

THE INTERNATIONAL *ARABIDOPSIS* FUNCTIONAL GENOMICS COMMUNITY

Arabidopsis researchers world-wide have already embarked on the functional genomics phase. In this section, brief descriptions of various national and transnational projects will be provided. Detailed information about the major projects can be found organized by country and project type at the website being developed by the Multinational *Arabidopsis* Steering Committee (site can be found at TAIR, http://www.arabidopsis.org/info/2010_projects).

Australia and New Zealand

MASC Contact: Geoffrey Wasteneys (geoffw@rsbs.anu.edu.au)

Australia

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. There is as yet no large-scale coordinated program in Australia. CSIRO's Division of Plant Industry (<http://www.pi.csiro.au/HomePage.htm>) funds major programs in Plant Genomics. Otherwise, funding is mainly available through the Australian Research Council's (ARC's) Discovery and Linkage Grant Schemes (<http://www.arc.gov.au/>) and the Grains Research and Development Corporation of Australia (GRDC) (<http://www.grdc.com.au/>). In addition, many Australian-based *Arabidopsis* researchers receive funding from international Agbiotech companies or collaborate with overseas colleagues.

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 (<http://www.pi.csiro.au/HomePage.htm>), the Australian National University (ANU) (<http://www.anu.edu.au/>), and CAMBIA (<http://www.cambia.org.au/>), is a formidable unit of fundamental, industrial and application-driven research. Despite the disappointing non-renewal a few years ago of the ANU-based Cooperative Research Centre for Plant Science, and the subsequent closure of Groupe Limagrain's Australian arm (www.limagrain.com), plant science research in Canberra remains very active.

The Australian Centre for Plant Functional Genomics is a major initiative announced in 2001. 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. Where this new entity will be located and whether it will incorporate *Arabidopsis* into its research program remains to be determined.

Funding Bodies in Australia supporting *Arabidopsis* Functional Genomics Research

- Australian Research Council (<http://www.arc.gov.au/>)
- CSIRO Plant Industry (<http://www.csiro.au>)



- Grains Research and Development Corporation (<http://www.grdc.com.au/>)
- The Australian Centre for Plant Functional Genomics (<http://www.arc.gov.au/acpfg/default.htm>)
- The Australian Genome Research Facility (AGRF) (<http://www.agrf.org.au/>)

New Zealand

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 (http://www.rsnz.govt.nz/funding/marsden_fund/index.php#Marsden) and the New Zealand Foundation for Research, Science and Technology (<http://www.frst.govt.nz/>).

Canada

MASC Contacts:

Bill Crosby (bcrosby@gene.pbi.nrc.ca)

Peter McCourt (mccourt@botany.utoronto.ca)

Functional genomics projects at the University of Toronto

(Coleman, McCourt, Berleth, Cutler, Goring, Guttman, Christendat, Provar)

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. Ongoing programs include:

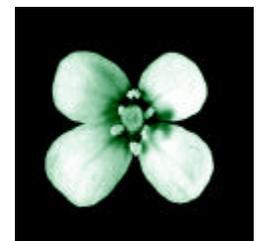
- Collection and characterization of random insertion GFP enhancer trap lines in *Arabidopsis* (Thomas Berleth)
- Collection and phenotypic characterization of inducible activation tagged lines in *Arabidopsis* (Peter McCourt)
- Bioinformatic analysis of transcript profiling and predictions of protein structure in *Arabidopsis* (Denish Christendat, Nick Provar)
- Functional genomics of protein localization in *Arabidopsis* (Sean Cutler)
- Functional genomics of receptor-like kinases in *Arabidopsis* (Daphne Goring)

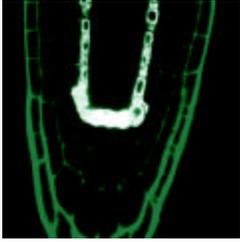
Functional Genomics Projects at the University of BC

(Bohlmann, Douglas, Ellis, Haughn, Li)

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 are listed below.

