the Chinese Academy of Sciences (CAS), was held in Shanghai. More than 30 researchers discussed and shared their results during the Workshop.

In 1999, a joint research team in Peking University and Chinese Agricultural University (Co-PIs: Zhangliang Chen, Li-Jia Qu and Weihua Wu) initiated a project for the generation of activation tagging lines by using a 35S enhancer construct. The project, funded for US\$ 3 millions by the Ministry of Science and Technology of China (MOST), was completed in 2002. Approximately 80,000 T-DNA lines (T1) have been generated by these researchers. In a separate effort, also funded by MOST for US\$ 350,000 (PI: Jianru Zuo, the Institute of Genetics and Developmental Biology, CAS), an inducible enhancer/promoter was used to generate activation tagging lines. The effort, aimed at the generation of 130,000 lines, is projected to be completed in 2005. Currently T1 seeds for 35,000 lines have been collected.

In 2002, the National Natural Science Foundation of China (NSFC) provided a grant of US\$1.5 millions for a major international collaborative project, aimed at the proteomic characterization and functional studies of approximate 1,600 *Arabidopsis* transcription factors. The project, headed by Xing-Wang Deng (the Peking University-Yale University-CAS Center for Plant Molecular Genetics and Agrobiotechnology; the PYC Center) and Yuxian Zhu (Peking University), will be completed in 2005.

Funding for *Arabidopsis* functional genomic research is available from MOST (www.most.gov.cn), NSFC (www.nsf.gov.cn), CAS (www.cashq.gov.cn) and other sources on a competitive basis.

European Union

The European Union has highlighted Functional Genomics approaches, including plant genomics, in previous "Framework" research funding programmes. In the current 5th Framework Programme (1998-2002) (FP5) a wide variety of fundamental and applied plant genomics research is supported under the 'specific programme' called 'Quality of Life and Management of Living Resources' - each project involves participation of several European countries. More information can be found by searching at http://db.cordis.lu/search/en/simple/EN_PROJ_simple.html. FP5 also currently supports about 30 young scientists with individual fellowships to carry out research on *Arabidopsis*. The following list illustrates some of the on-going funded research projects involving *Arabidopsis* (funding more than 40 million):

Molecular genetic analysis of transcription factors controlling seed maturation in *Arabidopsis thaliana*
Functional analysis of promoter sequences elements conserved between gibberellin 20-oxidase genes of *Arabidopsis* implicated in the regulation of GA biosynthesis
Homeotic-like conversions and expression of floral genes in alloplasmic, male sterile rapeseed lines.
Characterisation of BROMO, a respiratory burst oxidase in the development of root hair cells of *Arabidopsis*
Integrative plant biology: from genomes to development and plant physiology
New methodologies for assessing the potential of unintended effects in genetically modified food crops
Regulatory gene initiative in *Arabidopsis*
Exon trapping insert consortium
Controlling fatty acid breakdown in order to produce viable oilseeds with increased yields of novel oils
Enzyme discovery in hybrid aspen for fibre engineering
Associomics of Membrane Proteins in two Model Organisms, Yeast and *Arabidopsis*
Growth, vigour, environment - molecular breeding for plant growth and yield
European plant genome database network
Natural variation in *Arabidopsis thaliana*: resources for functional analysis
Development of systems to improve phytoremediation of metal contaminated soils through improved phytoaccumulation
Natural oxylipins and defence in ornamentals
Regulation of osmotolerance molecular breeding for improvement of plant drought, salt and cold stress tolerance
Compendium of *Arabidopsis* Gene Expression
Arabidopsis Genomic RNA Interference Knock-out Line Analysis
Functional analysis of *constans* and of related *Arabidopsis* transcription factors
Genes and proteins of meiosis in *Arabidopsis* and *Brassica*
Potentiation of plant defense responses during biocontrol bacteria-mediated induced systemic resistance in *Arabidopsis*
Functional analysis of a new class of MADS box genes in *Arabidopsis*
Integrated structural, functional and comparative genomics of the model legume *Medicago truncatula*
Upgrading of sugar beet pectins by enzymatic modification and molecular farming
Genetic determinism of maritime pine pulp and paper properties
Homologous recombination in plants

The 6th Framework Programme (2002-2006) is now well underway (see <http://fp6.cordis.lu/fp6/home.cfm>). Thematic areas in FP6 include Life sciences, genomics and biotechnology for health; Information society technologies; Nanotechnologies and nanosciences, knowledge-based multifunctional materials and new production processes and devices; Aeronautics and space; Food quality and safety; Sustainable development, global change and ecosystems; and Citizens and governance in a knowledge-based society. Further individual research fellowships are available as well.

