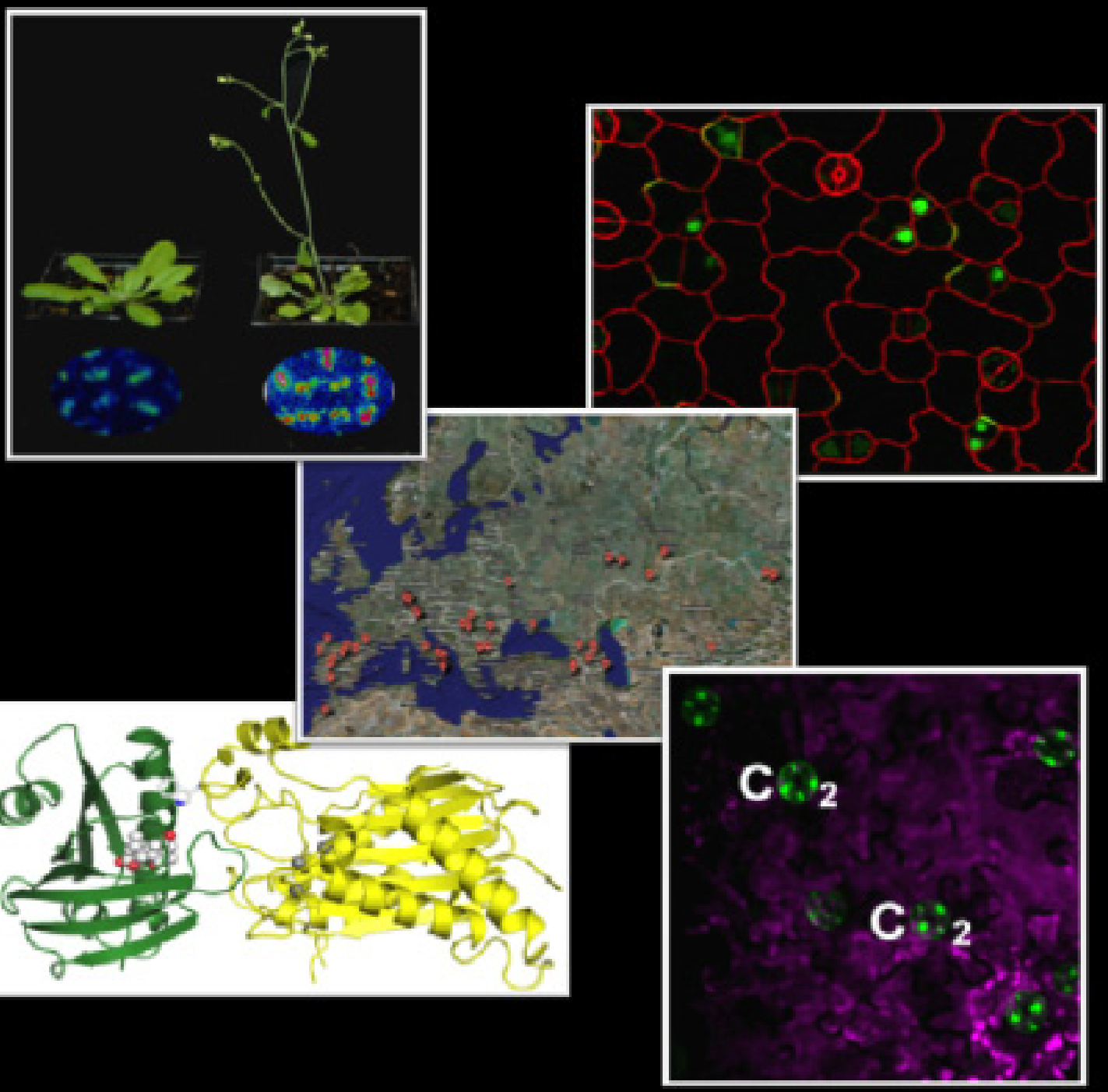
The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2010



The Multinational Arabidopsis Steering Committee

May 2010

The Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project

Annual Report 2010

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The Multinational Arabidopsis Steering Committee-May 2010

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Map
Courtesy of: Detlef Weigel (MPI for Developmental Biology, Tuebingen, Germany)
1001 Genomes Project for Arabidopsis thaliana - sequenced accessions

Arabidopsis plants
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The plant that doesn't feel the cold

Guard cells
Courtesy of: Dominique Bergmann (Stanford University, USA)
Setting up asymmetry by BASL

CO_2
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CO_2 transponder

PYL2/ABA/HAB1 complex
Courtesy of: Xu, Eric (Van Andel Research Institute, MI, USA)
PYL2, green; HAB1, yellow; ABA, grey balls

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Foreword to the Report

This is the 2009/2010 annual report of the **Multinational Arabidopsis Steering Committee (MASC)** on the status of the Functional Genomics Project. In 1990 nine scientists from the United States, Europe, Japan and Australia formed an *ad hoc* committee that initiated large-scale studies in *Arabidopsis thaliana*. A report outlining a plan for international cooperation was prepared and the Multinational Arabidopsis thaliana Genome Research Project (1990-2001) was initiated. This aimed to understand at the molecular level the physiology, biochemistry, growth and development of a flowering plant. A significant goal was to determine the complete sequence of the Arabidopsis genome by the year 2000, concurrent with the development of vital resources and collaborations. The international scientific community agreed to cooperate on several objectives including: the identification and characterization of the structure, function, and regulation of Arabidopsis genes; development of technologies for genome studies; establishment of biological resource centres; development of an informatics program to facilitate exchange of research results; and development of human resources and support of workshops and symposia. Most importantly, the community agreed that multinational cooperation was essential and must involve the free exchange of ideas and information through open communication and interactions. The Multinational Arabidopsis Steering Committee (MASC) was therefore established to implement overall research coordination and was charged with annually reviewing scientific progress and identifying needs and new opportunities for the global Arabidopsis research community. MASC also acts in an advisory capacity to various national funding agencies.

Following the success of the Multinational *Arabidopsis thaliana* Genome Research Project that led to completion of the sequencing of the reference Arabidopsis genome in 2000, the ambitious goal to determine the function of every Arabidopsis gene by the year 2010 was set by a new Project, the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. Numerous laboratories internationally have taken part in this project and very large datasets and resources have been generated leading to breakthroughs in understanding the fundamental processes underlying plant growth development and responses to the environment. The success of this project is the result of numerous factors, including the ease of manipulation of this organism, the synergistic development of a powerful set of tools, the ease of access to stocks and other key reagents, the collegiality of the Arabidopsis scientific community and the generous support from various national funded programmes. Whilst the function of every Arabidopsis gene has not yet been determined, the progress of studies at the level of the genome, transcriptome, proteome, metabolome and other '-omes' have been unprecedented. Studies originally conducted in Arabidopsis are increasingly being translated in the development of biotechnological tools that will help meet global challenges such as food security. As research continues, new large-scale funding mechanisms need to be in place to continue the promotion of discovery in this reference plant. Equally as important are the needs for strong funding in support of individual research labs doing creative work focused on a smaller scale, and for projects that link basic and applied approaches. Given the increasingly important role that Plant Science will play in all of our futures, new support mechanisms for Arabidopsis resources should be identified. For example, in 2010 MASC and NAASC are hosting two workshops to consider how the very large amount of data arising from Arabidopsis research can be managed (and funded) in a coordinated manner internationally. This is essential in order to fully leverage the impressive gains obtained thus far through Arabidopsis research and to maintain cutting edge research in plant biology.

This report details progress made over the last year by the international Arabidopsis functional genomics community including highlights from intensive efforts in basic research and advances in translating basic to applied research. Although the timeframe of translation into applied research is rather long, and the outcomes unpredictable, the very rapid increase in publication rate and patent filing in the last 15 years indicates what we might expect in the next decade. This report demonstrates the continued high level of cooperation that exists throughout the global community and the impressive returns that funding agencies gain from supporting Arabidopsis research.

The Multinational Arabidopsis Steering Committee
May 2010

Executive Summary

The increasing demands of a growing, prosperous world for improved agricultural products including food, fiber and fuel, intensifies the need for a thorough understanding of the basic biology and ecology of plants. As the first plant to have its entire nuclear genome sequenced, *Arabidopsis thaliana* has become the most important model system for plant biology and a vital resource for the study of other multicellular organisms. Arabidopsis research has increasingly impacted on our understanding of other plants and the intent has always been that the knowledge gained from this reference species would serve to advance understanding about others, particularly crop species. It can be expected that Arabidopsis research will translate into new and improved plant products and contribute to agricultural productivity. The transfer of knowledge from Arabidopsis is accelerating due to the efforts of a vibrant research community and the leveraging of advances and resources made over the last 15 years or more. Arabidopsis has shifted from model to reference organism - the plant in which the fundamentals are established and to which other plants are compared. Arabidopsis is now uniquely poised to address biological questions that range from the molecular to the ecosystem levels and resources currently available and under development will allow rapid experimentation to answer existing and future challenging questions. However, the utility of Arabidopsis extends far beyond the plant realm; researchers studying other organisms such as humans, flies, worms, fungi, and mice increasingly rely on the extensive collection of Arabidopsis resources and knowledge to inform their own research. Therefore, continued and expanded funding and international collaboration are critical to future success; maintaining and strengthening ties between researchers in all parts of the world, and between basic and applied scientists, are necessary to create the synergy needed to effectively meet the health and agricultural challenges facing us.

The highly active and enthusiastic Arabidopsis community around the world continues to attract new researchers. According to The Arabidopsis Information Resource (TAIR) there are currently about 20,000 Arabidopsis researchers in approximately 7,900 laboratories worldwide, with 9,168 people and 4,065 laboratories updated in the last five years. Arabidopsis continues to be an ideal training system for future generations of researchers with broadened expertise, for example, through the recent development of systems biology projects which combine classical 'wet lab' approaches with advanced computational methods. Resources must continue to be coordinated in order to maximize the efforts of the various labs around the world. It remains as true today as it was ten years ago at the release of the reference genome, that only sustained collaborations and timely sharing of data, stocks, and other resources will enable the Arabidopsis community to achieve its ambitious goals.

Highligths in Arabidopsis research

The past year continued to be strong for Arabidopsis publications. 3,093 Arabidopsis peer-reviewed research papers were published in 2009, nearly an 8-fold rate increase over 1994 (when 402 peer-reviewed papers were published; Fig. 1, page 9), and an increase of 50-fold in the last 20 years. This report includes summaries of just a few research highlights in the past year (pages 10-14) including:

- Discovery of the 'plant's thermometer' at the molecular level
- Identification of a segregating factor in plant asymmetric cell division
- Discovery of a novel defence mechanism involving fusion of the vacuolar membrane with the plasma membrane
- Identification of key regulators of meiosis
- Insight into nitrate perception and the first plant trans-ceptor
- Insight into the perception of increasing CO_2 levels
- Discovery of the ABA receptor and its mechanism

Examples of applications arising from Arabidopsis research

The knowledge gained from studies in Arabidopsis serves to advance our understanding of other plant species, particularly crop species, and thus translate into new or improved plant products and increased agricultural productivity. Importantly, basic research in Arabidopsis provides the foundation for applied studies. The filing of patents is one measure of potential commercial activity and while many patents worldwide acknowledge research on Arabidopsis, a widely-held myth is that few of these discoveries are ever turned into useful products. US utility patents referencing Arabidopsis patents increase: in 2009 there were 968 utility patents referencing Arabidopsis compared to 23 in 1994, a 42-fold increase (See Fig. 3, page 20). In the same timeframe, a 16- and a 10-fold increase have been recorded for European and world's published applications (i.e. patents) referencing Arabidopsis (See Fig.4 and Fig.5, page 21). It has been estimated to take up to 12 years or more to navigate the commercialization pipeline from initial discoveries to agricultural products. This report highlights a few examples of discoveries that demonstrate how basic research in Arabidopsis can be translated into real-world applications. Each study vitally depended on Arabidopsis data and resources (pages 21-24):

- Arabidopsis phytochromes allow spatio-temporal control in mammalian cells
- Fatter plants to meet biofuel demands
- Increased seed size to increase crop yields
- Discovery of human diseases through orthologous phenotype
- Single-parent plants to accelerate breeding of crop plants

New initiatives announced this year

- **Australia**- The Canberra and Adelaide phenomics nodes were officially opened in 2009.

- **Italy**- A new collaboration between the Italian groups of G.Serino/P.Costantino and G. Frugis with Q. Xie and LJ. Qu (Chinese Academy of Sciences) has been selected by the Italian Ministry of Foreign Affairs as one of the significant research projects within the frame of the Executive Programme of Scientific and Technological Cooperation between Italy and China.
- **UK**- BBSRC launched a new 5-year strategy which includes two out of three core areas relevant to plant science and Arabidopsis research.

Progress towards the goals of the Multinational Coordinated Functional Genomics Project

Since 2004, 'thermometer' illustrations have provided a visual way to track progress and describe a function for every Arabidopsis gene (see Fig.2 pages 18-19). The availability of high-quality genetic resources will facilitate future studies and contribute to our expanding pool of knowledge. Current progress includes:

- Sequence-confirmed homozygous mutant plant lines: with two or more insertions = 10,503 genes; with one confirmed homozygous allele insertion = an additional 7,218 genes, giving a total of 17,721 unique genes, or 62%, with at least one confirmed homozygous insertion.
- As of April, 2010, seeds from 33,747 homozygous insertion lines have been received by ABRC; so far 28,297 lines have been made available and are ready for distribution. 27,543 of 28,691 (96%) unique Arabidopsis genes contain at least one sequenced insertion element. Newly procured since last year are an additional 6% of genes with two homozygous insertions and an additional 4.4% with one homozygous insertion.
- Isolation of full-length cDNAs for 21,196 (74%) of genes; clones of 16,000 are currently being distributed.
- Availability of fully-sequenced ORF clones for 16,718 (58%) genes and partially-sequenced clones for 1,493 more.
- 27,257 (96%) of 28,691 genes whose expression has been detected by cDNA, EST, or smRNA data.

MASC Subcommittees

The MASC Subcommittees promote international cooperation in a number of areas of functional genomics research:

- Clone-based Functional Genomics (ORFeomics) - Progress towards obtaining full length cDNAs and open reading frame clones for all annotated Arabidopsis protein coding genes continues to be tracked (Table 1, page 28). Recent goals include further development of 'functional' clone sets for approaches including in planta overexpression and the opening of a public database searchable for ORF clones by AGI codes (Atxgxxxx).
- Proteomics - Subcommittee members continued to develop resources for the community including the further development of the subcommittee website to include a MediaWiki interface and a proteomic Aggregator, which is currently being developed to summarize the publicly available proteomic information specific to Arabidopsis for each AGI code.
- Systems Biology - An entire session entitled 'Plant Systems Biology' was chaired by the subcommittee Chair and Co-Chair at ICAR in Edinburgh in 2009.
- Phenomics - Subcommittee members continue to track progress by the various phenomics efforts underway worldwide including insertion lines, phenotyping platforms and facilities, databases, phenomics meetings, and community events.
- Bioinformatics - Subcommittee members have played a central role in the MASC Bioinformatics workshops (April 2010 in Nottingham, UK and May 2010 in Washington DC, USA) to evaluate the existing informatics resources and the future needs of the Arabidopsis and wider plant community.
- Metabolomics - In the light of the growing –omics integration, the subcommittee has defined new goals including the development of a website and participation by subcommittee members to non-plant specific metabolomics conferences.
- Natural Variation and Comparative Genomics - The most notable community advances continue to be in 'omics technologies: the 1001 Genomes Project has delivered the complete genome sequence of more than 80 accessions in the past year. The whole genome sequence of *A. lyrata* has been assembled, annotated and released. Unexpected genetic phenomena outside humans are being discovered.

MASC recommendations and goals for the next year

A number of recommendations for the scientific community were published by MASC in its 2009 report, and these are still valid. They included working towards homozygous mutant lines for all genes; a detailed analysis of their expression patterns and epigenetic control the large scale analysis of proteins and metabolites and their functions; the genomic analysis of wild accessions of Arabidopsis for a better understanding of genome evolution and adaptation; and the development of modelling tools. New recommendations for the coming year are as follows.

- The continued elaboration of a systems approach to plant biology, incorporating diverse data sets and using computational techniques to integrate data and predict plant function.
- The development of resouces for i) association mapping, ii) ecological genetics and iii) field experiments. Such resources include plant populations, appropriate and accessible statistical methods, good field sites, and sharing of knowledge.
- The development of an international policy to maintain bioinformatics and biological material resource centres, through sustainable funding models.
- The development of strategies to store, maintain, distribute and interpret the very large amounts of data that will be generated experimentally in the coming years.
- The effective translation of basic plant knowledge and tools, generated in Arabidopsis research, to crops in order to address the major global challenges of food and energy security in the face of climate change.

Progress and Activities of Multinational Arabidopsis Functional Genomics Projects

Progress and activities of MASC in 2009/2010

In 2009, Keith Lindsey (Durham University, UK) succeeded Joe Kieber (University of North Carolina-Chapel Hill, USA) to become the MASC Chair and Kazuo Shinozaki (RIKEN, Japan) became Co-chair. Prof Shinozaki will become the new MASC chair when Prof Lindsey steps down following the annual International Conference on Arabidopsis Research (ICAR) in June 2010. Dr Irene Lavagi (University of Warwick, UK) became the new MASC Coordinator in December 2009, replacing Dr Joanna Friesner.

To monitor the progress of the Functional Genomics Project an ICAR abstract submission process has been developed and has been in place since 2006. The system is hosted at The Arabidopsis Information Resource (TAIR) website. Thanks to this submission process it is possible to associate abstracts within TAIR to the genes listed, effectively monitoring the progress towards the goal of understanding the function of all Arabidopsis genes. For the 2008 ICAR, 336 of 628 submitted abstracts contributed 3,060 total distinct AGI codes, including 926 loci that were not already associated to the literature in TAIR at that time. In 2009, 645 of 646 abstracts were linked to 1,634 distinct AGI codes, including 25 loci that were not already associated to literature in TAIR.

Google Analytics were employed beginning June, 2007 to track the usage of MASC webpages at TAIR which are maintained by the MASC Coordinator. The community regularly visits the MASC pages: in the 1 year period between March 1, 2009 and March 1, 2010, 36 different MASC pages were viewed 8,871 times, an average of about 739 views a month. The top-viewed page (3,034 views) contains information on projects funded through the US NSF 2010 project (www.arabidopsis.org/portals/masc/projects.jsp). Another frequently viewed page was the Funding page, which received over 1,006 views over the last year (www.arabidopsis.org/portals/masc/funding.jsp).