- The exploitation of *Arabidopsis* as a model system for studying development, including metabolism and deposition of compounds of importance to wood fiber production in Conifers and *Populus* species (Ellis, Douglas, Bohlmann)





- Development of TILLING resources, in collaboration with Dr. Steve Henikoff (Fred Hutchinson Cancer Research Centre, Univ. Washington, Seattle) in support of the joint Genome Canada project concerned with Abiotic Stress of Crops (Haughn)
- Molecular biology of SAR response pathways in *Arabidopsis* (Li)

Functional Genomics Projects at the NRC-PBI

(Crosby, Risseeuw)

The PBI 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*. The following is a summary of the structural and functional genomics sub-programs:

- A limited EST program for *Brassica napus* (40,000 runs)
- Development of a T-DNA disrupted population of *Arabidopsis* (in collaboration with J. Ecker, Salk Inst., La Jolla, CA)
- Development of a genomic amplicon microarray for known and predicted genes of *Arabidopsis*
- Development of a 2-hybrid 'map' for proteins involved in the E3 Ligase functions in *Arabidopsis*
- Bioinformatics program including HPC (cluster) support, gene annotation and data integration tools
- Investigation of the role of ASK genes in SCF function in *Arabidopsis* (Risseeuw)
- Molecular biology of pathogen response signaling in *Arabidopsis* (Fobert, Dépres)

Functional Genomics Projects at Agriculture Canada, Saskatoon (AAFC-SRC)

(Lydiate, Parkin)

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
- Targeted EST programs in *Brassica* and *Arabidopsis*, with a biological emphasis on cold adaptation and biotic stress response (fungal pathogenesis; insect herbivory)
- Development of an *Arabidopsis* activation-tagged T-DNA insert population
- Development of SAGE libraries and tools for analysis of gene expression in *Arabidopsis* and *Brassica* crop species

China

MASC Contacts:

JiaYang Li (jyli@genetics.ac.cn)

ZhangCai Yan (yanzc@mail.nsf.gov.cn)

The National Natural Science Foundation of China (NSFC) has set up a major project to support functional genomics research on Transcriptional Regulators in *Arabidopsis*. The NSFC maintains a website at <http://www.nsf.gov.cn/english/english.html>.

European Union

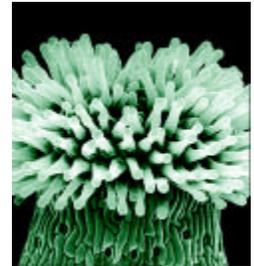
MASC contact: Bernard Mulligan (bernard.mulligan@cec.eu.int)

Information compiled by Karin van de Sande (kvd1@york.ac.uk)

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. The following list illustrates some of the on-going funded research projects involving *Arabidopsis* (funding more than €40 million):

- EXOTIC (Exon Trapping Insert Consortium)
- NATURAL (Natural variation in *Arabidopsis thaliana*: resources for functional analysis)
- REGIA (Regulatory Gene Initiative in *Arabidopsis*)
- ECCO (European cell cycle consortium)
- ASSOCIOPORT (Associomics of membrane proteins...in yeast and *Arabidopsis*)
- TF-STRESS (Transcription factors controlling plant responses to environmental stress conditions)
- CONFAB (Controlling Fatty Acid Breakdown in order to produce viable oilseeds with increased yields of novel oils)
- EDEN (Enzyme Discovery in hybrid aspen for fibre Engineering)
- GVE (Growth, Vigour, Environment)
- NONEMA (Making plants resistant to plant parasitic nematodes: no access - no feeding)
- GEMINI (Genetic determination of Maritime pine pulp and paper properties)
- EUROPECTIN (Upgrading sugarbeet pectins by enzymatic modification and molecular farming)
- GMO CARE (New methodologies for assessing the potential of unintended effects in genetically modified food crops)
- PLANET (European Plant genome Database Network)

FP5 also currently supports about 30 young scientists with individual fellowships to carry out research on *Arabidopsis*.



The EU Quality of Life Programme website can be found at: <http://www.cordis.lu/life/>. For a database of existing and past EU funded projects, please go to: <http://www.cordis.lu/en/home.html>

Planning of the 6th Framework Programme (2002-2006) is now well underway (see http://europa.eu.int/comm/research/fp6/index_en.html). Opportunities for plant science research will be available, for example, in several of the proposed 'priority thematic areas'. An invitation to submit expressions of interest for 'networks of excellence' and 'integrated projects' appropriate for the thematic priority areas of FP6 was recently published by the EU Commission (deadline of 7 June 2002). Further details are available on <http://www.cordis.lu/fp6/eoi-instruments>

France

MASC Contact: Ian Small (small@evry.inra.fr)

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 have recently been funded.