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The major source of *Arabidopsis* Functional Genomics project funding in France is Génoplante (<http://www.genoplante.org/>), a joint venture between public funding agencies (INRA, CNRS, CIRAD, IRD) and several French Agbiotech companies (Biogemma, Aventis CropScience, Bioplante).

Génoplante has joined forces with GABI, a similar German initiative, and several joint projects are being funded.

The Génoplante-Info database (<http://genoplante-info.infobiogen.fr/>) contains data from several *Arabidopsis* projects including FLAGdb, the FST database; PlantGene and GeneFarm, *Arabidopsis* gene annotation projects; ATOME, an ORFeome project; EST, SAGE and microarray data on transcription profiles.

Génoplante-funded programmes

- FLAGdb++, an *Arabidopsis* genomics database including an inventory of flanking sequence tags from the Versailles *Arabidopsis* T-DNA collection (<http://genoplante-info.infobiogen.fr/FLAGdb/>)
- CATMA, complete *Arabidopsis thaliana* microarray (<http://www.CATMA.org/>) (Programme involving several EEC countries and funded by Génoplante in France)
- ATOME: An *Arabidopsis* ORFeome (<http://www.evry.inra.fr/public/projects/Atome/index.html>)
- Analysis of the proteome of *Arabidopsis* (Contacts: Jacques Joyard, jjoyard@cea.fr and Michel Rossignol, rossignol@ensam.inra.fr)
- Metabolomics: several projects are starting that will analyse levels of various metabolites or protein co-factors in *Arabidopsis* mutants (The *Arabidopsis* metabolome by NMR and mass spectroscopy, R. Bligny, CEA, Grenoble; Cytochrome P450s, D. Werck, IBMP, Strasbourg; Glycoproteins, V. Gomord, U. de Rouen; Cell wall polysaccharides, H. Höfte, INRA, Versailles)
- Numerous other projects aimed at functional analysis of specific genes or gene families.

Major Generic Non-Génoplante Programmes

- A panel of sequenced *Arabidopsis thaliana* full-length cDNAs (Contact: Marcel Salanoubat, salanou@genoscope.cns.fr)
- AraCORE: Analysis of genetic variability between *Arabidopsis thaliana* ecotypes. Several hundred accessions, thousands of recombinant inbred lines, constitution of an *Arabidopsis* core collection based on SNP genotyping (Contacts: David Bouchez, bouchez@versailles.inra.fr, Dominique Brunel, brunel@versailles.inra.fr and Georges Pelletier, pelletie@versailles.inra.fr)
- AGRİKOLA: *Arabidopsis* Genomic RNAi Knock-out Line Analysis. Construction of resources for systematic RNAi in *Arabidopsis*. (<http://www.agrikola.org/> contact: Ian Small small@evry.inra.fr)

Germany

http://www.arabidopsis.org/info/2010_projects/Germany.html

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Research on *Arabidopsis thaliana* has a long history in Germany and many individual research groups have been using this plant for analysis of specific topics in plant biology. Individual groups and German members of the European sequencing consortia contributed to the *Arabidopsis* genome sequencing project. Functional genomics of *Arabidopsis* research has recently received strong support in Germany through the implementation of two major research programs supported by the Ministry for Education and Research (BMBF) and the German Research Foundation (DFG).