MASC subcommittees, proposed in 2002, were established to help track the progress made towards the goals outlined in the Multinational Coordinated *Arabidopsis thaliana* Functional Genomics Project. In the last 7 years, some committees were discontinued according to the evolving needs of the community. The minimum requirements for a subcommittee to be considered active include submission of an annual report and input at MASC annual meetings. A discussion regarding the reorganisation of inactive subcommittees took place at the 20th ICAR, held in 2009 in Edinburgh. It was decided that the MASC Chair should confirm leadership of the existing subcommittees and that, if necessary, new subcommittee chairs should be found. A 3-year minimum term for each subcommittee Chair was also instituted to provide continuity. Similarly, it was decided that the new Chair should confirm the interest of subcommittee members and that Co-chairs could help promote activity of the subcommittee. No new subcommittees have been formed over the last year and 2 subcommittees changed their Chairs: Bioinformatics, previously chaired by Heiko Schoof, is now chaired by Nicholas Provart, and Kazuki Saito now chairs the Metabolomics subcommittee, replacing Basil Nikolau. This report includes reports from the 7 current subcommittees: Bioinformatics, cDNAs and Clone-based Functional Proteomics (ORFeomics), Metabolomics, Natural Variation and Comparative Genomics, Phenomics, Proteomics, and Systems Biology.

Due to the evolving needs of the scientific community and the increasing importance of management of very large data sets, the Bioinformatics MASC subcommittee played a central role at the MASC and NAASC Bioinformatics workshops. The first MASC Bioinformatics workshop was held in Nottingham, UK (15-16 April 2010) and the second took place in Washington DC, USA (10-11 May 2010). A document that summarises the workshops discussions is in production and will be available at http://www.arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp. In addition, a Bioinformatics workshop organised by Nicholas Provart (Chair of Bioinformatics) and other members of MASC will be held at ICAR 2010 in Yokohama, Japan, to report on the MASC Bioinformatics workshops and develop further discussions. The MASC Proteomics subcommittee (MASCP) organized a workshop entitled 'Plant Proteomics - Breakthroughs in studying intra-cellular dynamics and environmental response in the Arabidopsis proteome' that was held at the 20th ICAR in Edinburgh, in 2009. The MASCP website (http://www.masc-proteomics.org/) has been further developed to include a MediaWiki interface and several other projects have been undertaken to integrate the existing proteomics resources. The former Systems Biology subcommittee Chair (Philip Benfey) together with Andrew Millar chaired a full conference session on 'Plant Systems Biology' at ICAR 2009 in Edinburgh. The ORFeomics subcommittee has been involved in numerous projects to track clone-based functional resources and facilitate additions to collections. A public database that allows ORF clone search using AGI codes (Atxgxxxx) has been opened (http://urgv.evry.inra.fr/ATOMEdb). Members of the Phenomics subcommittee continued to monitor the development of phenomics-based resources and were involved in a number of community events to promote international collaboration and outreach. The Metabolomics subcommittee has drawn new goals including a subcommittee website, assiduous participation to metabolomics-related meetings and a continuous dialogue among subcommittee members.

A full-time MASC Coordinator position, established in 2002, has been previously supported by the NSF (US) for 6 years and by DFG (Germany) for one year. The current Coordinator's position is UK-based and will be supported by BBSRC (UK) for the next three years. MASC webpages are hosted at TAIR (http://

www.arabidopsis.org/portals/masc/index.jsp) and are regularly updated. The 'Coordinator's Journal' webpage, established in 2007 by the previous coordinator, provides additional outreach and communication and also relays information of interest and relevance to the Arabidopsis community (http://www.arabidopsis.org/portals/masc/journal.jsp). The MASC Coordinator provides help and coordination to MASC, and the larger Arabidopsis functional genomics research community. Duties include (1) serving as the executive secretary of MASC, (2) providing assistance to local representatives in the organisation of the annual International Conference on Arabidopsis Research (ICAR), including help with sponsorship, (3) writing and editing of the annual MASC progress report with input from MASC members, (4) serving as liaison between members of MASC, the international research community, funding agencies, and databases and stock centres, and (5) maintaining and updating the functional genomics MASC website together with TAIR to inform the global research community about various opportunities, collaborations, large-scale activities and research progress.

Scientific Highlights of the Past Year

Following a 20-year period of steady increase, the annual number of publications involving Arabidopsis research appears to have reached a plateau. The annual number of peer-reviewed articles in 2009 in rice was similar to that of Arabidopsis. Evidencing the impact that Arabidopsis has had in the plant community and benefiting from the recently sequenced genomes, articles involving research on rice/oryza and corn/maize have increased while the number of papers focusing primarily on Arabidopsis has experienced a slight decrease in 2009. Over the past 20 years the Arabidopsis community has enjoyed the ease of manipulation of this plant and the availability of a wide range of resources that have been developed. Resources include chemically generated mutants; homozygous T-DNA insertion mutant lines; RNAi resources and the recently-developed artificial microRNAs; cDNA and ORF clones; large-scale microarray data; and RILs and other mapping populations. Resources that are more recent additions include expanded information about the Arabidopsis proteome, metabolome and methylome, and the natural diversity found in Arabidopsis accessions. Web-based databases and browsers are also proliferating, reflecting the need to manage the vastly increasing number of datasets put forth by the many worldwide Arabidopsis research groups. The constant development of resources that adapt to the evolving needs of the community have greatly facilitated a large body of cutting-edge research that allows for rapid advances in plant biology.

As the global demand for food and renewable energy supplies increases, governments across the world are allocating more money from their financial budget to plant science compared to previous years. In particular, food crop research with immediate applications is being encouraged. However, the time lapse between an original scientific discovery and its biotechnological application is often rather long and studying an organism that is easier to manipulate may be beneficial in the long term. Indeed, Arabidopsis lends itself exceptionally well to studying most aspects of basic plant biology; its well-known features include its small genome, size, high fecundity, diverse natural populations, ease of genetic manipulation and transformation, and short generation time. Studies in Arabidopsis have also greatly benefited from strong international collaborations first established over 40 years ago and strengthened during the Arabidopsis Genome project spanning the last decade across several countries and continents. With the release of the reference sequence in 2000, the 'genomic era' of Arabidopsis research truly began, allowing a rapid increase in discoveries and publications (Figure 1).

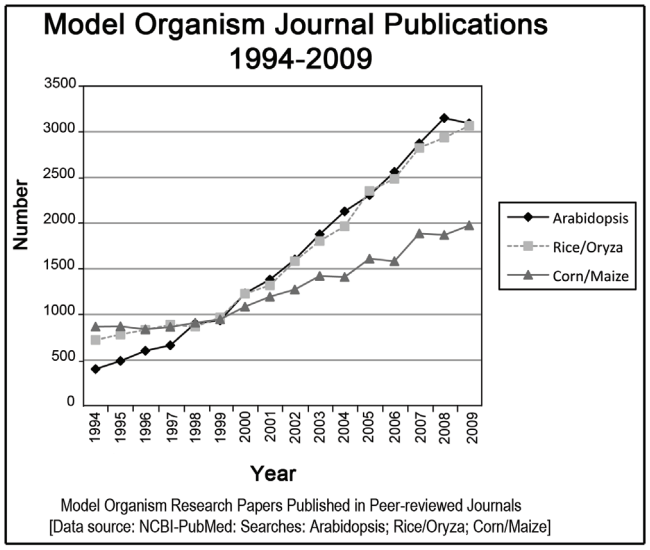

Figure 1: Model Organism Journal Publications (1994-2009)

Considered alongside classic model organisms such as corn, the Arabidopsis publication record remains impressive, reflecting its ease of use as a genetic system, advanced resources and datasets, and the collegiality of the worldwide community, each of which contributed to its development as the reference plant. Between 1994 and 2009, the number of peer-reviewed Arabidopsis publications increased nearly 8-fold, while rice and corn publications increased about 4-fold and 2-fold, respectively (Figure 1). Over 3,000 peer-reviewed Arabidopsis publications were produced in the past year, many of which contain exciting new breakthroughs that will no doubt have impacts on studies in plants and other species.

The following section provides summaries of just a few significant advances; notably, most publications involve collaborators from two or more countries, reflecting the collegiality and truly international nature of the Arabidopsis community.

The plant that doesn't feel the cold
By: Irene Lavagi, MASC Coordinator

The increasing global demand for food supplies coupled with varying climates across the planet make a full understanding of the molecular mechanisms that regulate plant responses to temperature changes a necessity. Plants are sensitive to temperature and can perceive differences of as little as 1°C. Although the effect of temperature on plants has been known for hundreds of years, the actual mechanism that regulates the sensing of temperature and fine-tunes the plant's responses had remained unknown until now.

In a recent publication by Kumar and Wigge, nucleosomes containing the alternative histone H2A.Z were found to be essential to perceive ambient temperature correctly (1).

In this study, a genome wide transcriptional analysis was followed by the characterization of the *Arabidopsis thaliana* mutant line *arp6* in the ambient temperature pathway for flowering. Arabidopsis *arp6* mutant lines displayed a cold insensitive phenotype, flowered with five leaves only and presented greatly enhanced architectural responses to temperature, including hypocotyl growth and petiole elongation, compared to wild type plants. Interestingly, the ambient temperature transcriptome of *arp6* mutant lines was found to be constitutively expressed even at 12°C. The *arp6* gene product is part of a highly conserved eukaryotic protein complex that is required for the insertion of the alternative histone H2A.Z into nucleosomes. H2A.Z nucleosomes are usually found at the transcription start site and appear to regulate the expression of quiescent genes by maintaining their promoters in a poised state ready for appropriate transcription. Extensive chromatin immunoprecipitation experiments revealed depleted H2A.Z nucleosome occupancy in *arp6* mutant lines, and showed that these temperature-dependent dynamics are specific to the H2A.Z histone. This suggests that H2A.Z is the major determinant of temperature responsiveness of chromatin. It was also found that the *FLOWERING LOCUS T* (*FT*) gene, an essential output of the thermosensory pathway for mediating early flowering, presents a promoter enriched in H2A.Z histones, which are depleted when plants are shifted to higher temperatures. This suggests an explanation for the early flowering observed in *arp6* mutant lines. Experiments with purified nucleosomes showed that H2A.Z confers distinct DNA-unwrapping properties on nucleosomes, so indicating a direct mechanism for the perception of light through DNA-nucleosome fluctuations. Therefore the alternative histone H2A.Z appears to act as the plant's thermometer. At lower temperatures, H2A.Z binds DNA more tightly, so preventing the transcription of some genes. As the temperature increases, H2A.Z dissociates from DNA and transcription of genes involved in the temperature response pathway can take place. A molecular understanding of the mechanism of temperature perception will enable us to understand how different species will respond to further increases in temperature and will be a key step toward breeding crops that are able to grow in a wide range of temperatures.

(1) Kumar SV, and Wigge PA (2010) H2A.Z-Containing Nucleosomes Mediate the Thermosensory Response in Arabidopsis. Cell (140): 136-147

BASL - a landmark in asymmetric plant cell division
By: Irene Lavagi, MASC Coordinator

Multicellular organisms must constantly generate differences between cells. Plants and animals can do this via the shared developmental mechanism of asymmetric cell division, which creates diverse cell types and maintains stem-cell populations. Typically, asymmetric cell division is achieved through either the asymmetric partitioning of materials (usually protein or RNA) within the mother cell and between the daughters, or by guidance from external signals. In animals, PAR proteins, well documented regulators of animal cell polarity, localise to restricted regions of the cell periphery and influence cell fate by guiding the localization of cell fate regulators so that that these determinants are segregated to one daughter only. Despite the fact that plants, like animals, use asymmetric divisions for development and self-renewal, a localized and segregated polarity factor was only identified and reported for the first time in a very recent publication in Cell (1). Differences in plant cell structure and the lack of homologues of the animal asymmetry regulators in plant genomes made it likely that plants would use novel regulators, a view supported by the discovery of this new segregated factor.

In plants, stomata, the structures involved in plant/atmosphere gas exchange, consist of two identical cells, guard cells, and the pore between them. In *Arabidopsis thaliana*, stomata are formed through a series of asymmetric cell divisions in a dedicated epidermal cell lineage, of which guard cells are the end-point. Dong and co-workers used Arabidopsis stomatal development as a system to identify plant cell asymmetry regulators (1). BASL (BREAKING OF ASYMMETRY IN THE STOMATAL LINEAGE), a novel protein with no obvious homologues outside of plants, was identified in a mutational screen for stomatal pattern defects. *basl* mutants displayed a clustered distribution of stomata and produced excessive stomatal precursor cells from cell divisions that lacked characteristic asymmetries. BASL expression, detected via transcriptional reporters, was highest in the asymmetrically dividing stomatal lineage cells. At the subcellular level, functional BASL-GFP reporter expression was dynamic, polarised and uniquely correlated with asymmetric divisions. BASL-GFP accumulated in the nucleus or in a crescent at the periphery of the cell, or in both locations depending on the identity and division behaviour of the stomatal lineage cell. From experiments expressing different portions of the BASL proteins, it was found that BASL is required for function at the cortex of the differentiating cell, whereas nuclear localisation of BASL was postulated to serve a sequestration function. BASL is, under its own regulatory sequences, expressed in the stomatal lineage and in the vasculature. When ectopically expressed in this study, however, BASL was found in a crescent at the periphery of many other cell types, suggesting that most plant cells possess the machinery for the trafficking and maintenance of BASL at specific, polarized locations. The identification of BASL represents a landmark in developmental plant biology as opens new opportunities to investigate cell polarity and the establishment of asymmetry.

As an aside, bioinformatics tools were used to accelerate the map-based cloning of *BASL*, and such tools also played an important role in the identification of *OSD1*, described below.

(1) Dong J, Macalister CA, Bergmann DC (2009) BASL Controls Asymmetric Cell Division in Arabidopsis. Cell (137): 1320-30

Fusing to attack

By: Irene Lavagi, MASC Coordinator

Unlike animals, plants lack mobile immune cells and have developed several defence strategies against pathogens. One of these strategies is the hypersensitive response, which leads to localised cell death. Plant vacuoles contain hydrolytic enzymes and are capable of discharging their contents into the cytoplasm in response to viral infection via a vacuolar collapse system. A vacuolar enzyme with caspase-like activity, previously shown to mediate the vacuolar collapse system, triggers the release of vacuolar hydrolytic enzymes into the cytoplasm to prevent viral proliferation and induces hypersensitive cell death. However, since this mechanism relies on the discharge of vacuolar contents into the cytoplasm, it cannot prevent bacterial proliferation outside the cells. Intriguingly, a variety of antibacterial proteins accumulate in plant vacuoles, suggesting that a mechanism for these molecules to come into physical contact with bacteria must exist. Although the activation of signal transduction pathways that lead to cell death in response to bacterial infection have been well documented at the molecular level, the actual mechanism through which cell death is accomplished had not been unveiled until recently. In a publication by Hara-Nishimura and co-workers, evidence of proteasome-mediated cell-autonomous immunity based on plant cell membrane fusion is presented (1).

In Arabidopsis leaf epidermal cells the vacuolar membrane fuses with the plasma membrane in response to bacterial infection. This fusion process creates an interconnection of vacuoles and the outside spaces of the plasma membrane, effectively allowing vacuolar contents to be discharged to the outside of cells. Ultrastructural observations of Arabidopsis epidermal leaf cells infected with avirulent *Pseudomonas syringae* bacteria revealed that at 3 h post-bacterial inoculation the vacuolar membrane is frequently fused with the plasma membrane. Concurrent with the typical features of the hypersensitive cell death response, cell shrinkage and cytoplasmic aggregation were observed 12 h after bacterial inoculation. In addition, this study provided evidence that membrane fusion in response to bacterial infection is proteasome-mediated. A plant enzyme with caspase-3 activity in plants, long reported to function in hypersensitive cell death, was identified for the first time in this study. Experiments involving silencing and pull-down analyses suggest that in Arabidopsis, like in animals and yeast, proteasome subunits have caspase-3-like sites well known to be involved in cell death. This work has uncovered a novel plant defence strategy that is mediated by the proteasome and triggered by bacterial infection. Fusion of the large central vacuole with the plasma membrane in response to bacterial infection leads to the accumulation of hydrolytic enzymes to the outside of cells and consequent hypersensitive cell death.

Due to the present extent of the destruction of crops and loss of subsequent harvest by bacterial infection, this work on a novel plant defence mechanism provides essential information for the future development of biotechnological tools that will help combat bacterial infection in plants.

(1) Hatsugai N, Iwasaki S, Tamura K, Kondo M, Fuji K, Ogasawara K, Nishimura M, Hara-Nishimura I (2009) A novel membrane fusion-mediated plant immunity against bacterial pathogens Genes Dev (23): 2496-506

Turning meiosis into mitosis

By: Irene Lavagi, MASC Coordinator

Successful clonal production of a specific genotype has been referred to as the holy grail of agriculture. Since the 1920s hybrid seeds obtained by cross-pollination have been employed in agriculture to improve specific traits, such as higher yield and disease resistance. However, hybrid seeds cannot be perpetuated, as seeds from the first generation of hybrid plants do not produce true copies in the following generations. New hybrid seeds must be purchased for each planting. Asexual reproduction through seeds gives rise to progeny that are clones of the maternal parent. Despite the occurrence of this phenomenon in over 400 species of angiosperms, introduction of this trait into sexual plants has proven very difficult.

Mercier and co-workers have identified a novel mutant phenotype in which meiosis is replaced by mitosis (1). Replacement of meiosis with mitosis is a key step towards the introduction of asexual reproduction in sexual plants. In a screen for genes involved in meiosis the *OSD1* gene was identified due to its coexpression with other known meiotic genes. Arabidopsis *osd1* mutants did not present any developmental defects and were capable of producing functional diploid gametes. The progeny of *osd1* Arabidopsis mutant plant were mostly tetraploid (84%) and no diploid plants were found. Observations at the cytological level and genotyping suggested that diploid gametes in *osd1* mutants are due to an absence of the second meiotic division. However, the gametes of *osd1* plants are genetically different from the mother plant. Combining the *osd1* mutation with previously described mutations in which the first meiotic division is replaced by mitotic-like division, a triple mutant where viable non-recombined diploid gametes are produced was obtained. Triple mutants, named *MiMe*, displayed a complete replacement of meiosis by mitotic-like divisions confirmed by observations of chromosome behaviour. Most intriguingly, all gametes of *MiMe* plants retained the mother plant heterozygosity for all tested genetic markers. However, successive generations increased in ploidy with a corresponding decrease in fertility.

To achieve the clonal production of seeds, both the production of unreduced gametes lacking recombination of chromatids, and the fertilisation-independent development of these unreduced gametes into embryos are required. The three mutant genes that contribute to the *MiMe* phenotype are highly conserved in plants, suggesting that it is possible to replace meiosis with mitosis in any plant species including crops. *MiMe* plants, capable of undergoing mitotic-like division instead of normal meiosis represent a major advance towards regulated clonal reproduction through seeds.

(1) d'Erfurth I, Jolivet S, Froger N, Catrice O, Novatchkova M, Mercier R (2009) Turning meiosis into mitosis. PLoS Biol (7): e1000124

How plants sense nitrate (NRT1.1- the first plant transceptor)
By: Irene Lavagi, MASC Coordinator

Plant growth is dependent on the ability of plants to acquire essential nutrients from the soil. Limited or reduced nutrient content of soil poses serious limitations to vigorous plant growth. Nitrogen is one of the major plant nutrients, and understanding nitrogen uptake and signalling is of vital importance for maximising crop yield. The major source of inorganic nitrogen for plant is nitrate. Despite the fact that nitrate transporters have been previously identified, the molecular mechanism mediating the sensing of nitrate concentrations in the soil and the subsequent response in gene expression of nitrate assimilatory enzymes and nitrate transporters has been poorly understood. Plant roots absorb nitrogen through low and high affinity nitrate transporters (3,7). The first identified plant nitrate transporter (NRT1.1 also known as CHL1 (8)) has regulated, dual affinity activity (5), and there is increasing evidence that the same nitrate transporter is also involved in nitrate signaling and sensing (1,4,6,9,10).