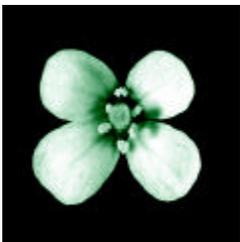
Non-Génoplante Programmes

- A panel of sequenced *Arabidopsis thaliana* full-length cDNAs (<http://www.evry.inra.fr/public/projects/cdna/cdna.html>)
- Analysis of genetic variability between *Arabidopsis thaliana* ecotypes (Contacts: David Bouchez, bouchez@versailles.inra.fr and Georges Pelletier, pelletie@versailles.inra.fr)
- AGRIKOLA: *Arabidopsis* Genomic RNAi Knock-out Line Analysis (<http://www.evry.inra.fr/public/projects/agrikola/agrikola.html>)

Génoplante-funded programmes

- FLAGdb/FST, an inventory of flanking sequence tags from the *Arabidopsis* T-DNA collection from Versailles (<http://flagdb-genoplante-info.infobiogen.fr/projects/fst/>)
- CATMA, complete *Arabidopsis thaliana* microarray (<http://jicbioinfo.bbsrc.ac.uk/CATMA/>) (Programme involving several EEC countries and funded by Génoplante in France)
- An *Arabidopsis* ORFeome (<http://www.evry.inra.fr/public/projects/orfeome/orfeome.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; Cytochromes P450, D. Werck, IBMP, Strasbourg; Glycoproteins, V. Gomord, U. de Rouen; Cell wall polysaccharides, H. Höfte, INRA, Versailles)

Génoplante-info database (<http://genoplante-info.infobiogen.fr/>) will contain data from the following *Arabidopsis* projects: FLAGdb, the FST database; GENEFARM,



a list of fully annotated *Arabidopsis* genome sequence data with other genomes; and AFPdb, the data produced by the proteome project.

Germany

MASC Contacts:

Thomas Altmann (altmann@mpimp-golm.mpg.de)

Gerd Jürgens (gerd.juergens@uni-tuebingen.de)

Research on *Arabidopsis thaliana* has a long history in Germany. Many individual German research groups have been using *Arabidopsis* for analysis of specific topics in plant biology. Furthermore, individual groups and German members of the European sequencing consortia contributed to the analysis of both its genome structure and its sequencing. Functional *Arabidopsis* genome analysis 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 aims and content of these two programs follow in the paragraphs below.

Genome Analysis in the Plant Biological System (GABI)

<http://www.gabi.de/>

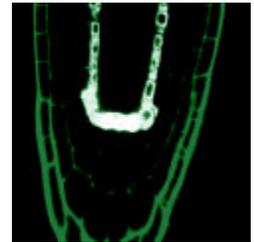
GABI Coordinator, Jens Freitag (freitag@mpimp-golm.mpg.de)

In 1999, the German plant genome program 'GABI' was initiated with the aim of strengthening plant genome research in Germany, establishing a network of competence (to include public and private research groups as well as business companies), enhancing international collaboration, and enhancing the transfer of knowledge into application. GABI is the acronym for "Genome Analysis in the plant biological System." Financial support for GABI is provided by the German ministry for education and research (about 90% contribution) and private business companies (about 10% contribution). Within the GABI initiative, about half of the 50 million Euro spent over a four-year period has been directed towards supporting work on *Arabidopsis thaliana*. In GABI, a one-programme-thesis is followed with respect to plant genome research. A fundamental principle of this initiative is to establish a seamless transfer of research results concerning the model organism(s) to real-life application in crop plants. Established rules (www.gabi.de/news/notifications/index_e.html) regulate the disclosure and use of research results obtained through GABI activities.

A major aim of GABI is the establishment and support of international co-operations. Developing a linking network of the various national research activities is of particular interest in Europe considering the current splintered structure of European research. A first step towards setting up direct collaborative efforts in Europe is to establish joint research projects between the French plant genome program, Génoplante and the German GABI initiative. Here, the model plant *Arabidopsis* serves as the front runner and provides a model for international cooperation. The first joint projects will start sometime this year.