The first of these programs is GABI, Genome Analysis in the plant biological System (<http://www.gabi.de/>). GABI was initiated in 1999 with the aims of strengthening plant genome research in Germany, establishing a network of competence including public and private research groups and corporations, enhancing international collaboration, and enhancing transfer of knowledge into application. GABI is funded by the German ministry for education and research (ca. 90% contribution) and private business companies (ca. 10% contribution); about 50% of funding provided by GABI is devoted to work on the model system *Arabidopsis thaliana*. The direct interlocking of research on the model organism(s) and the transfer of these results to crops plants is a fundamental principle of this initiative, and established rules regulate the disclosure and the use of research results obtained through GABI activities. Major recent contributions to the international efforts on *Arabidopsis* functional genomics by GABI projects are a large collection of sequence-indexed T-DNA insertion lines (GABI-KAT: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>), a database of membrane proteins (Aramemnon: <http://crombec.botanik.uni-koeln.de/index.html>), and extensive SNP information for 12 different *Arabidopsis* accessions (MASC-DB: <http://www.mpiz-koeln.mpg.de/masc/>). Maintenance and further development of MAtDB at MIPS <http://mips.gsf.de/proj/thal/> is also supported by GABI.

One of the major aims of GABI is the establishment of and support for international collaborations. A first step towards setting up direct collaborative efforts in Europe has been the establishment of joint research projects between the French plant genome program, Génoplante, and the German GABI initiative. This bilateral interaction is currently being expanded to a trilateral co-operation including the Spanish genome program.

The second major funding initiative for *Arabidopsis* functional genomics research is the *Arabidopsis* Functional Genomics Network (AFGN), which has been funded by the Deutsche Forschungsgemeinschaft (DFG). The AFGN, in close coordination with the 2010 Project of the United States National Science Foundation, has established a goal of elucidating the function of all *Arabidopsis* genes by the year 2010. In furtherance of this goal, *Arabidopsis* functional genomics projects were funded in 2001, and a further twenty projects in 2002. Information about the AFGN project can be found at <http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/AFGNHome.html>, and information about individual AFGN-funded projects can be found at <http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/Memebers.html>. AFGN has recently taken the lead in the setup of an international joint effort to establish a comprehensive genome-wide *Arabidopsis* transcriptome reference data base.

Italy

Italian research groups played an active role during the sequencing of the *Arabidopsis* genome, and many laboratories have now become actively involved in *Arabidopsis* functional genomics research. Funding provided by the Italian Ministry of Research (MIUR; www.miur.it), the Italian Space Agency, the European Space Agency, Institut Pasteur, and European Union Framework Programme 5 projects EXOTIC, REGIA and TF-Stress supports these labs in their efforts.

Research groups and the *Arabidopsis* projects with which they are involved:

Cella Group, Università di Pavia - Functional characterization of plant E2F factors and analysis of their role during cell cycle and development.

Cervone Group, University of Rome "La Sapienza" - Molecular mechanisms of plant defence and signal transduction in plant defence and development.

Chiurazzi Group, International Institute of Genetics and Biophysics, Consiglio Nazionale delle Ricerche (CNR), Naples - Discovery and characterization of genes involved in cellular DNA damage surveillance and repair functions.

Colombo/Kater Group, University of Milan - Ovule development in *Arabidopsis*; MADS box transcription factors; and TAF/TBP transcription factors.

Costantino Group, University of Rome "La Sapienza" - Characterization of three Dof transcription factor genes, *DAG1*, *DAG2*, and *AtBBF1*; Functional genomic analysis of *Arabidopsis* transcription factors with the EU REGIA consortium; *rold* and flower transition.

Migliaccio Group, CNR, Rome - Isolation and characterization of mutants disrupted in the gravitropic response, in auxin physiology, or in the basal process of circumnutation, including *AtRHA1*.

Mariotti Group, CNR, Rome - KNOX and NAC transcription factors

Morelli Group, National Research Institute for Food and Nutrition, Rome - Functional analysis of the HD-ZIP III family; Functional analysis of *GLABRA2*, a member of the HD-ZIP IV family.

Ruberti Group, IBPM-CNR, Rome - HD-Zip proteins; Functional genomic analysis of *Arabidopsis* transcription factors with the EU REGIA consortium and TF-stress project.

Soave Group, University of Milan: Study of proteins that interact with H-ATPases proton pumps, oxidative stresses and photoinhibition.