In a study by Ho and co-workers, evidence that NRT1.1 is a plant transceptor, which can act as a sensor independently of its transporter function, was presented (2). A genetic approach was used to distinguish and decouple the transport activity of CHL1 from its sensing activity. The novel mutant allele *chl1-9*, in which the nitrate transport activity of CHL1 is abolished, was found in a mutant screen and analysed. Assessment of *chl1-9* mutant Arabidopsis lines by the induction of the nitrate-responsive *NRT2.1* transport gene demonstrated that despite the loss of nitrate transport, nitrate signalling was not affected. Upon nitrate treatment, gene expression response, measured by the reporter NTR2.1, remained functional in Arabidopsis *chl1-9* mutant lines. These results indicated that the transport function can be separated from the sensing function. In Arabidopsis, CHL1 can exist in two states depending on the phosphorylation of the threonine residue at position 101 (T101). Phosphorylation was shown to occur in response to nitrogen availability in the soil and consequently both transport activity and gene expression are affected. At low nitrate levels, CHL1 was phosphorylated to control gene expression to respond to low nitrate concentrations, whereas at high nitrate concentrations CHL1 is not phosphorylated, triggering high nitrate response signalling.

This study provides evidence for a direct link between soil nutrient availability and gene expression. Together, the data indicate that CHL1 serves as a transceptor in Arabidopsis and unravel the mechanism that allows the CHL1 transporter/sensor to modulate the response to the nitrate signal according to the external concentrations in the root environment. Independent work has shown that NRT1.1 regulatory function is dependent on nitrogen in the growth media as N starvation for 24 h makes nitrate sensing NRT1.1-independent, indicating that there are yet more nitrate sensors beyond NRT1.1 to be discovered (10).

(1) Forde BG, Walch-Liu P (2009) Nitrate and glutamate as environmental cues for behavioural responses in plant roots. Plant Cell Environ (32): 682-93
(2) Ho CH, Lin SH, Hu HC, Tsay YF (2009) CHL1 functions as a nitrate sensor in plants. Cell (138): 1184-94
(3) Krouk G, Crawford NM, Coruzzi GM, Tsay YF (2010) Nitrate signaling: adaptation to fluctuating environments. Curr Opin Plant Biol (13): 1-8
(4) Krouk G, Tillard P, Gojon A (2006) Regulation of the high-affinity NO3- uptake system by NRT1.1-mediated NO3- demand signaling in Arabidopsis. Plant Physiol (142): 1075-86
(5) Liu KH, and Tsay YF (2003) Switching between the two action modes of the dual-affinity nitrate transporter CHL1 by phosphorylation. EMBO J (22): 1005-1013
(6) Remans T, Nacry P, Pervent M, Filleurce S, Diatloffc E, Mounier E, Tillard P, Forde BG, Gojon A (2006) The Arabidopsis NRT1.1 transporter participates in the signaling pathway triggering root colonization of nitrate-rich patches. PNAS (103): 19206-11
(7) Tsay YF, Chiu CC, Tsai CB, Ho CH, Hsu PK (2007) Nitrate transporters and peptide transporters. FEBS Lett (581): 2290-300
(8) Tsay, YF Schroeder, JI Feldmann, KA Crawford, NM (1993) A herbicide sensitivity gene CHL1 of Arabidopsis encodes a nitrate-inducible nitrate transporter. Cell (72): 705-713
(9) Walch-Liu P, Forde BG (2008) Nitrate signalling mediated by the NRT1.1 nitrate transporter antagonises L-glutamate-induced changes in root architecture. Plant J (54): 820-8
(10) Wang R, Xing X, Wang Y, Tran A, Crawford NM (2009) A genetic screen for nitrate regulatory mutants captures the nitrate transporter gene NRT1.1. Plant Physiol (151): 472-8

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How do plants sense increasing CO_2 levels?
By: Irene Lavagi, MASC Coordinator

Elevated CO_2 concentrations in leaves cause closing of stomatal pores in aerial plant tissues. Due to the rising atmospheric CO_2 concentration, this leaf CO_2 response is causing reduced stomatal apertures in plants on a global scale. Presently the atmospheric CO_2 concentration is already approximately 40% higher than before the industrial revolution and the CO_2 concentration is expected to double in the present century. The continuing rise in the atmospheric CO_2 concentration reduces stomatal pore apertures in leaves and thus globally regulates CO_2 influx into plants and the water use efficiency of plants. In addition reduced stomatal apertures reduce evaporative cooling of leaves, which can increase leaf heat stress. However, the CO_2-binding proteins that mediate CO_2 control of gas exchange between plants and the atmosphere had remained unknown. The cell type that responds to CO_2 within leaves, has also been a matter of debate, with a need for genetic investigation. The debated prime suspects being the photosynthetically active mesophyll cells or the guard cells that surround each stomatal pore.

By analyzing many candidate CO_2-binding proteins, Hu *et al* (1) discovered two CO_2 binding protein-encoding genes that mediate CO_2 regulation of stomatal pores (1). The authors demonstrated that Arabidopsis plants lacking the leaf and guard cell-expressed carbonic anhydrases β*CA1* and β*CA4* were greatly impaired in their response to increases in CO_2. Carbonic anhydrases are enzymes that bind CO_2 and convert CO_2 into bicarbonate and protons. Guard cell-targeted carbonic anhydrase over-expression plants exhibited an average enhanced instantaneous water use efficiency of 44%, while retaining wildtype-like CO_2 assimilation rates

(1). Thus guard cell-targeted over-expression causes an enhanced response to CO_2, allowing plants to take in CO_2, while reducing water loss via transpiration from stomatal pores. Remarkably, expression of an unrelated mammalian carbonic anhydrase in guard cells restored CO_2 control of stomatal movements in the *ca1ca4* double mutant plants. The authors also found guard cell anion channel activation by combined CO_2 and bicarbonate.

Together these data provide evidence that the mechanism of the CO_2 response is mediated by the catalytic activity of the carbonic anhydrases. These findings, together with epitasis analyses, provide strong evidence that the identified carbonic anhydrases function very early in the CO_2 signaling pathway as "CO_2 transponders" that mediate CO_2 control of transpirational water loss of plants and CO_2 influx into plants. This advance provides us with a new fundamental understanding of how plants are responding to the continuing global rise in the atmospheric CO_2 concentration. This advance may also enable engineering of C3 plants to make use of increased CO_2 levels, thus improving their water use efficiency.

(1) Hu H, Boisson-Dernier A, Israelsson-Nostroedm M, Boehmer M, Xue S, Ries A, Godoski J, Kuhn JM, Schroeder JI (2010) Carbonic anhydrases are upstream regulators of CO_2-controlled stomatal movements in guard cells. Nature Cell Biol. (12): 87-93

ABA receptor: the greatest hits

By: Irene Lavagi, MASC Coordinator

Plant hormones regulate numerous aspects of growth and development. They also regulate plant physiology allowing plants to respond to changes in the environment. Abscisic acid (ABA) is a plant hormone synthesized in response to low water availability, the most prevalent environmental stress factor for plants. ABA is also involved in developmental responses, including seed maturation and bud dormancy. The pivotal role played by ABA in plant physiology together with the varying climates and consequent fluctuating water supplies across the planet, make it a necessity to understand the ABA signaling pathway for future applications in agriculture.

Whilst receptors of the other plant hormones have been identified in the last decade, identification of the ABA receptor family had been hampered by redundancy. However, during 2009 a series of articles on ABA receptors flourished in high impact factor journals. Groundbreaking work that collectively contributed to the identification of the ABA receptor family (2,7), and subsequently provided insight into its structure and mechanism (3-5,8,11), was performed in laboratories across the world.

Discovery of the ABA receptor

Two independent studies published in May 2009 in *Science* reported the discovery of a new family of proteins, PYR/RCAR proteins, as candidate ABA receptors (2,7). These proteins were found to bind ABA and inhibit the activities of specific protein phosphatase enzymes, the type 2C plant PP2Cs, which have previously been characterized as components of the early ABA signaling pathway that negatively regulate ABA signaling. Phosphatases and kinases remove or add phosphate groups respectively thereby exerting regulatory effects. In the absence of ABA the phosphatase PP2C is a negative regulator of a family of kinases, which upon their phosphorylation regulate downstream targets (1,9-10).

In one study, Cutler and colleagues identified the class of receptors for ABA through a chemical genetics screen (7). A mutant resistant to the synthetic compound pyrobactin, which mimics the action of ABA by inhibiting seed germination, was identified. Pyrobactin Resistance 1 (PYR1) was found to be a novel protein of the START family (lipid-binding proteins). In the presence of ABA, PYR1 was shown to interact with and inhibit the phosphatase activity of HAB1, a PP2C family member. PYR1 therefore appeared to be a new class of ABA receptor, or ABA co-receptor together with a PP2C, that relieves repression of ABA signaling normally exerted through PP2Cs. PYR1 belongs to a 14-member gene family, the PYR/RCAR family and in addition to PYR1 several other members of the PYR/RCAR family were able to bind to the PP2C HAB1, suggesting significant functional redundancy. A quadruple knock out mutant in four *PYR/RCAR* genes showed a strong ABA insensitivity in ABA inhibition of seed germination and root growth.

In the second study, Grill and collaborators independently showed that RCARs function in ABA signaling through PP2Cs (2). Proteins that interact with the ABI1 and ABI2 phosphatases were identified in a yeast-2-hybrid screen for Arabidopsis proteins and named RCARs (regulatory components of ABA receptor) as they confer ABA inhibition to the phosphatases. RCARs and PYR1 are members of the same 14 member gene family. In response to the binding of ABA, RCAR1 represses the activity of PP2C, effectively resulting in the induction of ABA responses. In addition, single amino acid mutations, *abi1-1* and *abi2-1* that confer dominant ABA insensitivity, severely impaired PP2C interactions with RCAR1 and PYR1 (2,7). From binding studies it was also shown that a single ABA molecule binds per RCAR1. The biochemical evidence collected in this study demonstrated that RCAR1 down-regulates the PP2C activity of ABI1 and ABI2 in response to ABA, building a case for the heterotrimeric complex of RCAR1, PP2C and ABA to function as an ABA co-receptor. The manipulation of RCAR1 transcript levels achieved by over-expression or RNAi, resulted in altered ABA responses (increased and decreased sensitivity respectively), including the induction of stress defense genes, closure of stomata, inhibition of seed germination and vegetative growth (2).

Together, these results provided genetic and biochemical evidence that PYR/RCAR proteins function as ABA receptors or ABA co-receptors that bind PP2C proteins to inhibit their negative regulation of ABA signaling. ABA perception is therefore achieved through the PYR/RCAR family of proteins. A plant hormone signalling pathway that is initiated by phosphatases rather than kinases, was discovered. Research in which the ABI1 phosphatase complex of proteins was purified from Arabidopsis plants, led to the independent identification of nine of the 14 PYR/RCAR proteins as the major *in planta* protein interactors of the ABI1 PP2C (6). This study also showed that ABA triggers a rapid ABA-induced PYR1 interaction with the ABI1 PP2Cs *in vivo* in Arabidopsis and that PYR/RCARs are essential for ABA regulation of stomatal movements.

Discovery of structure and mechanism of the ABA receptor

Following the discovery of the ABA receptor family, a total of five studies were published in 2009, all contributing to the elucidation of

the structural and functional mechanisms by which ABA is sensed by this receptor (3-5,8,11). According to the current proposed model, in response to ABA binding the PYR/RCAR receptor binds to and represses PP2C, which results in the activation of the downstream SnRK2/OST kinase and subsequent phosphorylation of further downstream targets, effectively facilitating transcription of ABA-responsive genes. The model accounts for the perception of ABA by the receptor and inhibition of PP2C by ABA-bound receptor (2,7). The question whether PYR/RCARs function as outright ABA receptors or whether they form co-receptors for ABA together with PP2Cs, reminiscent of auxin co-receptors, remained to be determined. Five separate crystallographic studies generated high-definition structural images providing converging elements and complementary information that revealed the atomic structures of several PYR/RCAR proteins in different functional states (3-5,8,11).

Data obtained from this work along with NMR studies demonstrated that ABA binds within an internal pocket of a dimer of PYR/RCARs. Crystallization of PYR/RCAR proteins in the absence of PP2Cs, led to solving the structure of the proteins in the absence of ABA (unbound form) (5,8,11), resulting in the resolution of three major conformational changes including a “gate” or “proline cap” closing over this pocket, and a “latch” or “lock” forming on the gate/cap, and in addition an extension (“recoiling”) of an alpha helix. This conformation ensures the tight binding of the hormone and simultaneously exposes the surfaces of the PYR/RCAR protein that interacts with the phosphatase and interaction with the phosphatase active site. Unexpectedly, these studies showed that PYR/RCARs form homo-dimers in the crystal lattice, in solution and in plants (5,8,11). In 3 of the crystallographic studies, the complex formed by an ABA-bound receptor and the phosphatase was investigated (3,4,11). The interaction between the ABA-bound receptor and the phosphatase appeared to be mediated by a conserved tryptophan residue of the phosphatase, which effectively locks the gating loop of the receptor. The gating loop was shown to insert into the active site of the phosphatase, blocking its ability to bind and dephosphorylate its substrate. Interestingly, most of the amino acids of the PYR/RCAR proteins that come into contact with ABA are evolutionary conserved among PYR/RCAR proteins (3,5), and mutating the amino acid residues that directly form bonds with ABA causes loss of ABA receptor function (5,11), suggesting that the ABA-binding and open-to-close gating mechanisms are conserved and shared by most members of the ABA receptor family.

A unique structure of PYR1 with the non natural minus-ABA enantiomer was also resolved (5), providing the basis by which this non natural ABA isomer triggers signaling. The mechanism by which receptor homo-dimerization is disrupted *in vivo* upon ABA- and PP2C-interaction remains to be directly determined since the structures of PYR/RCARs complexed with PP2Cs do not reveal homo-dimers in the crystal lattice (3,4). Structural studies of the PYR/RCAR homo-dimer interface involves the flexible gating loop of the receptor, suggesting that homo-dimer dissociation may be functionally relevant for the ABA perception mechanism (5,8,11). Thus these studies have led to complementary findings on the ABA-unbound and ABA-bound receptors and the homo-dimeric PYR/RCAR organization (5,8,11) and the ABA-bound structures of PYR/RCARs with PP2Cs (3,4,11) and show that PYR/RCARs are direct ABA receptors.

Collectively, these studies have provided insight into the mechanism that regulates the inhibition of PP2C activity by PYR/PYL/RCAR proteins in response to ABA. These findings set the scene for the development of biotechnological tools that could lead to the generation of stress resistant crops.

(1) Fujii H, Chinnusamy V, Rodrigues A, Rubio S, Antoni R, Park SY, Cutler SR, Sheen J, Rodriguez PL, Zhu JK (2009) In vitro reconstitution of an abscisic acid signalling pathway. Nature (462): 660-664

(2) Ma Y, Szostkiewicz I, Korte A, Moes D, Yang Y, Christmann A, Grill E (2009) Regulators of PP2C phosphatase activity function as abscisic acid sensors. Science (324): 1064-8

(3) Melcher K, Ng LM, Zhou XE, Soon FF, Xu Y, Suino-Powell KM, Park SY, Weiner JJ, Fujii H, Chinnusamy V, Kovach A, Li J, Wang Y, Li J, Peterson FC, Jensen DR, Yong EL, Volkman BF, Cutler SR, Zhu JK, Xu XE (2009) A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. Nature (462): 602-608

(4) Miyazono KI, Miyakawa T, Sawano Y, Kubota K, Kang HJ, Asano A, Miyauchi Y, Takahashi M, Zhi Y, Fujita Y, Yoshida T, Kodaira KS, Yamaguchi-Shinozaki K, Tanokura M (2009) Structural basis of abscisic acid signalling Nature (462): 609-614

(5) Nishimura N, Hitomi K, Arvai AS, Rambo RP, Hitomi C, Cutler SR, Schroeder JI, Getzoff ED (2009) Structural Mechanism of Abscisic Acid Binding and Signaling by Dimeric PYR1. Science (326): 1373-9

(6 Nishimura N, Sarkeshik A, Nito K, Park SY, Wang A, Carvalho PC, Lee S, Caddell DF, Cutler SR, Chory J, Yates JR, Schroeder JI (2009) PYR/PYL/RCAR family members are major in-vivo ABI1 protein phosphatase 2C-interacting proteins in Arabidopsis. Plant Journal (61): 290-9

(7) Park SY, Fung P, Nishimura N, Jensen DR, Fujii H, Zhao Y, Lumba S, Santiago J, Rodrigues A, Chow TF, Alfred SE, Bonetta D, Finkelstein R, Provart NJ, Desveaux D, Rodriguez PL, McCourt P, Zhu JK, Schroeder JI, Volkman BF, Cutler SR (2009) Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. Science (324): 1068-71

(8) Santiago J, Dupeux F, Round A, Antoni R, Park SY, Jamin M, Cutler SR, Rodriguez PL, Márquez JA (2009) The abscisic acid receptor PYR1 in complex with abscisic acid. Nature (462): 665-8

(9) Umezawa T, Sugiyama N, Mizoguchi M, Hayashi S, Myouga F, Yamaguchi-Shinozaki K, Ishihama Y, Hirayamad T, Shinozaki K (2009) Type 2C protein phosphatases directly regulate abscisic acid-activated protein kinases in Arabidopsis. PNAS (106): 17588-17593

(10) Vlad F, Rubio S, Rodrigues A, Sirichandra C, Belin C, Robert N, Leung J, Rodriguez PL, Laurière C, Merlot S (2009) Protein Phosphatases 2C Regulate the Activation of the Snf1-Related Kinase OST1 by Abscisic Acid in Arabidopsis. Plant Cell (10): 3170-84

(11) Yin P, Fan H, Hao Q, Yuan X, Wu D, Pang Y, Yan C, Li W, Wang J, Yan N (2009) Structural insights into the mechanism of abscisic acid signaling by PYL proteins. Nat Struct Mol Biol (16): 1230-6

Community Arabidopsis Projects and Resources

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

By: Eva Huala, TAIR Director

TAIR Funding:

In mid-2009 TAIR was granted a renewal from NSF that provides level funding for the current year (September 2009 - August 2010) followed by steeply decreasing budgets (approximately 75%, 50% and 25% of the current year) for the remaining three years. The steep decreases in TAIR's NSF funding beginning in September 2010 will require severe cutbacks in the services provided by TAIR unless additional funding can be found. The following timeline shows how TAIR's activities will be cut back to match the available funding:

September 2010: Curators will no longer gather gene function information from published articles. Manual curation of Arabidopsis gene structures will also end but computational updates to gene structures will continue for one additional year with a final genome release planned for summer 2011. We will continue to support TAIR's journal collaborations and load gene function data submitted to TAIR spontaneously or through journal collaborations. **Impact:** Beginning in September 2010 the TAIR database will begin to fall rapidly out of date with regard to gene function, phenotypes, gene names, allele symbols and expression patterns. Staff layoffs will impact our ability to recover from the funding crisis even if new funding is found after this date.