Plant technology and resource developments:

- GABI - KAT (Cologne *Arabidopsis* T-DNA tagged lines) – Contact: Bernd Weishaar (weissaha@mpiz-koeln.mpg.de)
- GABI - LAPP (GABI Resource Centre: "Large-scale automated plant proteomics") – <http://www.molgen.mpg.de/~gabi/>



- The Resource Center and Primary Database in GABI – <http://www.rzpd.de/>

GABI Bioinformatics centers:

- GABI Primary Database (GABI-PD) – <http://gabi.rzpd.de/>
- GABI-Info – Werner Mewes (mewes@gsf.de) and Klaus F.X. Mayer (kmayer@gsf.de)

GABI-funded *Arabidopsis* research projects: <http://mips.gsf.de/proj/gabi/projects/index.html#arabidopsis>

Joint Génoplante - GABI projects:

- Sharing sequence data and computer resources on T-DNA transformants of *Arabidopsis thaliana* – Bernd Weishaar (weissha@mpiz-koeln.mpg.de) and Alain Lecharny (Alain.Lecharny@evry.inra.fr)
- Functional genomics of membrane transporters - A European genomics and proteomics resource for plant membrane transporter – Ulf Ingo Flügge (ui.fluegge@uni-koeln.de) and Jacques Joyard (Jjoyard@cea.fr)
- Cell wall: Interactions between components, identification and functional analysis of cell wall proteins and polysaccharide – Martin Steup (msteup@rz.uni-potsdam.de) and Rafael Pont-Lezica (lezica@smcv.ups-tlse.fr)
- Functional genomics of nitrogen utilisation and nitrogen signaling – Mark Stitt (stitt@mpimp-golm.mpg.de) and Françoise Vedele (vedele@versailles.inra.fr)
- A fifth joint French - German project is in discussion and will come up soon. The working title of this project is: "Evaluation of natural diversity in *Arabidopsis* accessions for traits of agronomic or basic importance". The coordinators of this project will be: Georges Pelletier (pelletie@versailles.inra.fr), Mark Stitt (stitt@mpimp-golm.mpg.de) and Thomas Altmann (altmann@mpimp-golm.mpg.de)

Arabidopsis Functional Genomics Network (AFGN)

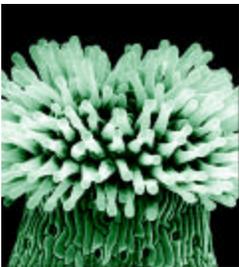
<http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/AFGNHome.html>

AFGN Coordinator: Lutz Nover (nover@cellbiology.uni-frankfurt.de)

In addition to the GABI program funded by the BMBF, another initiative discussed a year ago has attracted attention in Germany. The Deutsche Forschungsgemeinschaft (DFG) - German Research Foundation – is coordinating with the US National Science Foundation (NSF) to support projects on *Arabidopsis* functional genome analysis. AFGN, the *Arabidopsis* Functional Genomics Network, has been established in order to achieve the enormous goal of elucidating the function of all *Arabidopsis* genes within the next ten years. This will undoubtedly only be possible if additional programmes in other countries also participate.

Information about AFGN-funded projects:

<http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/Memebers.html>



Italy

MASC Contact: Fernando Migliaccio (fernando.migliaccio@milib.cnr.it)

Groups involved in *Arabidopsis* functional genomics research in Italy:

Chiurazzi Group (chiurazzi@iigb.cnr.it)

- Investigation into the possibility that the mechanism controlling nodule development in legumes might be derived from processes common to all plants.

Costantino Group (paolo.costantino@uniroma1.it)

- Dof proteins – Dr. Paola Vittorioso (paola.vittorioso@uniroma1.it)
- Functional genomic analysis of *Arabidopsis* transcription factors with the REGIA network of the EU Framework 5 – Dr. Paola Vittorioso (paola.vittorioso@uniroma1.it)
- *roLD* and flower transition – Dr. Maurizio Trovato (maurizio.trovato@uniroma1.it)

Funding from the EU FP5 Programme REGIA project, Ministry of Research grants, and Institut Pasteur -Fondazione Cenci Bolognetti grant.

Marmioli Group (marmirol@ipruniv.cce.unipr.it)

- Isolation of mutants showing resistance to heavy metals from T-DNA tagged collections

Migliaccio Group (fernando.migliaccio@milib.cnr.it)

- Investigations into the process of gravitropism and auxin physiology

Funding from the European Space Agency (ESA) and the Italian Space Agency (ASI).

Morelli Group (morelli@inn.ingrm.it)

- Functional analysis of the HD-ZIP III family – Dr. Simona Baima (baima@inran.it)
- Functional analysis of the GLABRA2 (HD-ZIP IV family) – Dr. Renato Rodrigues Pousada (pousada@inran.it)

Funding from Ministry of Research grants.