Tonelli Group, University of Milan: Development of a large-scale exon-trapping system; Functional analysis of MYB and NF-Y transcription factors in *Arabidopsis*.

Japan

http://www.arabidopsis.org/info/2010_projects/Japan.html

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For many years, Japan has been a worldwide leader in *Arabidopsis* science, and is continuing that tradition by moving forward into the world of functional genomics.

Programs for *Arabidopsis* functional genomics in Japan are ongoing at RIKEN Genomic Sciences Center Plant Functional Genomics Research Group (<http://pfgweb.gsc.riken.go.jp/>), RIKEN Plant Science Center (<http://www.psc.riken.go.jp/indexE.html>), Kazusa DNA Research Institute (<http://www.kazusa.or.jp/en/plant/>), and the CREST program of the Japan Science & Technology Corporation. Both RIKEN Genomic Sciences Center Plant Functional Genomics Research Group and Kazusa DNA Research Institute have ongoing bioinformatics programs as well.

Arabidopsis functional genomics research at RIKEN Genomic Sciences Center (GSC) includes the collection and phenotype analysis of Ds-tagged lines and collection of full-length cDNAs, the collection and phenotype analysis of activation tagging lines and full-length-cDNA-overexpressing transgenic lines, structural proteomics of plant regulatory proteins with novel structures, and transcriptome analysis of genes expression in response to both abiotic and biotic stress using RAFL full-length cDNA microarray analysis. Further work on reverse proteomics for functional analysis of in vitro expressed proteins is taking place at RIKEN GSC in collaboration with a group at Ehime University. The RIKEN Plant Science Center is active in phenotype analysis of Ds-tagged lines in collaboration with RIKEN GSC.

At the Kazusa DNA Research Institute, ongoing projects include the collection of T-DNA tagged lines, *Arabidopsis* and Lotus ESTs. A major project is the genomic sequencing of *Lotus*. Research on comparative genomics using *Arabidopsis* and *Brassica* is also taking place.

Several groups at other centers and universities are also involved in *Arabidopsis* functional genomics, with projects involving metabolic profiling in *Arabidopsis* at Chiba University, genome-wide analyses of both the two-component system and homeobox genes in *Arabidopsis* and rice at Nagoya University, genome-wide analysis of the cell wall genes at Tohoku University, and genome-wide analysis of transcription factor function using repressor domain at the Agency of Industrial Science & Technology in Tsukuba.

The RIKEN Bioresource Center started in 2002 collecting *Arabidopsis* resources produced in Japan, such as: full-length cDNAs; Ds tagging lines and Activation tagging lines produced at the RIKEN Genomic Sciences Center; various ecotypes and mutants from Sendai *Arabidopsis* Seed Stock Center (PI: Prof. Nobuharu Goto); and T-DNA tagging lines from Kazusa DNA Research Institute. The PI for the RIKEN Bioresource Center is Masatomo Kobayashi (kobayasi@rtc.riken.go.jp).

Funding opportunities for *Arabidopsis* functional genomics in Japan include CREST of Japan Science and Technology Corporation (<http://www.jst.go.jp/EN/>), the Program of Promotion of Basic Research Activities for Innovative Biosciences (<http://www.brain.go.jp/welcome-e.html>), and Grants-in Aids for Science of the Ministry of Education, Science, Culture and Sports.

The Netherlands

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In 2002 many previously established research groups continued active research using *Arabidopsis* studying a wide variety of topics from signal transduction to ecological questions. These groups are located at the universities of Amsterdam, Leiden, Nijmegen, Groningen Utrecht and Wageningen. An annual meeting of the so-called ARANED group is held every year and is attended by almost 100 participants.

Important for *Arabidopsis* research was extra funding provided by two genomics initiatives: one by NWO, the Dutch NSF and by a novel initiative of the Dutch government to promote genomics. In the latter program a large grant was awarded to the CBSG (Centre for Biosystems Genomics) headed by Prof WJ Stiekema (www.biosystemsgenomics.nl). This program aims at genomics research in tomato and potato but also has a strong *Arabidopsis* part, which provides additional funding for eight *Arabidopsis* groups. CBSG can be considered as the Dutch counterpart of other European programs such as Garnet, Gabi and Genoplante.