September 2011: All gene structure and function updates will end except those resulting from community data submissions. Existing tools and databases will be maintained and kept available, loading of community data submissions and user support will be continued, all other activities will end. **Impact:** Beginning in mid- 2011 the Arabidopsis genome annotation will be static, with no incorporation of newly discovered genes or other genomic features.

September 2012: Existing tools and databases will be maintained and kept available, loading of community data submissions and user support will be continued.

August 2013: Current TAIR grant ends. The TAIR website will no longer be available after August 31, 2013.

Other funding sources:

Efforts to find additional funding for TAIR are underway but no source of funding has yet been identified that could serve as a sustainable alternative to grant funding. Some possible revenue sources we are exploring include corporate sponsorships or subscriptions and licensing of TAIR software to companies but to date it appears unlikely that more than a small fraction of TAIR's costs could be recovered from these sources. Advertising has been ruled out due to the low potential for bringing in revenue and its incompatibility with our host institution's non-profit status. Although we have considered the possibility of requiring academic subscriptions we believe the negative impact on our ability to provide data releases to other groups and effectively solicit community data contributions to TAIR precludes this option as a viable long-term funding source.

TAIR Usage Statistics and Surveys:

TAIR usage continued to grow over the past year, with an average of 37,600 unique visitors to the TAIR website each month in 2009, an increase of 12% over the number of visitors in 2008. The number of registered TAIR users also continued to grow: as of March 22 there were 20,241 registered users (including 9836 that have been added or updated in the past 5 years) and 7836 labs (including 4899 that have been added or updated in the past 5 years). Surveys conducted in November 2009 and March 2010 via email to registered TAIR users and posting of the survey link on the TAIR website indicate that 74% of respondents consider TAIR to be essential to their research or teaching. Approximately 99% of survey respondents were affiliated with an academic institution, nonprofit research institution or government agency and only 0.8% were affiliated with a company. Use of the TAIR website to gather information saved the respondents an average of 1-3 hours per week. This suggests that TAIR saves approximately 1 million hours of researcher time each year (9836 active registered users x 2 hours saved per week x 52 weeks = 1,022,944 hours of researcher time). If the average salary of a researcher is $20 per hour this translates to a savings of 20.5 million dollars per year or approximately 12 times the annual cost of supporting TAIR at 1.6M/yr.

Curation of gene function data:

In the past year TAIR has added 6059 new gene function annotations based on experimental data to 1708 Arabidopsis genes. Of these, 402 genes had no previous annotations based on experimental data. As of March 25, 2010 a total of 9024 Arabidopsis genes have been annotated with Gene Ontology terms based on direct experimental data. If experimental data on gene expression patterns is also included 20,373 genes (71% of all TAIR8 genes excluding transposon genes and pseudogenes) now have experimental annotations in TAIR. These annotations were generated in part by TAIR's in-house article curation efforts and in part from TAIR's collaboration with the journal *Plant Physiology* (see below). Annotations made by TAIR curators in the past year were based on experimental results reported in 545 published research articles. The set of articles curated by TAIR staff represents approximately 32% of all articles published in that period with experimental data on the function of Arabidopsis genes. The articles were chosen for curation by TAIR staff based on their content, with higher priority given to articles describing the function of previously uncharacterized genes.

TAIR Journal Collaboration Program

TAIR's new journal collaboration program aims to gather Arabidopsis gene function data directly from authors whose articles have just been accepted for publication. The program was launched in early 2008 with the journal *Plant Physiology*, and in the last 12 months (March 09 - February 10) TAIR has received direct author submissions of gene function or expression information for 422 genes drawn from 104 articles, resulting in 609 new gene function annotations in TAIR. Although the rate of initial compliance by *Plant Physiology* authors was only 21% in the first year, we have

clarified the author instructions resulting in an improvement to 50% compliance, with further improvement expected as authors gain familiarity with the submission process. The journal collaboration program was expanded in the past year to include The Plant Journal and work is underway to include six additional plant journals. A new interactive web form and an improved pipeline for reviewing and loading community annotations is currently under development.

Curation of gene structures and genome assembly:
The most recent genome release, TAIR9, was made public on June 19, 2009. A description of this release can be found in the 2009 MASC report or on the TAIR news page (http://arabidopsis.org/doc/news/breaking_news/140). The TAIR10 release is planned for summer 2010 and will include updates to gene structures based on proteomics and RNA-seq data from the Mockler, Ecker, Briggs and Baginsky labs. No updates to the chromosome assembly are planned for the TAIR10 release.

Other new data and tools:
A synteny viewer (gbrowse_syn, developed by Sheldon McKay) displaying aligned genomes of *Arabidopsis lyrata* and *A. thaliana* was released in July 2009. An update to the synteny viewer in November 2009 added alignment data for poplar. The *A. lyrata* and *P. trichocarpa* alignment were kindly provided to TAIR by Pedro Pattyn, a student in the Van de Peer lab at the University of Ghent, Belgium. RSS feeds for TAIR news and job postings were also added to TAIR in November 2009. NBrowse, a tool for visualizing interaction partners developed by Mark Gibson in the Gunsalus lab at New York University, was released on the TAIR site in March 2010. The new synteny and interaction viewers are available from the TAIR Tools dropdown menu and the RSS feeds can be accessed from the Breaking News section of the TAIR home page, the TAIR news archive and the Job Postings page.

The Arabidopsis Biological Resource Center (ABRC, http://abrc.osu.edu/)

By: Erich Grotewold, ABRC Director

The Arabidopsis Biological Resource Center (ABRC) collects, preserves and distributes seed and DNA resources of Arabidopsis and related species. Current ABRC seed stock holdings include insertion lines covering 25,000+ genes, the 11,000+ lines of the Arabidopsis TILLING service, 360 natural accessions which are genetically fingerprinted and 80 received from 1001 Genomes Project, 27 recombinant inbred populations, a set of near-isogenic lines, new Wisconsin Ds-Lox T-DNA lines, RNAi lines, and related species. DNA resources at ABRC include full-length ORF and cDNA clones for about 16,000 genes, BACs covering the entire genome, BACs of nine related species, the AGRIKOLA GST entry clones, various sets of expression clones and 8,000 amiRNA clones. The ABRC has also recently initiated the distribution of cells in culture, as well as chips generated by S. P. Dinesh-Kumar (Yale Univ.) containing more than 5,000 proteins. The distribution of seed and DNA stocks exceeded 90,000 in 2009.

ABRC is presently conducting a so far very successful stock donation campaign with emphasis on the improvement of the published mutant collection. Toward this end, we have greatly streamlined the donation process. The new simplified form and procedure can be found at http://arabidopsis.org/submit/abrc_submission.jsp. We encourage everyone to participate by sending their published mutant stocks. Donations of other seed stocks as well as clones continue to be welcome. ABRC continues to focus on functional genomics. The J.Ecker laboratory (Salk Institute, http://signal. salk.edu/gabout.html) is genetically purifying to homozygosity 50,000 T-DNA insertion knockout lines. To date, 33,747 of these lines have been received. The stocks being utilized for this project include the J.Ecker (SALK) population plus lines from Syngenta (SAIL), B. Weisshaar (GABI-Kat) and P. Krysan/R. Amasino/M. Sussman (Wisconsin Ds-Lox). Initial members of sets of the confirmed SALK T-DNA lines have been distributed to laboratories for forward screening. So far 28,297 lines have been made available and are ready for distribution, and several sets of confirmed SALK lines have been made available during 2009. Of note are recent additions, which include Saskatoon activation-tagged T-DNA lines, MAGIC recombinant inbred lines and a set of Wave lines expressing subcellular localization markers. Receipt and distribution of Entry and Expression full length/ORFeome clones remain a priority. ORF clones lacking a stop codon are being received from members of the Arabidopsis Membrane Interactome Project, with 2,106 received to date. The extensive expression ORF collections from S. P. Dinesh Kumar and S. Clouse continue to be received, with over 16,400 of these currently in-house. Further additions to the amiRNA collection are also anticipated. We are pleased to report that 10,000 loci are now represented by clones in both a GatewayTM entry vector and the pUNI51 vector, 4,000 loci are represented only by a clone in a GatewayTM entry vector and 2000 are represented only by a clone in the pUNI51 vector.

Measuring Gene Function

By Irene Lavagi, MASC Coordinator

In 2003, MASC members agreed that it would be useful to establish an improved means to update gene function knowledge and quantify the number of genes with known function. Since the 2004 MASC annual report this was illustrated by thermometers to provide visual illustrations of the progress in Arabidopsis functional genomics efforts. This year, the thermometers are measured against the new TAIR9 genome release and include the number of loci (1) containing sequence-indexed insertion elements (T-DNA), (2) targeted by RNAi constructs, (3) with full-length cDNA clones, sequencing status and availability, (4) with Open Reading Frame (ORF) clones available as stocks and (5) with gene expression detected. The thermometers are updated with data available at the end of April 2010.

It is likely that the thermometers do not include all existing data and resources given that there are individual labs and private companies that have not publicly shared information, as well as publicly available resources that are not easily accessible. In 2007, MASC re-evaluated the usefulness of the tracking thermometers and the majority opinion was that in general, the thermometers are useful even if they are an underestimate of the existing resources. MASC also felt that (1) the thermometers should not track data and resources that are not freely shared as their emphasis is on readily available resources, (2) a caveat that not all existing resources are included should be noted and the sources for the thermometers should be listed, and (3) researchers with currently inaccessible data and resources must be encouraged to submit them to major public repositories so they can be tracked. Based on this discussion we have included updated thermometers for 2010 with the sources of data and resource counts listed accompanied by the caveat that they do not represent all existing data and resources in the listed categories but do represent a large proportion of what is publicly available in large repositories and databases.

As the Arabidopsis 2010 project draws to its end, the progress in generating resources over the past year is shown in the tracking thermometers below alongside knowledge of gene function. During the past year advances have been made in expanding resources to knockout or knockdown gene expression including the isolation of two or more confirmed homozygous insertion mutants for an additional 6% of genes, and isolation of insertion mutants with at least one confirmed homozygous insertion for an additional 4.4% of genes. This brings the current total to 17,721, or nearly 62% of unique genes, with one or more confirmed homozygous insertions, comprising 10,503 genes with two or more homozygous insertion sites and an additional 7,218 genes with one homozygous insertion site. To date, more than 33,747 lines have been received by ABRC. In total, 27,543 of 28,691 unique Arabidopsis genes (almost 96%) contain at least one sequenced insertion element. Increases in the other resource categories have been much more modest which likely reflects the conclusion of several large-scale projects. However, there is some information about the majority of unique Arabidopsis genes; for example, numerous gene expression studies and resources available demonstrate confirmed expression for 27,257 of 28,691 genes (95%), including new input from a project that is sequencing small RNAs.

Tracking Thermometers

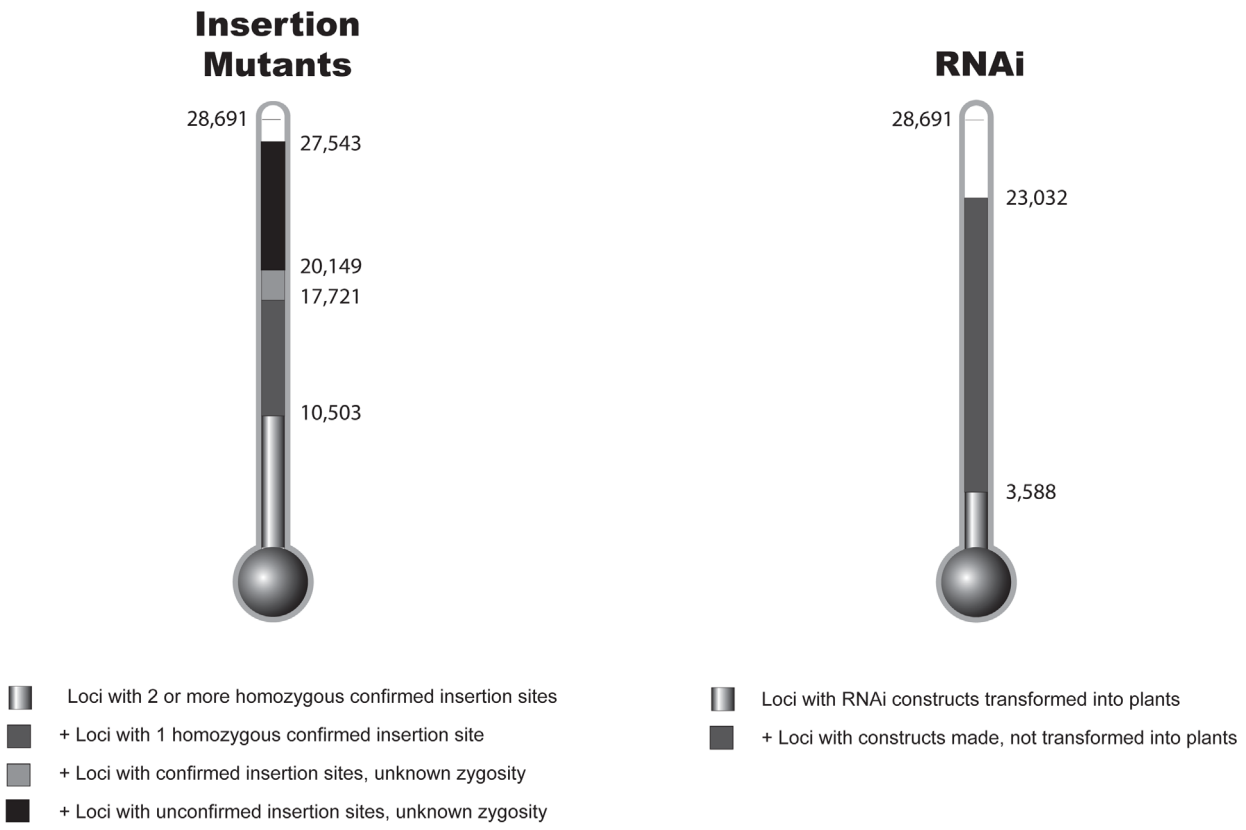

Figure 2: Measuring Arabidopsis Genomic Resources

All data are as of April 2010. For consistency, all resources are measured against the TAIR9 genome release (including noncoding RNAs and organelle-encoded genes but excluding transposon genes and pseudogenes, a total of 28,691 genes). Five categories are included: (A) Loci with insertion mutants – 10,503 genes with two or more homozygous confirmed insertion sites, an additional 7,218 genes with one homozygous confirmed insertion site, an additional 2,428 genes with confirmed insertion sites and homozygous status unknown, and an additional 7,394 genes with unconfirmed insertions, homozygous status unknown (data from Huaming Chen/Joe Ecker, SIGnAL, including data from the Salk collections, the Arabidopsis community, and GABI); (B) Loci with targeted RNAi knockdowns - 3,588 genes with RNAi constructs transformed into plant lines and an additional 19,444 genes with RNAi knockdown constructs made but not transformed into plant lines, (data from Emma Knee/Randy Scholl (ABRC), the 2010 amiRNA project (CSHL), Martine Vanhoucke/Pierre Hilson (PSB/LMBP), Ian Small (AGRIKOLA), Graeme Gill/Sean May (NASC), and chromDB project); (C) Loci with full length cDNA clones - 18,327 genes with full length cDNAs fully sequenced and known to be available for ordering, an additional 1,925 genes with cDNAs not fully sequenced but known to be available and an additional 944 genes with fully sequenced cDNAs but stock availability unknown, (data from Huaming Chen/Joe Ecker, SIGnAL); (D) Loci with ORF clones - 16,718 genes with fully-sequenced ORF clones and an additional 1,493 with partially sequenced ORF clones (data from Huaming Chen/Joe Ecker, SIGnAL); (E) Expression detected – 21,115 loci with cDNAs (data from Eva Huala, TAIR), an additional 3,611 loci with ESTs, an additional 2,531 loci with expression detected only by small RNA (smRNA) sequencing (data from Eva Huala/TAIR)

Note: Detailed information on ORF, cDNA, and other projects can be found in the ORFeomics and Phenomics Subcommittee Reports (pages 27-32).

Full-length cDNA clones

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

ORF

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

Expression

Loci with cDNAs
+ Loci with ESTs
+ Loci with smRNA expression

Broader Impacts of Arabidopsis Research

Impacts on Industry

Arabidopsis research has increasingly impacted the study of other plants. The knowledge gained from this reference plant serves to advance our understanding of other plant species, particularly crop species, and thus translate into new or improved plant products and increased agricultural productivity. Importantly, basic research in Arabidopsis provides the foundation for applied studies, many of which take place within private companies. This division of labour between the public and private sector is successful due to their complementary approaches; publicly funded basic research, typically performed in universities, benefits from relative freedom to explore a broad range of hypotheses and to develop novel tools and approaches. This curiosity-driven approach facilitates discoveries that can be leveraged by private companies whose research programs are more focused on applications with commercial value. In this system, basic research thrives on open exchange of information and resources while private companies are structured to maintain confidentiality. Companies commonly make their findings publicly known only during later stages of the commercialization process and such disclosures may contain few details unless they are conveyed through peer-reviewed publications. This presents a predicament to Arabidopsis research supporters who want to understand the usefulness of basic research to commercial applications. Compounding challenges include the relatively long time from discovery to application and the pervasive reality that commercial products are often not explicitly defined by the contributions derived from Arabidopsis studies.

When evaluating the success of Arabidopsis as a means of advancing applied research, it is important to keep the realities of public vs. private research and relatively long timeframe from discovery to product in mind. Similarly, it can take a bit of sleuthing to uncover the ways in which Arabidopsis research plays important roles in the success of commercial products, or any research project that in the end, focuses on another species. Importantly, while the recent advances in Arabidopsis research have been phenomenal, it is worth remembering that it is still a fairly new model organism. According to the National Center for Biotechnology Information (1), 25 years ago there were 263 and 465 publications citing rice or corn, respectively, but only 5 citing Arabidopsis. Similarly, the US Patent and Trade Office (2) listed 545 patents referencing rice and 1,491 referencing corn at that time. In comparison, the first U.S. utility patent referencing Arabidopsis was filed in 1989, six years later.

An indication of what we might expect from translating basic Arabidopsis research into crop species and commercial products in the next decade is informed by the rapid increase in publication rate and patent filing in the last 15 years, the timeframe in which Arabidopsis became established among other classic model organisms such as rice and corn. Between 1994 and 2009, the number of peer-reviewed Arabidopsis publications increased by 8-fold, while rice and corn publications increased roughly 4-fold and 2-fold, respectively (Fig. 1, page 9). In that same timeframe, while the number of U.S. patents referencing rice and corn increased 2.4-2 fold, the number of patents citing Arabidopsis increased 42-fold (Figure 3).