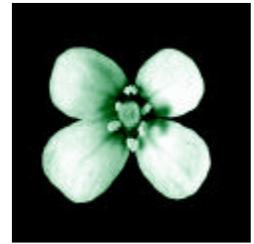
Ruberti Group (ida.ruberti@uniroma1.it)

- HD-Zip proteins – Dr. Monica Carabelli (monica.carabelli@uniroma1.it) and Dr. Giovanna Sessa (giovanna.sessa@uniroma1.it)
- Functional genomic analysis of *Arabidopsis* transcription factors, with the REGIA network of the EU Framework 5 – Dr. Monica Carabelli (monica.carabelli@uniroma1.it) and Dr. Giovanna Sessa (giovanna.sessa@uniroma1.it)

Funding from the EU FP5 Programme REGIA project, the EU FP5 Programme TF-stress project, and Ministry of Research grants.

Soave Group (carlo.soave@unimi.it)

- Study of proteins that interact with H-ATPases proton pumps



- Isolation of *Arabidopsis* mutants altered in the sensitivity to the photoinhibition
- Isolation of knock-out mutants altered in the active oxygen scavenging processes, in the sensitivity to UV-B radiation

Tonelli Group (chiara.tonelli@unimi.it)

- Large-scale Exon-trapping System – Dr. Massimo Galbiati (massimo.galbiati@unimi.it)
- Functional analysis of MYB and NF-Y transcription factors in *Arabidopsis* – Dr. Katia Petroni (katia.petroni@unimi.it)

Funding from the EU FP5 Programme, Exotic Project, the EU FP5 Programme, REGIA Project, and the Italian Ministry of University and Research.

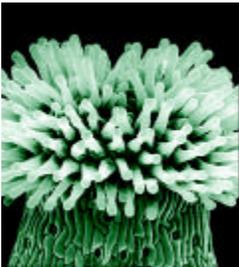
Japan

MASC Contact: Kazuo Shinozaki (sinozaki@rtc.riken.go.jp)

Arabidopsis Functional Genomics efforts in Japan:

- Collection and phenotype analysis of Ds transposon-tagged lines with the goal of making a library of phenotypes, and collection of full-length cDNAs at RIKEN Genomic Sciences Center (Contacts: Kazuo Shinozaki, sinozaki@rtc.riken.go.jp and Motoaki Seki, mseki@rtc.riken.go.jp)
- The Functional Genomics Research Group of RIKEN Genomic Sciences Center, in collaboration with the *Arabidopsis* SPP Group of the United States (<http://sequence-www.stanford.edu/ara/SPP.html>), have made about 8,000 sequenced, full-length cDNAs publicly available through the RIKEN Bioresource Center (Contact: Masatomo Kobayashi, kobayasi@rtc.riken.go.jp)
- Collaborating with the RIKEN group on the phenotypic analysis project is the group of Kiyotaka Okada at the RIKEN Plant Science Center (Contact: Kiyotaka Okada, Kiyoko@ok-lab.bot.kyoto-u.ac.jp)
- Collection of activation tagging lines at RIKEN Genome Science Center (Contact: Minami Matsui, minami@postman.riken.go.jp)
- Genome-wide analysis of the cell wall genes (Contact Kazuhiko Nishitani, nishitan@mail.cc.tohoku.ac.jp)
- Analysis of the Homeo-box genes of *Arabidopsis* and rice (Contact Makoto Matsuoka, makoto@nuagr1.agr.nagoya-u.ac.jp)
- Collection of T-DNA tagged lines created by the Kazusa group, *Arabidopsis* and Lotus ESTs (Contact Satoshi Tabata, tabata@kazusa.or.jp)
- Distribution and Data accumulation of *Arabidopsis* cDNA arrays (Contact JCAA, Japan *Arabidopsis* Array Consortium@isize.egroups.co.jp)

The RIKEN Bioresource Center started in 2002 to collect *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 Mobuharu 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). For distribution and data accumulation of *Arabidopsis* cDNA arrays, contact the JCAA (Japan *Arabidopsis* Array Consortium@isize.egroups.co.jp).



United Kingdom

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Ian Furner (ijf@mole.bio.cam.ac.uk)
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Sean May (arabidopsis@nottingham.ac.uk)
Compiled by Karin van de Sande

GARNet, the Genomic Arabidopsis Resource Network (<http://garnet.arabidopsis.org.uk>)

GARNet is establishing the 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. The services will move onto a cost recovery basis when BBSRC funding is finished. All GARNet services and resources are publicly available and data created using the GARNet resources will be made publicly available via various databases designed and held at the Nottingham *Arabidopsis* Stock Centre (AGR, NTP) and the The John Innes Centre (ATIdb).