In addition NWO awarded a grant to the Wageningen Phytoinformatics group (also headed by Stiekema) dealing with bioinformatics issues related to plants. This group is also involved in the EU PLANET project that aims to develop and deliver a high level plant genome database for the systematic exploration of *Arabidopsis* and other plants.

Resources have been developed in ongoing research. The generation of new recombinant inbred line populations as part of the EU project natural (www.natural-eu.org) by Koornneef and co-workers and the generation of a large activation tag population using the En transposon within the EU EXOTIC project by Pereira (Wageningen) deserve mentioning. Dutch researchers (Angenent, Smeekens) also participate in the EU REGIA project looking at areas such as functional interdependences among transcriptional factors.

At Utrecht University a facility for *Arabidopsis* microarray analysis was set up (Weisbeek) which is linked to the EU CATMA and CAGE projects. One of the groups that will use this facility is the NWO funded project QTL-Express (coordinator Koornneef), which combines the analysis of natural variation with gene expression analysis and which includes 5 groups from Wageningen and Utrecht University. The same NWO genomics program also supports work on the role of chromatin (Bisseling coordinator).

Other EU projects having Dutch participants and that use *Arabidopsis* as a model are the EU APOTOOL project coordinated by de Vries (Wageningen) aimed at a deeper understanding of apomixis using *Arabidopsis* and to apply this knowledge as a novel tool in plant breeding. Hooykaas (Leiden) is involved in the EU PLANTREC project aiming at homologous recombination in plants.

Nordic Arabidopsis Network

All the Scandinavian countries have their own national research funding system. The Nordic Research Academy (NorFA, Nordisk Forskerutdanningsakademi) is funding the Nordic Network for groups who are involved in research with *Arabidopsis*. The Nordic *Arabidopsis* Network aims at keeping the groups in regular contact with each other and also offers small mobility grants for graduate students and post docs for short-time exchange between the groups.

Norway has initiated a national functional genomics program, FUGE. A Norwegian *Arabidopsis* Research Centre was created. Proteomics is performed in Oslo (UIO, Aalen lab), mutant/clone-collection at the Agricultural University (NLH, Rognli lab) and genomics in Trondheim (NTNU, Bones lab). The intention is that these three labs will serve the plant community in Norway (coordinated by Prof. Atle Bones, University of Trondheim).

In Sweden, the Umeå Plant Science Center (UPSC) has been created by moving plant groups from the Umeå University and Swedis University of Agricultural Sciences (Umeå) to the same building. Groups there have also received National Center of Excellence status and funding for functional genomics. The activities are mainly concentrated in trees (hybrid poplar), but *Arabidopsis* functional genomics is heavily utilized for the determination of the function of poplar genes that have a well-conserved counterpart in *Arabidopsis*. The UPSC is also a partner in the European CATMA-project. Groups in Uppsala University are involved in two EU-projects that aim in the elucidation of several transcription factors groups in *Arabidopsis*.

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. Groups are using genomics and proteomics to determine that plant defense and adaptation to biotic and abiotic stresses, and in the determination of the function for the proteins in chloroplast thylacoid membranes. The Finnish Plant Functional Genomics Research Program, mainly aiming at participating in the European functional genomics activities, was created spring 2003. The Finnish groups are also planning to join the European CATMA consortium.

The Icelandic investigators involved in *Arabidopsis* research have promoted *Arabidopsis thaliana* as a model research plant in recent years within the Icelandic research community. The Danish activities in *Arabidopsis* functional genomics are mainly concentrated on plant-pathogen interactions and plant defense responses and in photosynthesis.

United Kingdom

The major funding agency for plant science in the UK is the Biotechnology and Biological Science Research Council, BBSRC. The BBSRC is encouraging applications that use genomic technologies. To stimulate research in this area they have launched several initiatives. The BBSRC Exploiting Genomics Initiative now funds several *Arabidopsis* functional genomics projects. Other initiatives include metabolomics, proteomics, and e-science. More information about these can be found at <http://www.bbsrc.ac.uk/science/initiatives/>.