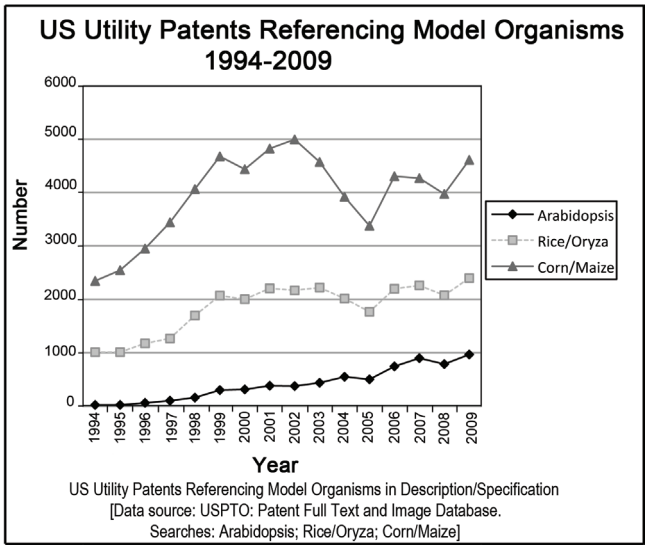

Figure 3: US Utility Patents Referncing Model Organisms 1994-2009

To reflect the international cooperation and effort of the Functional Genomics Project, this year we have included data on patents referencing model organisms from other parts of the world. Whilst searches for US utility patents have been performed as in previous years, data on patents filed in other countries had to be retrieved via a different database. Although using different databases poses some limitations, the insight gained from a global perspective outweighs them. The European Patent Office database esp@cenet (3) currently allows the searching of three databases to gather information on the existing patents across the world: 1) EP-complete collection including full text of European published applications 2) Worldwide- full collection of worldwide published applications from 80+ countries 3) WIPO complete collection including full text of PCT published applications. In the U.S. the correct term for a patent is 'utility patent', whereas in Europe they are referred to as 'published applications'. Most of the world's countries are signatories to the Patent Cooperation Treaty (PCT). The PCT is an international patent law treaty (London, 1970) that provides a unified procedure for filing patent applications and protects

inventions in each of its contracting states. As of September 2009, there were 142 contracting states to the PCT. A patent application filed under the PCT is called an international application, or a PCT application. The number of European published applications (i.e. patents) and PCT published applications referencing model organisms have been included, searching for the keyword of interest in the full-text option, as it corresponds more closely to the US Description/Specification field (Figure 4 and 5).

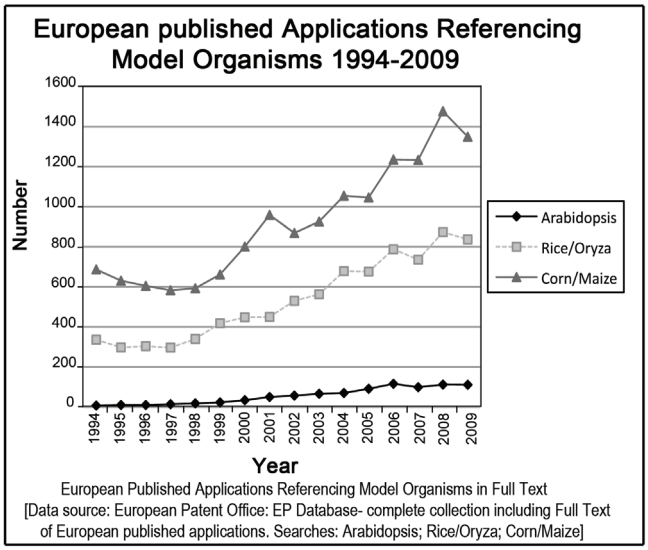

Figure 4: European published Applications Referencing Model Organisms 1994-2009

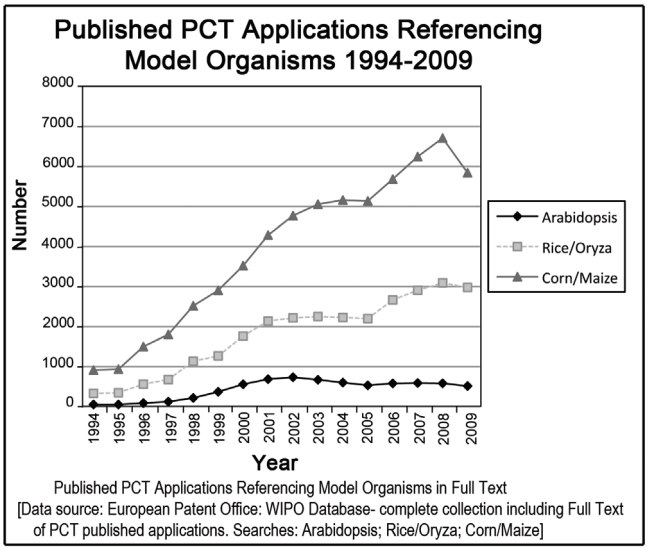

Figure 5: Published PCT Applications Referencing Model Organisms 1994-2009

The worldwide search option was not included in this report as both the country published application and the PCT published applications are included, increasing the number of multiple hits for any given published application. The number of European and world's published applications also increased in the period between 1994 and 2009. Interestingly, a 16-fold increased was registered for European published applications referencing Arabidopsis, whereas a 2.5 and a 2 fold increase occurred for rice and corn respectively. From a world's perspective (or PCT perspective), published applications referencing Arabidopsis increased by 10-fold, whereas rice and corn registered a 9- and 6.4 fold increase respectively. The absolute number of patents citing rice and corn exceed those citing Arabidopsis. This reflects how access to a reference sequence enables both applied and basic research and illustrates how strong funding of Arabidopsis as a model organism by numerous funding bodies has been central to developing Arabidopsis as a reference for plant biology, and for leveraging the knowledge gained in Arabidopsis for studies in other plant species.

The importance of basic Arabidopsis research cannot be understated and it is clearly an invaluable reference to applied research efforts. The upcoming decade will likely yield a number of commercial advances based on Arabidopsis studies. In this report, we have chosen just a few recent examples of discoveries that demonstrate the importance of basic Arabidopsis research to applied research, and how knowledge gained in this reference organism can be translated into real-world applications.

(1) http://www.ncbi.nlm.nih.gov/sites/entrez?db=PubMed
(2) http://patft.uspto.gov/netahtml/PTO/search-adv.htm
(3) http://ep.espacenet.com:80/advancedSearch?locale=en_EP

Examples of Translation Research Using Arabidopsis

Lighting up with Arabidopsis
By: Irene Lavagi, MASC Coordinator

The ability to control cellular events and manipulate them with high spatio-temporal resolution is a goal that both experimental biologists and medics wish to fulfil. Being able to influence the activity of one specific molecule within a cell is a very attractive prospective. Over the past decade optical reporters such as proteins fused to fluorescent chromofluore, have been extensively used to observe and measure cellular states. Reporters fused to the green fluorescent protein GFP and its derivatives have helped to elucidate the subcellular localisation of molecules and served as reporters for the quantitative measurement of cellular activities. In all the above examples light was used to track cellular activities. Recently, the inverse challenge, which is to use light to exert control over cellular activities, has been explored. Two recent *Nature* publications demonstrated that the naturally occurring light responsive domains of plant proteins can be exploited to introduce light-dependent control of cell functions. In the first of the papers Wu and colleagues demonstrated a light-gated system, which exploited the light-sensitive domain of phototropin 1 from *Avena sativa* to control Rac activity (1).

This approach was taken further in research by Levskaya and co-workers that utilised the Arabidopsis phytochrome signaling machinery as a switch to control cellular behaviour in mammalian cells (2). Arabidopsis phytochromes are photoreceptive signalling molecules that detect red (650 nm) and infrared (>750 nm) light. The conformation of Arabidopsis Phytochrome B (PhyB) changes

depending upon the wavelength of light to which it is exposed. Only the red-light conformation of PhyB allows PhyB to bind the transcription factor PIF3. The heterodimeric PhyB-PIF3 complex translocates to the nucleus where it modulates directly the transcription of light response genes. In this study the Phy-PIF3 interaction was optimised using a domain from another transcription factor (PIF6) fused to YFP and mCherry tagged PhyB localised to the plasma membrane via a C-terminal motif. Upon exposure to red light PhyB undergoes a conformational change that allows it to bind PIF3 and triggers the subsequent translocation of the YFP-PIF domain to the plasmamembrane. Rapid binding and reversibility by exposure to infrared light were also obtained and optimised. High spatio-temporal control was achieved by focusing a spot of red light on one particular area of the cell, whilst bathing the cell in infrared light. This optimised system that allows light-gated translocation of the molecules of interest with micrometre spatial resolution and at a timescale of seconds, was shown to be efficient for the localised activation of regulators of Rho GTPases, which control the actin cytoskeleton, to reshape and direct the cell morphology of mammalian cells.

These recent studies involving the light-sensitive domains of plant proteins provide very promising tools to exert unprecedented levels of control over cellular biological processes, which are of particular interest in medicine.

(1) Wu YI, Frey D, Lungu OI, Jaehrig A, Schlichting I, Kuhlman B, Hahn KM (2009) A genetically encoded photoactivatable Rac controls the motility of living cells. Nature (461): 105-8

(2) Levskaya A, Weiner OD, Lim WA, Voigt CA (2009) Spatiotemporal control of cell signalling using a light-switchable protein interaction. Nature (461): 997-1001

Fatter plants to fuel your car

By: Irene Lavagi, MASC Coordinator

The ever-increasing demand for fuel requires the rapid development of sustainable and renewable sources of energy. According to the goal set by the US, by 2025 one third of all liquid fuel should be generated from renewable sources. It is estimated that 1 billion tonnes of biomass would be needed to meet this requirement. Increased biomass is therefore a highly desirable trait that should be engineered in plants. Turner and colleagues from the University of Manchester (UK) have identified Arabidopsis genes that could be engineered in plants to greatly increase biomass.

Controlling the orientation of the cell division plane is key to the development of plant organs. Despite the crucial importance of differential cell growth the mechanisms regulating this process are not well understood. Work conducted by Etchells and Turner on cell division of the vascular bundles of Arabidopsis led to the identification of new genes that are responsible for its radial growth (1). During vascular development the orientated division of the long thin meristematic cambial cells down their long axis generates files of cells along the radial axis. Receptor-like kinases and ligands belonging to the CLE family have been shown to be required for these oriented cell divisions. However, the signaling mechanism that controls the orientation of cell division had remained unknown. The receptor kinase PXY is normally expressed in the dividing meristematic cells of the procambium, whereas *CLE41* expression localizes to the adjacent phloem cells. In this study it was demonstrated that the interactions between PXY and CLE41 determine the orientation of the division plane. *CLE41* expression is localized to phloem cells, it is perceived by PXY and is required for ordered vascular development. Misexpression of *CLE41* in the xylem was shown to result in the loss of cell division orientation and the consequent compromised development of the vascular tissues. Importantly, overexpression of *CLE41* in the phloem, its normal localization, increased the number of cell divisions without compromising the orientation, leading to an increased but correctly patterned vascular development. This work also provided evidence that expression of *PXY* is down regulated by CLE41 in a negative feedback loop mechanism that allows the integration of PXY signaling roles, including the control of xylem differentiation and the regulation of vascular cell division.

This work therefore sheds new light on the regulation of the radial growth of Arabidopsis. Translation of this knowledge into other plant species could make trees grow thicker in less time, leading to increased wood biomass for biofuels. The team is currently assessing the system for increased outwards growth in poplar trees to develop an efficient way to increase wood production.

(1) Etchells JP, and Turner SR (2010) The PXY-CLE41 receptor ligand pair defines a multifunctional pathway that controls the rate and orientation of vascular cell division. Development (137): 767-774

Unlocking seed size to increase crop yield

By: Irene Lavagi, MASC Coordinator

The increasing world population requires continued improvement in crop yields. A key aspect of this is the ability to control seed size. Although larger seeds tend to be less easily dispersed, they are more likely to contain a greater percentage of storage products of nutritional advantage in a food crop and provide the germinating seedling with an increased competitiveness during seedling establishment. Seed development in plants is a complex process that requires the coordinated controlled growth of the embryo, endosperm and the maternal tissue.

In a recent study by Adamski and co-workers, maternal cytochrome P450 KLUH (KLU) was shown to regulate seed size in Arabidopsis (1). KLU had been previously shown to promote the growth of leaves and floral organs. Promoter fusions studies revealed that *KLU* is expressed within the base of the nucleus and the inner integument of the ovules throughout their development. Loss of function of KLU leads to seeds that are 13% lighter and 16% smaller than wild-type, whilst increased expression of *KLU* results in 11% and 10% increase in weight and size of seed respectively. These results indicate that the level of KLU activity positively correlates with seed size. Although *KLU* is also expressed in developing embryos, experiments involving numerous plant crosses demonstrated that the embryo and endosperm genotype for KLU do not influence seed size, instead KLU provided by the mother plant promotes seed growth. Experiments involving a rescue transgene in the *KLU* loss of function transgenic line demonstrated

that the changes in seed size are not due to global changes in plant resources. In addition, KLU action was found to be independent of other maternal factors that alter integument cell proliferation.

Data obtained from this study show that the level of KLU-dependent growth factor signalling determines the size of ovules and seeds. These findings are all the more pertinent giving the potential implications on crop improvement to ensure food security in the future. Indeed, increased seed or grain size is key to increasing the yield of crops to cope with an increasing world population. Scientists are already looking at translating these findings into crop plants. Plant Bioscience limited (PBL) has patented this discovery and licensed it to agricultural biotechnology companies for use in major crop species.

(1) Adamski NM, Anastasiou E, Eriksson S, O'Neill CM, Lenhard M (2009) Local maternal control of seed size by KLUH/CYP78A5-dependent growth signalling. PNAS (106): 20115-20

Unravelling human diseases using Arabidopsis

By: Irene Lavagi, MASC Coordinator

Model organisms have a history of being used to study human diseases particularly when the model has a close similarity to the disease. Searching for models of human disease may have recently taken a huge step forward due to a technique that involves screening genetic databases to find links to organisms that are as far removed from humans as plants (1). The new technique draws upon data from existing databases and then qualitatively and systematically identifies non-obvious equivalences between mutant phenotypes in different species based on overlapping groups of orthologous genes from human, mouse, yeast, worm and plant. This approach allows researchers to identify genes in non-human species that are likely to contribute to human disease. As one would expect many specific and obvious phenologs were found through this analysis, particularly through the comparison of mouse and human phenotypes. However, the disruption of function in conserved genes may give rise to different phenotypes in different species, as illustrated by the disruption of human RB1 which causes cancer of the retina, whereas mutation of the nematode orthologue results in the mislocalisation of worm genitalia. Nevertheless, this technique still offers very powerful insights into potential gene function.

Indeed, work from this research group has suggested less obvious phenologs. These include the use of a yeast model for the study of angiogenesis defects, a worm model for breast cancer, a mouse model for autism, and a plant model for the study of neural crest defects that are associated with Waardenburg syndrome. With specific regard to the plant model, genes involved in gravity sensing were found to be linked to those associated with human Waardenburg syndrome, which causes the abnormal pigmentation of the skin and hair, in addition to cleft palate and lip, and hearing loss, which accounts for 2-5% of cases of deafness. Identification of the phenolog suggested that three plant genes involved in plant growth in response to gravitational signals, may direct neural crest cell migration and differentiation in animal embryos. One of the three proteins, STX12, is known to interact with the protein of the *pallid* gene in mice, whose mutational phenotypes include pigmentation and ear defects, consistently with Waardenburg syndrome. The other two genes had not previously documented and the three mammalian orthologs of theses genes were evaluated using *in situ* hybridisation in *Xenopus*. It was found that *sec23ip* was expressed in migrating neural crest cell and that reduced expression of the *sec23ip* gene caused severe defects in the migration patterns of neural crest cells, thus confirming gene function. The success rate of 50% for genes relevant to Waardenburg syndrome is a 550-fold improvement upon the current accepted rate of 1 in 1100 genes. Importantly, regardless of disparate phenotypes, phenologs can identify functionally consistent gene sets that predate the divergence of plants and animals.

This approach will clearly be most useful in determining subtle associations related to complex diseases. One major hope is that it will expedite the identification of disease pathways and drug discovery, as undertaking research on organisms such as plants and yeast is much cheaper and rapid than studying mice and humans.

(1) McGary KL, Park TJ, Woods JO, Cha HJ, Wallingford JB, Marcotte EM (2010) Systematic discovery of nonobvious human disease models through orthologous phenotypes. PNAS (107): 6544-9

Single-parent plants

By: Irene Lavagi, MASC Coordinator

An observation in Arabidopsis chromosome research has lead to the generation of a technique for producing plants that possess genetic information from one parent (1). This discovery is of particular value as it could rapidly accelerate the breeding of crop plants, and is a clear example of the value of translational research. The molecular principles of genome elimination are not known. However, one theory is that centromeres from one of the parent plants interacts unequally with the mitotic spindle, leading to selective chromosome loss. The generation of a haploid plant carrying chromosomes from one parent has been discussed for decades: it is highly desirable as plants would be instantly homozygous, therefore removing the necessity for generations of inbreeding.

The work of Ravi and Chan has demonstrated that haploid Arabidopsis can be generated through seeds by the manipulation of the centromere specific histone protein CENH3. The crossing of *cenh3* null mutants with wild type leads to the eradication of chromosomes from the mutant, therefore yielding haploid progeny. Meiotic non-reduction spontaneously produces fertile diploids from haploids, enabling genotype continuation. Furthermore, it has been demonstrated that it is possible to reduce a natural tetraploid Arabidopsis line (Warschau-1) to a haploid through centromere-mediated genome elimination, thus simplifying breeding.

CENH3 is universally present in eukaryotes, making the findings unearthed through this 'blue skies' research very favourable to the production of haploids in other plant species. CENH3 is not highly conserved between species and is among the fastest-evolving sequences in the genome leading to the suggestion by Chan and co-workers that centromere differences may create barriers to breeding between species.

This work has opened up new avenues of research for the group which plan to test this theory through the crossing of

closely related species. In addition to expediting research, the findings should impart benefits to the crop sector, by providing a possible mechanism for creating haploid inducing lines in any plant species.

(1) Ravi M and Chan SWL (2010) Haploid plants produced by centromere-mediated genome elimination. Nature (464): 615-9

The Past 10 Years in Arabidopsis Research

By: Irene Lavagi, MASC Coordinator

As we approach the end of the NSF-funded Arabidopsis 2010 initiative, it is an appropriate time to reflect on what we have achieved in the past ten years in Arabidopsis research. Over the past twelve months alone Arabidopsis has featured in 3,093 research publications, including an entire issue of the *Plant Journal* dedicated to Arabidopsis to celebrate the 10th anniversary of the publication of the fully assembled Arabidopsis nuclear genome sequence. Arabidopsis has also been in the headlines and editorials of key journals such as *Nature,* highlighting the concerns for reduced funding opportunities for Arabidopsis research and the need to grow and respond to the evolving needs of the wider plant community.

On the 10th Anniversary of the Multinational Cooordinated *Arabidopsis thaliana* Functional Genomics Project, MASC evaluates the last ten years of Arabidopsis research via interviews the MASC Coordinator undertook with a number of individuals that have played a central role in the Arabidopsis story over the past ten years, including funding officers and researchers, to discover what were the high and lows of the last decade and what the future might hold. A summary of these interviews is outlined here in the last Annual Report of this 10-year project.