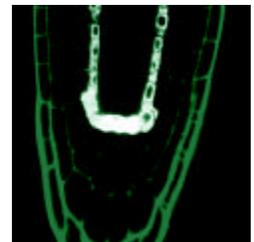
Services available at GARNet include:

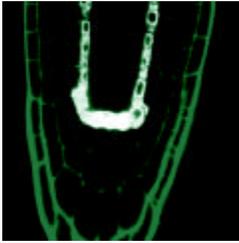
- Transcriptome analysis service (using GSTs from CATMA, <http://jic-bioinfo.bbsrc.ac.uk/CATMA>) – Sean May (arabidopsis@nottingham.ac.uk), GARNet is also taking part in, and funding the UK part of, the CATMA project, aiming at creating a Complete Arabidopsis Transcriptome Micro Array – Jim Benyon (jim.benyon@hri.ac.uk) and Martin Trick (martin.trick@bbsrc.ac.uk)
- Proteome analysis service – Paul Dupree (p.dupree@bioc.cam.ac.uk) and Kathryn Lilley (ksl23@cam.ac.uk)
- Metabolite analysis – Mike Beale (mike.beale@bbsrc.ac.uk)
- Tools for forward and reverse genetics:
 - dSPm line generation – Jonathan Jones (jonathan.jones@bbsrc.ac.uk)
 - SINS (Sequence of INsertion Sites) Database (<http://www.jic.bbsrc.ac.uk/staff/michael-bevan/atis/index.htm>) – Mike Bevan (michael.bevan@bbsrc.ac.uk), Jonathan Jones (jonathan.jones@bbsrc.ac.uk), and Jonathan Clarke (jonathan.clarke@bbsrc.ac.uk)
 - GeTCID (Gene Transfer Clone Identification and Distribution service) – Ian Bancroft (ian.bancroft@bbsrc.ac.uk)
- Bioinformatics resources include databases for the proteomics, metabolomics and transcriptomics data that are being developed and held at NASC

The BBSRC Exploiting Genomics Initiative

The BBSRC launched a targeted initiative to allow researchers in the UK to assemble consortia to use Functional Genomics approaches to tackle their research priorities. Below are the plant-related projects funded in this programme.

- Functional genomics of shoot meristem dormancy (Leyser, H. M. O., M. Holdsworth, and M. M. Campbell)





- Exploiting genomics to make glycosidic bonds in vitro and metabolic engineering in vivo (Bowles, D.J., G. Davies, R. Edwards, B. G. Davis, and H. J. Gilbert)
- Computational approaches to identifying gene regulatory systems in *Arabidopsis* (May, S.T., M.W. Bevan, and G. C. Cawley)
- Prediction of protein function in plant genomes using data mining (King, R., H.J. Ougham, and S.T. May)

European Union Framework

Scientists in the UK participate in European collaborations through the European Union's Framework research opportunities, including CONFAB, EDEN, EXOTIC, GVE, NATURAL, NONEMA, PLANET and REGIA (see European Union section for more information).

Databases

AGR: *Arabidopsis* Genome Resource (<http://ukcrop.net/agr/>)

UK CropNet: The UK Crop Plant Bioinformatics Network (<http://ukcrop.net/>)

ATIdb: *Arabidopsis* Transposon Insertion database (<http://stein.cshl.org/~x-pan/atidb/index.html>)

Web sites

GARNet: <http://garnet.arabidopsis.org.uk/>

Plant-GEMs: <http://plant-gems.org/>

NASC: <http://arabidopsis.org.uk/>

JIC: <http://www.jic.bbsrc.ac.uk/>

Newsgroup

Arab-uk, the UK mailing list to discuss anything *Arabidopsis* (Arabuk@lists.bbsrc.ac.uk)

United States

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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) (<http://www.nsf.gov>) 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 (see <http://www.nsf.gov/bio/pubs/awards/2010fy01.htm> for a list of awards) in 2001. 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. NSF award information can be found at <https://www.fastlane.nsf.gov/a6/A6AwardSearch.htm>. The U.S. Department of Agriculture (<http://www.reeusda.gov/nri/pubs/abstracts/programlinks01.htm>), the U.S. Department of Energy (<http://www.sc.doe.gov/production/bes/eb/ebhome.html>) and the National Institutes of Health (<http://www.nih.gov>), 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).