GARNet, the Genomic *Arabidopsis* Resource Network, has established infrastructure and expertise to provide reliable and efficient user-driven and publicly available functional genomics resources for *Arabidopsis* research. GARNet started in January 2000 with funding from the UK BBSRC (Biotechnology and Biological Sciences Research Council) for a three year period. Funding has recently been extended for a further three years to allow establishment of cost recovery systems from GARNet users. Information on GARNet is available via the GARNet web pages at <http://garnet.Arabidopsis.org.uk>. GARNet Resources include a transcriptome analysis service, a proteome analysis service, and a metabolite analysis service. Large insert clone libraries and a screening service are available from GeTCID (<http://www.jic.bbsrc.ac.uk/staff/ian-bancroft/arabIGF.htm>), and additional insertional mutagenesis populations generated in the first funding period are now available at NASC, The Nottingham *Arabidopsis* Stock Centre. Also available at NASC is a large database with results from GARNet Affymetrix experiments. Databases for proteomics and metabolomics are being developed.

In addition to the GARNet programme, many leading Universities and Institutes in the UK have established their own functional genomics resource centers.

NASC (<http://Arabidopsis.info/>) makes a wide range of material available to the Research Community such as seeds, DNA and database information. NASC has an agreement with the ABRC in that they both stock the same lines as safety copies and the onus of acquiring/curating/bulking/distribution is shared. Distribution from NASC alone is about 30,000 tubes of seed per year worldwide. Data resources made available from NASC include AGR, the *Arabidopsis* Genome Resource, and NASCArray, a database of Affymetrix GeneChip™ data.

Arabidopsis research groups in the UK are involved in several Europe-wide research initiatives. UK groups participate in European Union Framework Programme 5 research projects REGIA, EXOTIC, CONFAB, EDEN, GVE, PLANET, NATURAL and NONEMA. In addition, several genome-related applications have been submitted for Framework Programme 6 research projects. Finally, GARNet has teamed with GABI, the German plant functional genomics initiative, and Génoplante, the French functional genomics program to organize an annual international functional genomics meeting called PlantGEMs. In 2003, PlantGEMs will take place in York, UK (<http://www.york.ac.uk/res/garnet/plantgems2.htm>).

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The *Arabidopsis* research community in the United States is coordinated by the North American *Arabidopsis* Steering Committee, consisting of 6 elected members who serve two-year terms. Two members rotate off every year. Two members of the Committee represent U.S. on the Multinational *Arabidopsis* Steering Committee.

The National Science Foundation (NSF) initiated the *Arabidopsis* 2010 Project in fiscal year 2001. The program's goal is to determine the function of 25,000 genes in *Arabidopsis* by the year 2010. The current foci of the Project are to determine the function of a network of genes and to develop research tools and resources that enable the entire research community to participate in the 2010 activities. NSF requires that the 2010 awards be coordinated with similar activities world-wide, that the investigators post publicly the identity of genes under investigation, and that the outcome of the awards (data, information and materials) be made available to the public according to the timetable approved by NSF. Twenty-seven projects were funded under this program in 2001, and a further twenty projects in 2002. Abstracts can be found at http://www.arabidopsis.org/info/2010_projects/2010_Abstracts.html. The NSF expects to continue the *Arabidopsis* 2010 Project for 10 years, although the focus of the Project may change.

In addition to the *Arabidopsis* 2010 Project, other activities related to *Arabidopsis* research are supported by various programs at NSF, including individual research projects, workshops/meetings, information resources and informatics tools development, and the biological resource center, ABRC. The Center for Eukaryotic Structural Genomics (<http://www.uwstructuralgenomics.org/>) has been funded by the NIH to solve three-dimensional structures for many of the proteins of the *Arabidopsis* proteome.

NSF award information can be found at <https://www.fastlane.nsf.gov/a6/A6AwardSearch.htm>. The U.S. Department of Agriculture, the U.S. Department of Energy and the National Institutes of Health, especially the National Institutes of General Medical Sciences, support many research projects involving *Arabidopsis*, although they do not have a funding program specifically targeted to *Arabidopsis* research. NIH awards can be searched at http://commons.cit.nih.gov/crisp3/Crisp_Query.Generate_Screen

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