The past ten years of Arabidopsis research have been very fruitful in both answering long-standing questions in plant biology and opening new avenues of research and applications. Scientific highlights of the past 10 years include the identification of the nature of receptor molecules of the major plant hormones, the discovery of florigen, a greatly enhanced understanding of the key players of many developmental pathways, an in-depth comprehension of transcriptional regulation of processes such as circadian rhythms, a contribution to the understanding of small RNAs, DNA methylation and the paradigm for natural variation. As outlined by Ottoline Leyser, "our knowledge of regulatory pathways and networks in Arabidopsis has developed to the point that a more holistic understanding is emerging", an idea that Machi Dilworth (NSF) reiterates: "Arabidopsis research has opened up the era of systems biology for plants. This is consistent with the tradition that Arabidopsis research has played as a scientific trail blazer". In addition, improved crop varieties are often the result of the application of discoveries first made in Arabidopsis, highlighting the importance of translational research. As Kazuo Shinozaki notes: "translational research for application in crops and trees will be built upon basic knowledge accrued in Arabidopsis".

Whilst in many ways advances in Arabidopsis over the past ten years have exceeded expectations, some areas outlined ten years ago have not delivered as expected. One notable example is the characterisation of every gene in the genome, reflecting on this limitation of the Functional Genome Project Philip Benfey commented: "It was an understandably naïve view that characterizing the phenotype of mutations in every gene would lead to an understanding of their function. We had no way of predicting the high degree of functional redundancy that exists". However, this is not surprising as most of the times the complexity of a research project is unravelled as the project itself develops.

Similarly, studies in diversity and evolution did not develop as predicted for example, as Detlef Weigel notes "no genomes of close relatives for functional annotation" were obtained until late in this decade. Despite the wealth of information that could be uncovered from the natural variation available across wild Arabidopsis ecotypes, it has remained relatively under- appreciated during the Functional Genomics projects. In fact, we are only just beginning to mine this remarkable resource, as exemplified by The 1001 Genomes Project for *Arabidopsis thaliana* that aims to discover the whole genome sequence variation in 1001 Arabidopsis strains and enable researchers to link phenotypic differences with genotypic variation in the plant.

Despite these and other limitations of the project, the success of the Functional Genomics Project have been numerous, especially the wealth of publicly available data, tools and resources that have been generated, including mutant collections of homozygous T-DNA insertion mutant lines; RNAi resources and artificial microRNAs; cDNA and ORF clones; large-scale microarray data; expanded information about the Arabidopsis proteome, metabolome and methylome; web-based databases and browsers. This plethora of resources has been central to a number of key advances in Arabidopsis research in the past decade as well as developing new paradigms in science. However, the almost exponential increase in data has created problems of its own, with the necessary infrastructure for data management, storage and access not growing at a rate comparable to that of data generation. This situation is the result of a combination of factors, including low numbers of bioinformaticians compared to biologists, a relatively weak demand (until recently) from pure biologists for the development of platforms that would be able to cope with very large data sets in an integrative manner and the concurrent development of equipment that was able to yield very large amounts of data. All these factors left Arabidopsis scientists short of time to tackle long-term data management issues before they arose. However, this situation is not unique to the Arabidopsis community as Machi Dilworth comments: "Since the need to manage data/information is great for everyone, I expect that someone outside the Arabidopsis community will develop better data management tools and novel ways to convert the database to a knowledgebase in the near future. I still hope that the richness of Arabidopsis information resources will inspire bright information scientists to work with forward-thinking

Arabidopsis researchers to advance the field of bioinformatics to the next level using Arabidopsis as an experimental model".

An integral component of the 2010 project was to promote national and international collaboration and much has been accomplished in this area over the past ten years, particularly as a result of the large datasets and resources that have been generated by Arabidopsis researchers for the wider community to utilize and exploit. As Detlef Weigel points out, "there is in general a lot more collaboration in the Arabidopsis field than in other fields", whilst Machi Dilworth believes that the "secret to the success of Arabidopsis research is openness among the world Arabidopsis researchers. They have shared information, materials, and ideas freely, and together they have built a cohesive international project whose sum is truly bigger than its parts". International collaboration has been actively promoted by MASC, which "has served a critical role as a clearing house for information about Arabidopsis research and as the primary body for organizing the international meetings and reaching out to funding agencies" says Philip Benfey. Ottoline Leyser adds: "international co-ordination is extremely important to minimize redundancy and maximize synergy in the Arabidopsis community. In addition, a clear and unified voice is very powerful in efforts to secure funding for important tools and resources". Funding official Machi Dilworth agrees: "MASC played a key role in fostering the international cooperation and collaborations with assistance of the MASC Coordinator. Funding agencies around the world who support Arabidopsis research have used the MASC reports in justifying funding Arabidopsis research in their own countries. In conclusion, I think the MASC and a cohesive international community have been extremely important for Arabidopsis research".

So what does the future hold for Arabidopsis research?

Among the interviewees there appeared to be a general agreement that the future of Arabidopsis research is "integrative, comparative and translational" as Ottoline Leyser summarizes. Behaviour of the plant in a dynamic, natural environment including other plant species and enemies (systems biology), cellular-resolution maps of RNA, protein, metabolite content and the intersection of natural variation are all areas that are expected to blossom in the next decade. Inspirationally Machi Dilworth says: "I have always thought that by the time a funding agency official like myself can identify where a field is going, the critical research is already underway […]. Arabidopsis research will continue to answer longstanding major questions in biology, to open up new fields of research, and to discover novel concepts and principles in biology. My sincere hope is that Arabidopsis research will take biology to a totally new plain that no one can even imagine today".

Reports of the MASC Subcommittees

Clone-based Functional Genomics Resources (ORFeomics)

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

Activities of the ORFeomics subcommittee have produced some additions to the existing very large set of Open-Reading Frame (ORF) clone set. Large scale ORF clone production has transitioned from ORFeome production to the construction of large set of 'destination' or 'functional' clone sets (Table 1). Examples of functional clone collections may include clone sets in planta overexpression, yeast two-hybrid interactome mapping, tagged ORF expression, etc. that are derived from the ORFeome collection.

Regarding unique ORF clone production (gene ORF clones not currently available in any form) and deposition during the past year, 620 Gateway ORF entry clones produced from the ATOME project (http://urgv.evry.inra.fr/ATOME/index.cgi) were deposited with ABRC. As part of the ORFeome project at URGV, a public database searchable for ORF clones in the collection using AGI codes (Atxgxxxx) directly linking to ordering from the ABRC or CNRGV stock centres has been opened (http://urgv.evry.inra.fr/ATOMEdb).

The RIKEN Plant Science Centre (PSC) project to collect full-length cDNAs (clone with 5' and 3' UTRs) from *Arabidopsis thaliana* (the so-called RAFL clones) has come to completion and all clones have been deposited to RIKEN Bio Resource Center (BRC) (http://rarge.psc.riken.jp/cdna/cdna.pl). In addition, the RIKEN PSC group has collected full-length cDNAs from various crops and trees for comparative genomics and genome annotation. Recently, they collected full-length cDNAs from wheat and soybean. The wheat and soybean full-length cDNAs are now available from Kihara Institute for Biological Research, Yokohama City University and the National Bioresource Project for Lotus/Glycine in Japan, respectively (Lotus: http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp, Glycine: http://www.legumebase.agr.miyazaki-u.ac.jp) Regarding 'functional' *Arabidopsis thaliana* ORF clone collections, several new large "destination" vector clone sets have been deposited into the public domain during the past year: The Arabidopsis 2010 Associomics project (http://associomics.org) donated 2,100 Gateway clones without stop codon (therefore allowing C-terminal fusions) to ABRC. Another 1,000 are available and will be submitted to ABRC. From the Arabidopsis 2010 LRR RLK project (Steve Clouse, North Caroline State University), 258 new ORF Gateway clone constructs, designed for expression in E. coli to create N-terminal Flag tagged kinases for in vitro biochemical assays, were deposited with ABRC. (http://www4.ncsu.edu/~sclouse/Clouse2010.htm). This bringing the total number of clones received from the LRR RLK project to 782. These include five types of clones: 1. full-length LRR RLK cDNAs in the Gateway Entry Vector pDONR/Zeo 2. 179 cytoplasmic kinase domains only in the Gateway Entry Vector pDONR/Zeo 3. 138 cytoplasmic kinase domain clones in a bacterial expression vector with N-terminal Flag tag 4. 140 full-length cDNAs with CaMV35S promoter, C-terminal Flag tag and BASTA resistance for expression in Arabidopsis plants 5. 152 full-length cDNAs with CaMV35S promoter, C-terminal GFP tag and hygromycin resistance for expression in Arabidopsis plants. In addition, 5000 TAP-tagged clones produced by the Yale group (Dinesh-Kumar et al.) were deposited with ABRC. This brings the total Yale clones to 15,000 ORFs. Most of the Yale ORFs were derived from the SSP/SALK ORFeome collection clone but a significant number of clones in this collection are derived from genomic DNA.

TAIR/ABRC RESOURCE FOR cDNA/ORF clones (http://www.arabidopsis.org/servlets/Order?state=catalog#dna)

References:

(1) Gou X, He K, Yang H, Yuan T, Lin H, Clouse SD, and Li J (2010) Genome-wide cloning and sequence analysis of leucine-rich repeat receptor-like protein kinase genes in Arabidopsis thaliana. BMC Genomics (11): 19

(2) Kawaura K, Mochida K, Enju A, Totoki Y, Toyoda A, Sakaki Y, Kai C, Kawai J, Hayashizaki Y, Seki M, Shinozaki K, and Ogihara Y (2009) Assessment of adaptive evolution between wheat and rice as deduced from full-length common wheat cDNA sequence data and expression patterns. BMC Genomics (10): 271

(3) Mochida K, Yoshida T, Sakurai T, Ogihara Y, and Shinozaki K (2009) TriFLDB (http://trifldb.psc.riken.jp/): A database of Clustered full-length coding sequences from triticeae with applications to comparative grass genomics. Plant Physiol. (150): 1135

(4) Umezawa T, Sakurai T, Totoki Y, Toyoda A, Seki M, Ishikawa A, Akiyama K, Kurotani A, Yoshida T, Mochida K, Kasuga M, Todaka D, Maruyama K, Nakashima K, Enju A, Mizukado S, Ahmed S, Yoshihara K, Harada K, Tsubokura Y, Hayashi M, Sato S, Anai T, Ishimoto M, Funatsuki H, Teraishi M, Osaki M, Shinano T, Akashi R, Sasaki Y, Yamaguchi-Shinozaki K, and Shinozaki K (2008) Sequencing and analysis of approximately 40,000 soybean cDNA clones from a full-length enriched cDNA library. DNA Res. (15): 333

Table 1: Arabidopsis ORF and cDNA clone repertoires

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP consortium & Salk Institute	Univector pUNI51		Full sequence	14,398	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	http://interactome.dfci.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/sheenweb/category_genes.html	ABRC
Steve Clouse	Gateway expression	N-terminal Flag tagged kinases		782	http://www4.ncsu.edu/~sclouse/Clouse2010.htm	ABRC
Frommer et al.	Gateway entry, no stop	Membrane protein genes	5' and 3' seq. (long reads)	2,100	http://associomics.org	ABRC
cDNA clones						
RIKEN/SSP/Salk Insitute	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	25,000	www.brc.riken.go.jp/lab/epd/Eng/order/order.shtml	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/Arabidopsis	CNRGV

Stock centres distributing Arabidopsis clone repertoires

- Arabidopsis Biological Resource Center (ABRC, USA), http://www.biosci.ohio-state.edu/pcmb/Facilities/abrc/abrchome.htm
- RIKEN BioResource Center (BRC, Japan), http://www.brc.riken.jp/lab/epd/Eng/catalog/pDNA.shtml
- GABI Primary Database (GABI/RZPD, Germany), http://gabi.rzpd.de/
- National Resources Centre for Plant Genomics (CNRGV, France), http://cnrgv.toulouse.inra.fr/ENG/index.html
- European Arabidopsis Stock Centre (NASC, United Kingdom), http://arabidopsis.info/
- BCCM/LMBP Plasmid and DNA library collection (BCCM/LMBP, Belgium), http://bccm.belspo.be/db/lmbp_gst_clones/
- Open Biosystems Inc., www.openbiosystems.com/

Natural Variation and Comparative Genomics

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

Arabidopsis thaliana serves not only as a model system for understanding the genetic, molecular and biochemical functions underlying plant life, but also for determining the mechanisms by which these functions (and variation in them) contribute to ecological and evolutionary success. The ease of genetic manipulation, abundant natural variation, and rich understanding of genetic and biochemical pathways all point to the suitability of Arabidopsis and its relatives for ecological, quantitative genetic, and evolutionary studies. Indeed Arabidopsis and its relatives represent an ideal system for understanding environmental adaptation, quantitative genetic variation, and microevolution at the mechanistic level.

Natural variation and comparative genomics studies are required for true understanding of how genes function. For example, understanding how genes are used to build an *A. thaliana* plant requires knowledge not only about molecular functions in *A. thaliana*, but also an understanding of why *A. thaliana* genes do not make a plant that looks more like *Capsella*, or *Brassica*, or *Cleome*, or cotton. Thus, understanding the genetic basis of developmental, metabolic, or physiological differences between species is at the very crux of plant biology. Finally, diverse species with different structures, life histories, and environmental adaptations provide tools for exploring gene function (in the molecular sense), that complement those traditionally deployed in *A. thaliana*.

More generally, *A. thaliana* is second only to humans when it comes to knowledge and ability to exploit sequence variation. *A. thaliana* surpasses humans when it comes to tools available for understanding how sequence variation affects biological processes. *A. thaliana* indeed is serving as a useful model for developing methods that will be applicable in medical genetics.

Notable Advances and New Resources

- Characterization of variation in 'omics traits, and determining loci responsible for that variation continues at the transcriptome, metabalome, ionome, and of course genome levels. Short-read sequencing is being used to sequence many Arabidopsis accessions. The 1001 Genomes Project mentioned last year is now running in full force (http://1001genomes.org/) with the complete genome sequence of more than 80 accessions already released. Whole genome sequence of *Arabidopsis lyrata*, noted last year, has been assembled, annotated and released (http://genome.jgi-psf.org/Araly1/Araly1.home.html).
- A multiparent mapping, inbred mapping population for Arabidopsis has been developed that allows increased resolution and captures far more diversity than standard recombinant inbred line populations (Kover *et al.*, PLoS Genetics, 2009).
- Sureshkumar *et al.* (Science, 2009) reported the first triplet repeat expansion associated genetic defect outside humans, demonstrating the usefulness of *A. thaliana* natural variation for studying unexpected genetic phenomena.
- Moving on to comparative genomics, Borhan *et al.* (Molecular Plant Pathology, 2010) were able to directly show the applicability of Arabidopsis research to Brassica crops. Specifically, a disease resistance gene (*WRR4*) from Arabidopsis was shown to confer resistance in transgenic brassicas, to a major pathogen of oilseed production in India and North America. This establishes transgenic testing of the first gene of a complex trait in brassicas, and recommends cloning of the underlying genes as an approach for capturing the full and potentially durable source of white rust resistance.
- Hauben *et al.* (PNAS, 2009) demonstrated that quantitative traits having agronomic impact are able to be recursively selected through recurrent selfing in isogenic lines of Canola (*B. napus*). They key finding is that observed stably inherited phenotypic variation is associated with epigenetic variation at the level of DNA methylation as well stable inheritance of histone marks. The authors maintained selection for respiration and were able to improve the trait of energy use efficiency, with gains of 5% yield increase beyond that achieved by heterosis.
- Cheung *et al.* (Plant Cell, 2010) compared homoeologous regions of *Brassica rapa*, *Brassica oleracea*, and allopolyploid *Brassica napus*.

Needs and recommendations

Development of resources for i) association mapping, ii) ecological genetics and iii) field experiments. Such resources include plant populations, appropriate and accessible statistical methods, good field sites, and sharing of knowledge.

- Survey of epigenetic variation both in Arabidopsis and in Brassica.
- With the increase in high throughput 'omics characterization, high throughput phenotyping remains a significant bottleneck. Infrastructure for archiving, organizing, analyzing, and displaying the huge amount of sequence data that will be generated in the next few years is needed. We are pleased to note that the iPlant Collaborative has also recognized this need and has included a NextGen Sequence Pipeline and visualization tools in their current projects. Additionally, techniques for analyzing, resolving, and common nomenclature for discussing structural variation, especially that not seen in "reference" genomes (e.g. Vlad *et al.*, PLoS Genetics, 2010).
- For the last several years we have discussed the need for a "fingerprinting" method for identifying *A. thaliana* stocks. SNP chip genotyping or short-read sequencing will provide the reference data, but we need to develop an inexpensive way for individual labs to fingerprint their own stocks.
- Last year we commented that an integrated database for storing and retrieving QTL data and results, especially for 'omics traits is needed. Ideally this would use a common mapping framework to facilitate comparison among experiments and populations. This also is being worked on by the iPlant collaborative ("genotype to phenotype" project) and we are optimisitic that their work will fulfill this need.
- A community-driven initiative, called the Brassica Map Alignment Project (BMAP), has been started to organize a list of genomes to sequence in the Brassicaceae. Organized by J. Chris Pires, Rod Wing, and Detlef Weigel, the first meeting was held at the Plant and Animal Genome meetings in San Diego in January 2010. A second meeting in March 2010 was held in Tubingen, Germany. A third meeting is being planned for 8 June, 2010, in Japan in parallel with the next ICAR meeting. If you wish to participate or make suggestions, please contact the BMAP organizers.
- Long term and stable funding for resources such as TAIR and the anticipated iPlant infrastructure discussed above is critical.

References:

(1) Borhan MH, Holub EB, Kindrachuk C, Omidi M, Bozorgmanesh-Frad G, Rimmer SR (2010) WRR4, a broad-spectrum TIR-NB-LRR gene from Arabidopsis thaliana that confers white rust resistance in transgenic oilseed brassica crops. Molecular plant pathology (11): 283-291

(2) Hauben M, Haesendonckx B, Standaert E, Van Der Kelen K, Azmi A, Akpo H, Van Breusegem F, Guisez Y, Bots M, Lambert B, Laga B, De Block M (2009) Energy use efficiency is characterized by an epigenetic component that can be directed through artificial selection to increase yield. PNAS (106): 20109-20114

(3) Cheung F, Trick M, Drou N, Lim YP, Park JY, Kwon SJ, Kim JA, Scott R, Pires JC, Paterson AH, Town C, Bancroft I (2009) Comparative Analysis between Homoeologous Genome Segments of Brassica napus and Its Progenitor Species Reveals Extensive Sequence-Level Divergence. Plant cell (21): 1912-1928

(4) Kover PX, Valdar W, Trakalo J, Scarcelli N, Ehrenreich IM, Purugganan MD, Durrant C, Mott R (2009) A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in Arabidopsis thaliana. PLoS Genetics (5): e1000551

(5) Sureshkumar S, Todesco M, Schneeberger K, Harilal R, Balasubramanian S, Weigel D (2009) A Genetic Defect Caused by a Triplet Repeat Expansion in Arabidopsis thaliana. Science (323): 1060-1063

(6) Vlad D, Rappaport F, Simon M, Loudet O (2010) Gene transposition causing natural variation for growth in Arabidopsis thaliana. PLoS Genetics (In Press)

Phenomics

Prepared by Eva Huala (Co-chair, huala@acoma.stanford.edu)

Phenomics seed and DNA resources

The T-DNA homozygous collection presently consists of 33,747 confirmed lines which have been shipped to the Arabidopsis Biological Resource Center (ABRC) from The Salk Institute Genome Analysis Laboratory (SIGnAL). This set of completed lines provides at least two homozygous insertion alleles for 10,458 genes, and a total of 18,516 genes are currently covered by at least one homozygous insertion. In addition to single inserts, ABRC is now making available larger sets of lines for bulk phenotyping assays by the Arabidopsis community. SIGnAL staff are continuing to screen new lines including segregating lines from Wisconsin (WiscDsLox and WiscDsLoxHs) and Saskatoon collections.

A remaining hurdle to the completion of the T-DNA homozygous collection is the lack of any insert lines for 3300 protein coding genes. To recover new inserts for these lines, SIGnAL has developed a method for deep-sequence indexing of large T-DNA collections. They have screened over 10,000 T-DNA insert lines and have identified over 300 new inserts in genes for which no insert was previously known. In an initial test, over 80% of these newly identified lines were recovered. Ultimately, a total of 80,000 T-DNA lines will be screened with this approach, and based on initial numbers recovery of 2000 new insertion lines is expected. Additionally, the SIGnAL team will recover new inserts representing second alleles for genes for which no additional insert is currently available. Considering that some portion of these genes disruptions may not be recoverable due to homozygote lethality, recovery of an insert in every single gene is unlikely, but this new method, along with the continuing screening of the existing collections, will greatly advance us towards of goal of creating a collection consisting of two alleles for every gene.

A complete set of the lines as well as a one-allele per locus ("unigene") set are being made available from ABRC. The second instalment of the confirmed SALK sets was released at the end of 2009. Together with the first instalment, ABRC have released a total of almost 11,000 one-allele, as well as about 3,500 second-allele confirmed SALK lines as sets. The confirmed population is also being organized into pools of different sizes to allow efficient forward phenotypic screening for traits that can be identified within larger populations. This activity is planned for September 2010.

For the first time this year a number of researchers will have a unique opportunity for phenotypic analysis of 5,000 confirmed and segregating T-DNA lines planted by ABRC at the OSU greenhouses (http://abrc.osu.edu/MutantHunt.html). Similar "mutant hunts" will be conducted periodically.

Tools for Association Mapping

Magnus Nordborg, University of Southern California and Gregor Mendel Institute, Vienna:

A database of phenotypes and association results is being generated. Part of the data will become public pending the publication of a Nature paper that describes association mapping of 107 different (community-generated) phenotypes using 250k SNPs in 96-192 accessions. Community submission of further phenotypes is encouraged, and results will be made available upon publication. The database will also incorporate further polymorphism data generated by the 1,001 genomes project.

Phenomics community events

In November 2009 the Jülich Plant Phenotyping Center organized the EPSO-Workshop on Plant Phenotyping (http://www.plantphenomics.com/phenotyping2009/). The workshop brought together the phenotyping community including deep, high-throughput and field phenotyping as well as users and developers of phenotyping technologies and concepts. The workshop was followed by the ETNA School on Plant Phenotyping (http://www.plantphenomics.com/ETNA/), which provided hands-on experience with state-of-the-art technology to Ph.D. students and postdoctoral fellows.

The Jülich Plant Phenomics Centre (JPPC) and the Australian Plant Phenomics Facility (APPF), are co-organizing an International Plant Phenomics Initiative (IPPI; http://www.plantphenomics.com/) to provide a stronger vehicle for international collaboration. Members of this Initiative are currently working to develop an agenda and will organize a meeting later in 2010 to decide on priorities and actions. The agenda will likely include exchanging protocols, validating systems, exchanging staff for technical education and developing collaborative funding bids. Please contact Bob Furbank (Robert.Furbank@csiro.au) or Ulrich Schurr (u.schurr@fz-juelich.de) for further information on the Initiative.

The 2nd International Plant Phenotyping Conference will be held in Jülich (Germany) in 2011.

High throughput phenotyping projects and data

Bob Furbank, Australian Plant Phenomics project:

The two nodes of the Australian Plant Phenomics Facility (APPF, www.plantphenomics.org.au) have now been commissioned. The High Resolution Plant Phenomics Centre (HRPPC) in Canberra was opened in August 2009 while the Plant Accelerator (TPA) in Adelaide opened in January 2010. The HRPPC model plant module specializes in medium to high throughput digital growth analysis, pulse modulated chlorophyll fluorescence imaging and FIR imaging under a variety of growth cabinet environmental conditions, using trays of 20 plants. Three Arabidopsis projects are currently underway in the HRPPC. At TPA "smart houses" provide high throughput glasshouse based screening of single pots and trays of plants using digital growth analysis plus imaging modules for near infrared, far infrared and steady state variable chlorophyll fluorescence. The Phenomics Ontology Driven Database development has progressed with a pilot implementation for model plant data occurring early in 2010. This database will house all the outputs of the APPF and will be the vehicle for interfacing to international databases and collaborators in the International Plant Phenomics Initiative. A special issue of Functional Plant Biology entitled Plant Phenomics has been published based on the International Plant Phenomics Symposium (IPPS) held in Canberra in 2009 (http://www.publish.csiro.au/nid/103/issue/5005.htm).

Ulrich Schurr, Jülich Plant Phenotyping Center (http://www.fz-juelich.de/icg/icg-3/jppc/):

A fully automated growth chamber-based screening system for leaf growth was established and used for a number of projects using Arabidopsis and other species. A FluoGrowScreen system (Jansen et al. (2009) Functional Plant Biology 11, 902-914) was implemented. This system allows simultaneous analysis of rosette growth, rosette characteristics (compactness, number of leaves, etc.) as well as chlorophyll fluorescence parameters in high throughput (presently up to 2500 plants per run). More imaging and analysis systems are presently installed in this platform.

A root system analysis platform for high-throughput (300 plants analyzed in 12 min) was established and utilized in characterization of Arabidopsis genotypes. Quantitative data obtained characterize the root system by parameters of root length, branching as well as dynamic parameters of growth and structure of the root systems. The system provides an *in silico* representation of the entire root system in Agar-based cultivation systems.

All data are integrated into database systems, transferred into quantitative parameters of leaf, shoot and root characteristics and provided in a graphical representation to the user. All systems are integrated in high-accuracy environment simulation systems.

Pierre Hilson, Christine Granier, AGRON-OMICS project:

Probing the reproducibility of leaf growth and molecular phenotypes: a comparison of three Arabidopsis accessions cultivated in ten laboratories. A major goal of the life sciences is to understand how molecular processes control phenotypes. Because understanding biological systems relies on the work of multiple laboratories, biologists implicitly assume that organisms with the same genotype will display similar phenotypes when grown in comparable conditions. In the frame of the European AGRONOMICS project, we investigated to what extent this holds true for leaf growth variables, metabolite and transcriptome profiles of three *A.thaliana* genotypes grown in ten laboratories using a standardized and detailed protocol. Our comparative analysis revealed that small variations in growing conditions (light quality principally) and handling of plants can account for significant differences in phenotypes and molecular profiles obtained in independent laboratories. It underscores the challenge of describing, monitoring and precisely controlling environmental conditions but also demonstrate that dedicated efforts can result in reproducible data across multiple laboratories. Results of this comparative experiment will be published in *Plant Physiology* in 2010.

Update on the PHENOPSIS platform and associated database. The PHENOPSIS platform in INRA-LEPSE (Montpellier, France) is now equipped with 3 robots each capable of weighing, accurately irrigating and digitally imaging more than 500 individual *A. thaliana* plants grown in pots under rigorously controlled environmental conditions. The platform produces more than 1500 images of plants per day and collects more than 15,000 data points for soil water content (measured several times a day) and meteorological conditions (incident light, air temperature, air humidity) measured in the chambers every 20 minutes. In addition, plants are regularly measured for several variables (phenological stages according to Boyes *et al.* (2001), photosynthesis, stomatal conductance, infrared thermal Imaging etc). Measurements requiring destruction of the plant are also carried out (area and number of epidermal cell, stomata density, leaf thickness, leaf and root biomass, biochemical or molecular measurements). PHENOPSISDB was created using the DataBase Management System MySQL 5.0 for data storage, data browsing, download of data and online data analysis (http://bioweb.supagro.inra.fr/phenopsis/Accueil.php). Automated SQL insert statements have been developed to update the database in real time using data collected from the chambers (meteorological data) and from the robots (soil water content data and images of the plants). Other data are inserted manually by the operator. Tools to analyse the data (R scripts) and images (image J macros) are available via the database and some can be used online.

Minami Matsui, RIKEN:

A comprehensive new database called the RIKEN Hub Database (https://database.riken.jp) has been developed by Dr. Tetsuro Toyoda to provide an integrated access point for RIKEN data. The new database includes a section on activation-tagged lines (http://activation.psc.database.riken.jp) or formally (http://amber.gsc.riken.jp/act/top.php) which contains phenotype data and insertion site information for 500 activation-tagged lines found to have visible phenotypes (Miki Nakazawa, Youichi Kondou and Eli Kaminuma). A set of Ac/Ds transposon lines including 200 visible phenotypes and flanking sequence information for 18,000 integration sites is described at http://rapid.psc.database.riken.jp (Takashi Kuromori and Eli Kaminuma). Another section of the new database (http://nazunaarabifox.psc.database.riken.jp) contains information on 1,500 visible phenotypes and 9,000 integrated full-length cDNAs for Arabidopsis FOX (Full-length cDNA over-eXpressor gene) lines (Takanari Ichikawa, Youichi Kondou and Eli Kaminuma).

RIKEN BRC (Bioresource center; Masatomo Kobayashi) has begun to distribute 5,000 of the Arabidopsis FOX lines, see http://www.brc.riken.go.jp/lab/epd/Eng/species/arabidopsis.shtml for ordering information. The “Rice FOX Arabidopsis mutant database” is now freely accessible at http://amber.gsc.riken.jp/ricefox/. Information is included on 11,000 rice full-length cDNAs that have been expressed in Arabidopsis, along with the resulting phenotypes which have been categorized into subsets using various criteria.

Olivier Loudet, INRA Versailles, IJPB

Thanks to funding from the European Research Council (ERC), we are setting up a unique combination of 2 ‘Phenoscope’ robots, modeled after the prototype developed at INRA Versailles to study Arabidopsis growth in controlled conditions, a challenging task due to the small size of the plant (very sensitive to micro-environmental heterogeneity existing in any growth room) and its high plasticity.

The new Phenoscope robotic system is capable of handling ~750 individual pots (each containing a single Arabidopsis plant). Conveyor rails use automaton to move each plant across all positions on the table through the chamber every 4 hours, ensuring that all individuals will perceive exactly the same conditions over a day. This robot is also equipped with a weighting/watering station that, for each cycle, adjusts water and nutrients for each individual plant on the table to the level pre-programmed by the user. Very precisely controlled physiological conditions at any level of stress

(or standard conditions) can be reproduced and finely adjusted, for comparison of hundreds of plants at once. Finally, a camera takes bird's eye photographs of rosettes and the computer stores and dynamically measures projected leaf area as an estimation of shoot growth. Of course this entirely computer-controlled robot does not only save time but enables experiments that would not be reproducible or perhaps even possible if done by hand. The robots are now set up in a single growth chamber and will be used in quantitative genetics approaches to decipher the genetic bases of Arabidopsis natural variation for growth and response to the environment, including water and nutrient levels.
http://www.inra.fr/vast/projects.htm

Justin Borevitz, University of Chicago
A new tool, GigaVision, has been developed to enable photographic archiving for ecologic and phenologic studies (http://borevitzlab.uchicago.edu/resources/gigavision). This simple, yet very effective system provides a method to conduct phenotyping of entire plant populations in a field site or within a greenhouse. We have used the gigapan.org panoramic tripod mount and Canon Powershot SX10IS camera to take sand dune blowout ecosystem panoramics at almost weekly intervals through 2009. Gigavision aims to increase this to hourly intervals through the growing season. The high resolution (~ 32Gb memory card swapped weekly) will allow plant level zoom and play. Thumbnails are being transmitted in real time for habitat level observations. We expect to share several Tb of GigaVision data through a local server.

Proteomics

Prepared by Wolfram Weckwerth (Co-chair, wolfram.weckwerth@univie.ac.at), Harvey Millar (Co-chair, harvey.millar@uwa.edu.au), Sacha Baginsky (Co-chair, sbaginsky@ethz.ch), Klaas van Wijk (Co-chair, kv35@cornell.edu) and Joshua Heazlewood (Co-chair, jlheazlewood@lbl.gov)

The MASC subcommittee for *Arabidopsis thaliana* proteomics was established to coordinate research efforts and provide points of contact for the community. The MASC Proteomics (MASCP) members have been responsible for establishing and maintaining an array of proteomics based resources to the community through online repositories that together represent the largest collection of proteomics information in Arabidopsis. These resources include protein subcellular localization, protein modifications, tissue based protein 'expression' data and a vast collection of proteotypic peptides. While providing specific functional information at the protein level, collectively these data provide direct experimental evidence for 16,700 proteins (50%) of the 33,410 proteins (TAIR9) currently predicted to be coded for by the Arabidopsis genome (see Table 1).

The past year has seen a number of significant reports using Arabidopsis that have advanced the potential of proteomics as a technique (see below). While such advanced uses of the technology can require large investment in infrastructure, it is likely that access to this technology will generally become more widespread with the continued establishment of user facilities. A number of recent studies demonstrate the role that this technique can play

Database	Number of Proteins	Unique Proteins
SUBA	4,685	361
AtProteome	13,029	5,754
PPDB	6,425	1,775
ProMEX	1,032	ND
PhosPhAt	4,859	1,256
Total (unique)		9,146
Total (shared)		7,554
Total (non-redundant)		16,700

Table 1. Proteins with proteomic data from MASCP associated databases as of 2009. Updates are in progress for all databases.

Recent activities:

- Meetings and the organization of proteomics workshops have been established on a regular basis at the International Conference on Arabidopsis Research. A well attended workshop was held in 2009 in Edinburgh titled "breakthroughs in studying intra-cellular dynamics and environmental response in the Arabidopsis proteome" organised by Harvey Millar, Wolfram Weckwerth, Joshua Heazlewood and Alex Jones. The workshop included research presentations by MASCP members and others which included attendees who submitted proteomics-related abstracts and were selected for oral presentation. A workshop is planned for ICAR 2010 in Yokohama focusing on Arabidopsis phosphoproteomics and is being organised by MASCP members Joshua Heazlewood, Alex Jones and Hiro Nakagami.
- The first International Workshop on Plant Peroxisomes was held in Edinburgh, 30 June 2009, where a number of MASCP members discussed advances in analysis of the peroxisome proteome in plants.
- Three new members have been invited to join the subcommittee, Waltraud Schulze (MPIMP, Germany), Katja Baerenfaeller (ETHZ, CH) and Nicolas Taylor (UWA, Australia).
- The MASC Proteomics Subcommittee (MASCP) website has been further developed to include a MediaWiki interface creating a more dynamic interface where members can directly contribute information. The website represents a useful resource for the Arabidopsis proteomics community and includes a summary of guidelines and standards for data interpretation, links to proteomic resources, meetings and workshops, funding opportunities, links to MASCP members and news section highlighting interesting reports relating to proteomics in Arabidopsis (see http://www.masc-proteomics.org/).
- The MASCP website will shortly host a proteomic data Aggregator that is designed to briefly summarize publicly available proteomic information specific to Arabidopsis for each AGI. The initiative is led by Joshua Heazlewood (Berkeley Labs, USA) and has involved a coordinated effort amongst MASCP members to ensure standardisation of MASCP administered Arabidopsis proteomic resources.
- MASCP members have played significant roles in establishing many of the major proteomic resources in Arabidopsis. The proteomic databases associated with MASCP include AtProteome (http://www.AtProteome.ethz.ch); PPDB (http://ppdb.tc.cornell.edu); SUBA (http://suba.plantenergy.uwa.edu.

au); ProMEX (http://promexdb.org) and PhosPhAT (http://phosphat.mpimp-golm.mpg.de). All of these resources have continued to be updated and expanded during 2009-2010; with significant developments and additions being made to PhosPhAt and PPDB in 2009.

- A major focus of MASCP is the integration of current proteomic resources with emerging protein interaction databases. A number of large scale protein-protein interactomes are currently underway and it is likely that in the next few years these resources will become available and their integration into existing proteomics resources.

There were a number of significant papers published in the last year (2009-2010) that advanced proteomics in Arabidopsis. These include:

- Zybailov B, Sun Q, van Wijk KJ (2009) Workflow for large scale detection and validation of peptide modifications by RPLC-LTQ-Orbitrap: application to the *Arabidopsis thaliana* leaf proteome and an online modified peptide library. Anal Chem. (81): 8015-8024. *Demonstrating the power of high resolution, high mass accuracy mass spectrometry for the identification of proteins and protein modifications in Arabidopsis leaf samples.*
- Ferro M, Brugière S, Salvi D, Seigneurin-Berny D, Court M, Moyet L, Ramus C, Miras S, Mellal M, Le Gall S, Kieffer-Jaquinod S, Bruley C, Garin J, Joyard J, Masselon C, Rolland N (2010) AT_CHLORO: A comprehensive chloroplast proteome database with subplastidiallocalization and curated information on envelope proteins. Mol Cell Proteomics (in press). *New insights into the chloroplast through in depth proteomic characterization of plastid sub-compartments using semi-quantitative mass spectrometry techniques.*
- Reiland S, Messerli G, Baerenfaller K, Gerrits B, Endler A, Grossmann J, Gruissem W, Baginsky S (2009) Large-scale Arabidopsis phosphoproteome profiling reveals novel chloroplast kinase substrates and phosphorylation networks. Plant Phisiol. (150): 889-903. *Uncovering signal transduction networks through the identification of over 3000 phosphopeptides in Arabidopsis seedlings.*
- Ren Y, Lv J, Wang H, Li L, Peng Y and Qu LJ (2009) A comparative proteomics approach to detect unintended effects in transgenic Arabidopsis. Genet Genomics (36): 629-639. *Utilization of proteomics to characterize changes in the proteome due to genetic manipulation.*
- Kierszniowska S, Seiwert B, Schulze WX (2009) Definition of Arabidopsis sterol-rich membrane microdomains by differential treatment with methyl-ß-cyclodextrin and quantitative proteomics. Molecular and Cellular Proteomics (4): 612-623. *Utilization of quantitative proteomics techniques to characterize composition and changes in the membrane proteome.*
- Chen Y, Hoehenwarter W, Weckwerth W (2010) Comparative analysis of phytohormone – responsive phosphoproteins in Arabidopsis thaliana using TiO2-phosphopeptide enrichment and MAPA. Plant Journal (in press). *Utilization of a novel quantitative label-free shotgun proteomics technique called MAPA (mass accuracy precursor alignment) to characterize composition and changes in the soluble and membrane phosphoproteome in Arabidopsis in response to phytohormone treatments.*

References:
(1) Polge C, Jaquinod M, Holzer F, Bourguignon J, Walling L, and Brouquisse R (2009) Evidence for the Existence in Arabidopsis thaliana of the Proteasome Proteolytic Pathway: ACTIVATION IN RESPONSE TO CADMIUM. J Biol Chem (284): 35412-35424
(2) Zhao H, Xing D, and Li QQ (2009) Unique features of plant cleavage and polyadenylation specificity factor revealed by proteomic studies. Plant Physiol (151): 1546-1556

Systems Biology

Prepared by Rodrigo A. Gutiérrez (Co-Chair, rgutierrez@uc.cl) & Andrew Millar (Co-Chair, Andrew.Millar@ed.ac.uk)

Systems biology can be defined as the exercise of integrating the existing knowledge about biological components, building a formal model of the system *as a whole* and using the model both to understand details of the system and to extract broader organizational principles that explain the form and function of living organisms. More practically speaking, a systems approach to understand biology can be described as an iterative process that includes (1) experimentation at a global level, (2) data collection and integration, (3) system modeling and (4) generation of new hypotheses to initiate a new cycle of experimentation at a global level. Given the limitations of global assays for many biological processes, Systems Biology research often focuses on subsystems and aims to test all components of the subsystem, often across spatial scales. The promise of systems biology is that by using this global integrative and iterative approach we will greatly increase our understanding of biological systems, both by broadening the scope of understanding to include more biological components, and by deepening understanding of systems that are complex enough to limit research progress that is unaided by models.

A primary goal of the Systems Biology Subcommittee is to further the use of Systems Biology among Arabidopsis researchers. Arabidopsis-focused scientists are leading high-profile Centres and Projects in Systems Biology, such as the CSBE and CPIB in Edinburgh and Nottingham (UK), the IGSP at Duke (USA) and the SystemsX.ch project PGCE (Switzerland). Community action on standards and accessibility (of data, models and software tools), on training, and communicating to the public will be important to build on the opportunities that this presents.

The former MASC Systems Biology Subcommittee chair (Philip Benfey, Duke) and Andrew Millar chaired a full session on 'Plant Systems Biology' at the Arabidopsis conference in Edinburgh, 2009. The premier conference on Systems Biology in 2008, ICSB in Gotheborg, Sweden, also included a Plant Systems Biology session for the first time, organized with input from the subcommittee.

The Systems Biology Subcommittee has a Wiki at http://arabidopsis.info/wiki/index.php/Plant_Systems_Biology, for community input.

Systems Biology publications in the past year include, amongst many others:

- Prusinkiewicz P, Crawford S, Smith RS, Ljung K, Bennett T, Ongaro V, and Leyser O (2009) Control of bud activation by an auxin transport switch. PNAS USA (106): 17431-17436
- Curien G, Bastien O, Robert-Genthon M, Cornish-Bowden A, Cardenas ML, and Dumas R (2009) Understanding the regulation of aspartate metabolism using a model based on measured kinetic parameters. Mol Syst Biol (5): 271
- Salazar JD, Saithong T, Brown PE, Foreman J, Locke JC, Halliday KJ, Carre IA, Rand DA, and Millar AJ (2009) Prediction of photoperiodic regulators from quantitative gene circuit models. Cell (139): 1170-1179
- Jones AR, Kramer EM, Knox K, Swarup R, Bennett MJ, Lazarus CM, Leyser HM, and Grierson CS (2009) Auxin transport through non-hair cells sustains root-hair development. Nat Cell Biol (11): 78-84

Bioinformatics

Prepared by Nicholas Provart (Chair, nicholas.provart@utoronto.ca) with input from Eva Huala huala@acoma.stanford.edu, Sean May (sean@arabidopsis.info), Tetsuro Toyoda (toyoda@base.riken.jp)

Many of the Arabidopsis bioinformatic tools and database sites described in Brady and Provart (2009) added new data, which continue to be generated at a brisk pace. These data sets include genome-wide cell-type-specific expression profiles, such as those for pollen germination (Yadav *et al*., 2009) and shoot apical meristems (Qin *et al*., 2009), and more specifically for cell-type-specific "translatomes" in response to hypoxia (Mustroph *et al*., 2009). Further data sets included whole genome tiling array circadian rhythm (Hazen *et al*., 2009), abiotic stress (Zeller *et al*., 2009), and expression level polymorphism (Plantegenet *et al*. 2009) data. Genomic sequence data from the 1001 Arabidopsis Genomes project also started to be released (1001genomes.org; Weigel and Mott, 2009), as were metabolome data over the course of Arabidopsis development (Matsuda *et al*., 2009). One final large scale data set of note was for MAPK targets, generated using protein microarrays (Popescu *et al*., 2009). All of these data sets will be useful in the context of hypothesis generation for plant biology.

New bioinformatic tools, for Arabidopsis and other plant research, were also published, such as PLAZA for plant comparative genomics (Proost *et al*., 2009), ATTED-II for identifying coexpressed genes (Obayashi *et al*., 2009), or predicted and documented protein-protein interactions in the PAIR database (Lin *et al*., 2009). The use of coexpression tools to identify novel genes associated with a researcher's given process of interest was well summarized in Usadel *et al*. (2009). Many other publications appeared in which bioinformatics played a role in gene function discovery and/or elucidating other aspects of plant biology.

With this as a background, a big event this year was the announcement of funding cuts to TAIR by the U.S. National Science Foundation. A recent survey of the Arabidopsis community showed that TAIR was used on a regular basis by more than 90% of the 295 researchers that responded to the survey (just behind literature databases and ahead of gene expression databases). While TAIR is one of the most popular bioinformatic resources for Arabidopsis researchers, its funding is not just an issue for TAIR to resolve, as the larger question of how to fund online resources sustainably affects all such resources once their grant funding runs out. The survey asked the community how they would be willing to support online resources. Of several options, the greatest number indicated that they would be willing to pay a surcharge on seed stocks, while the second greatest number indicated that the sites should continue to be supported by government (and perhaps private benefactors and sponsors), given that most of the data sets were generated with public money in the first place.

Model 1: Surcharge on Seed and other Stocks from the ABRC/NASC

While a surcharge on seed stocks is at first glance an attractive option, several issues arise with this in practice. First, researchers typically use grant funds to buy seed stocks, so why fund bioinformatic resources indirectly instead of directly through funding agencies in the first place? The second is that even a doubling of seed charges would only generate enough funds to support one bioinformatician for the whole world at most. Third, increasing fees would likely decrease the number of stocks being ordered, thus already exacerbating the stock centres' precarious financial situation.

Model 2: Subscription

Most researchers (about 50%) indicated willingness to pay $50 a year for a "really useful" bioinformatic site. This is lower by a factor of 10 than the level that would be required to fully fund just TAIR's work, not to mention other big plant bioinformatic sites that are out there. Several bioinformatic resources are located in countries other than the U.S., and if a subscription model were adopted in the case of TAIR, and other countries' bioinformatic resource were kept publicly funded, it would create an unfair system whereby Country X would be subsidizing the use of its resources for the world for free, while TAIR would be charging Country X's users for access. Finally, clawing back the resources provided to TAIR and other publicly-accessible sites and forcing them to charge user fees goes against the mandate of many federal funding agencies that require data to be made publicly-available, and against UPSIDE principles (Cozzarelli, 2004; Chandras *et al*., 2009). It seems anomalous that another U.S. bioinformatic resource, the NCBI, receives government funding to support complete and unfettered access to data, while a similar resource, arguably equally important for human health, should have its funding cut.

Other Models: Advertising Revenue and Donations/Sponsorship

Donation and ad-based funding models are unlikely to generate large amounts of revenue. Experience with the BAR website shows that such ads can generate just a very small fraction (less than 1%) of the funds necessary to pay for a bioinformatic technician, in spite of more than 50,000 uses of that site a month. There do not appear to be enough private plant biotechnology corporations to generate sufficient donation amounts to fully support the many

sites out there, although this option is currently being investigated by TAIR and other online resources in a sponsorship context.

Perhaps the answer lies in a combination of licensing to corporate users – an avenue currently being explored by several plant bioinformatics resources – and corporate sponsorship, with access remaining free for academic use, including undergraduate and high school teaching. Such an answer might also include transnational governmental/institutional funding for such resources, in a manner similar to the way the DNA Database of Japan, the European Bioinformatics Institute of EMBL, and GenBank share the responsibility for DNA sequence submission to and curation of a common database, or to how some other online resources are funded, see Table I (it is not clear how this differs from the current situation whereby each national government funds different bioinformatic resources, each with their own particular strengths). What is clear is that charging everyone for access would likely result in the fragmentation of Arabidopsis genomic resources and disruption of the utility of highly cross-referenced and cross-linked data sets, between TAIR, RIKEN, SIGnAL, the BAR and the many others, on which Arabidopsis and plant research in general is increasingly reliant and due to which plant research has become much more productive. Finally, it should be pointed out that the well-funded iPlant Collaborative will also be relying on third-party sites such as TAIR for high-quality annotations and data, not generating them itself.

Table I – 2009 funding levels and sources for Model Organism Databases

Database Name	Species	Annual Funding[1]	Funding Sources[2]
MGI	Mouse	$6,331,237	NIH
FlyBase	Fruit fly	$4,901,508	NIH, MRC (U.K.), other
SGD	Yeast	$3,803,362	NIH
WormBase	Nematode	$3,688,258[3]	NIH, MRC (U.K.)
ZFIN	Zebrafish	$2,893,050	NIH
UCSC Browser	Human	$2,207,501[4]	NIH, HHMI, other
RGD	Rat	$1,791,904	NIH
TAIR	Arabidopsis	$1,600,000[5]	NSF

Notes: 1. Including indirect costs; 2. U.S. funding agency unless otherwise indicated. HHMI – Howard Hughes Medical Institute , MRC – Medical Research Council (U.K.), NIH – National Institutes of Health, NSF – National Science Foundation; 3. NIH funding amount only; 4. NIH funding amount only; 5. TAIR funding level prior to funding cut.

Metabolomics

Prepared by Kazuki Saito (Chair, ksaito@psc.riken.jp) & Wolfram Weckwerth (Co-chair, wolfram.weckwerth@univie.ac.at)

Aims

Since metabolomics is an important component of Arabidopsis '-omics', a continuous major goal of this subcommittee will be to promote metabolomics research in Arabidopsis leading to functional genomics and systems biology. For this purpose we plan to establish a website for the initial process of consolidating Arabidopsis metabolomics activities making them more visible for the community. Full integration of Arabidopsis-based metabolomics research with the activity of the Metabolomics Society (http://129.128.185.121/metabolomics_society) is also an important goal of this subcommittee. Several members of the subcommittee are involved in drawing up the plant biology specific documentation for the Metabolomics Society. In addition, this committee aims to establish a mechanism that allows the dissemination of metabolomics datasets to the wider Arabidopsis community and encourage and facilitate initiatives for the integration of metabolomic datasets with other '-omic' datasets. This will involve depositing Metabolomic data in a usable form for data integration.

To achieve these goals, we aim to establish the subcommittee website for more efficient exchange of information and dissemination of the subcommittee's activity. Subcommittee discussions will not be limited to an annual meeting at ICAR, a continuous dialogue among subcommittee members will be encouraged through the participation in numerous other metabolomics-related meetings.

In 2010 Kazuki Saito replaced Basil Nikolau, whom we thank for his contributions as Chair over the past years, to become the new Chair of the Metabolomics with Wolfram Weckwerth as Co-chair. In the past, the following conferences related to Arabidopsis metabolomics have been held: The 5th International Conference of Plant Metabolomics in Yokohama, Japan, July 2008; The 4th Scientific Meeting of the Metabolomics Society in Boston, USA, September 2008; The 5th Scientific Meeting of the Metabolomics Society in Edmonton, Canada, September 2009. The Metabolomics 2010 meeting, which will be held in Amsterdam, The Netherlands, June 27-July 1 2010 (http://www.metabolomics2010.com/) is the first joint conference that integrates The Metabolomics Society, The Plant Metabolomics Platform, The Metabolic Profiling Forum and a number of additional groups involved in metabolomics research.

Updates

A MS/MS spectral tag database of Arabidopsis metabolome (Plant J. (57): 555–577 (2009)) and an Arabidopsis metabolome expression database 'AtMetExpress development' have been established (Plant Physiol. (152): 566-578 (2010)) at http://prime.psc.riken.jp/. A web portal (plantmetabolomics.org) at http://lab.bcb.iastate.edu/sandbox/pbais05/alpha/plantmetabolomics_trimmed/index.php that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants has been launched.

Two substantial EU funded consortia projects, METAPHOR http://www.meta-phor.eu/ and DEVELONUTRI http://www.develonutri.info/welcome, although not focused on Arabidopsis, are technology orientated and aim to provide platforms to coordinate the data collection of plant metabolomic data across different laboratories. Activities of this sort should be encouraged for Arabidopsis to facilitate the integration of data from different sources.

The International Arabidopsis Functional Genomics Community

Country Highlights

Argentina
An expedition in Patagonia was organized to search for local ecotypes of Arabidopsis. Javier Botto has identified spots of Arabidopsis close to the lakes in the Andes. Analysis of the collected specimens is expected to provide cues to identify genes that allow plants to cope with the extreme environmental conditions of this region.

Australia and New Zealand
- The Canberra and Adelaide phenotyping facilities were officially opened in 2009. International collaborations are being organized and encouraged.
- XVIII International Botanical Congress, Melbourne 23-30 July 2011.
- Arabidopsis 2013 – The 24th International Conference on Arabidopsis research will be held in Australia. Tentative dates are 8-12 July 2010, possible venue is Cairns, the gateway to the Great Barrier Reef.

Austria
- New Research network: "Towards sustainable food and bioenergy security for society: Establishing an academic compound screening platform in Vienna to characterize and modulate Strigolactone synthesis in plants" WWTF-Project
- The 7th Tri-National Arabidopsis Meeting will be held in Salzburg , 15-18 September 2010.
- Arabidopsis 2012 – The 24th International Conference on Arabidopsis research will be held at the Hofburg Palace in Vienna, 3-7 July 2012.

Belgium
- VIB, the Flanders Institute for Biotechnology provides significant support to the Department of Plant Systems Biology, approximately 6 million Euro per year.
- The Department of Plant Systems Biology continues to develop and disseminate a collection of destination vectors designed for the functional analysis of genes in plant cells. It also coordinates the EU project AGRON-OMICS.

Canada
- Genome Canada funding was not renewed in the 2009-2010 Federal budgetary year. The 2010 budget included a modest allocation of CDN$75Million to support Technology Platforms and projects in the Forestry and Environment sectors.
- BAR (Bio-Array Resource) expanded its collection of bioinformatics tools for large-scale data sets from Arabidopsis.

China
The National Science Foundation of China (NSFC) granted 12 projects to laboratories using Arabidopsis as a model system. The National Transgenic Crop Development Initiative founded many other plant laboratories.

France
- Most of the plant genomics projects funded by the National Research Agency over the past year are on crop plants and only two on Arabidopsis. Arabidopsis projects have been founded by the blue-sky call for proposals within the 'Blanc' programme.
- Noteworthy publications: Bikard *et al*. (2009) Divergent Evolution of Duplicate Genes Leads to Genetic Incompatibilities within *A. thaliana*. Science (323): 623-626. Teixeira *et al*. (2009) A Role for RNAi in the Selective Correction of DNA Methylation Defects. Science (323): 1600 – 1604. Matsuno *et al*. (2009) Evolution of a novel phenolic pathway for pollen development. Science (325): 1688-1692. d'Erfurth *et al*. (2009) Turning meiosis into mitosis. PLoS Biol (7): e1000124.

Germany
- The successful AFGN project has come to its end. The most important resource created during its course is the AtGenExpress transcriptome data set.
- Over 120 PhD students and postdoctoral researchers have been trained in functional genomics in Germany and 8 PhD students were hosted between 1-3 months in the US on the AFGN-2010 Young Researcher Exchange Programme.

Israel
- BARD announced that no more than 25% of awards could go to "proposals whose outcomes are expected to have application in more than seven years", making it very unlikely for Arabidopsis research to be funded via this channel.
- The Manna Center for Plant Biosciences, growth and analyses facility, was opened at Tel Aviv University.
- New public resource for Arabidopsis – The Arabidopsis Co-Expression database at http://ibis.tau.ac.il/AthMod/

Italy
- A new collaboration between the Italian groups of G.Serino/P. Costantino and G. Frugis with Q. Xie and LJ. Qu (Chinese Academy of Sciences) has been selected by the Italian Ministry of Foreign Affairs as one of the significant research projects within the frame of the Executive Programme of Scientific and

Technological Cooperation between Italy and China.
- Outreach conference: C. Tonelli organized the 5th conference on the future of Science, Venice 20-22 September 2009
- Noteworthy publications: P.Vittoriosos/P. Costantino, Plant Journal, on the regulation of GA biosynthesis. A. Carpaneto, Plant Journal, on the development of a new technique to measure calcium permeation in cation channels. F. Cervone/G. de Lorenzo, PNAS, on the molecular recognition between pathogen-derived polygalacturonases (PGs) and plant polygalacturonase-inhibiting proteins (PGIPs).

Japan
- Kazuo Shinozaki and Kazuko Yamaguchi-Shinozaki received the JSPP award from the Japanese Society of Plant Physiologists. Kiotaka Okada received the BSJ Award of the Botanical Society of Japan. Nobuharu Goto received a Special Award from the Botanical Society of Japan for his service to the research community as former Director of the Sendai Arabidopsis Seed Stock Centre.
- Japan will host the 21st International Conference on Arabidopsis Research (ICAR2010, http://arabidopsis2010.psc.riken.jp/) on June 6-10, 2010 in Pacifico Yokohama, Yokohama, Japan. ICAR 2010 will highlight recent advances in Arabidopsis research and its translation into research in crops and trees.

The Netherlands
- One NWO-VENI innovation grant was awarded to an Arabidopsis project of a junior scientist.
- Overall Dutch Arabidopsis scientists published 70 papers in the past year. Notable highlights: Kaufmann *et al*. (2009) Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biol. (7): e1000090. Immink RG *et al*. (2009) SEPALLATA3: the 'glue' for MADS box transcription factor complex formation. Genome Biol. (10): R24. Fu J *et al*. (2009) System-wide molecular evidence for phenotypic buffering in Arabidopsis. Nat Genet. (41): 166-7. Tessadori F *et al*. (2009) Phytochrome B and histone deacetylase 6 control light-induced chromatin compaction in *Arabidopsis thaliana* PLoS Genet. (5): e1000638

Spain
- A collection of 1000 transgenic lines, each expressing a different TF under the control of an estradiol inducible promoter is being prepared and will be made available through the NASC stock centre (TRANSPLANTA Programme).
- A tilling facility for *Landsberg erecta* ecotype has been now operative for 2 years (Carlos Alonso Blanco)
- The two most important results from Spanish researchers have been the identification of the chemical nature of the active Jasmonate (Fonseca, Nature Chemical Biology, 2009) and the contributon to the identification and functional and structural characterisation of ABA receptor (Santiago *et al*.(2009) Nature; Park *et a*l. (2009) Science. Fujii *et al*. (2009) Nature).

United Kingdom
- The new 5-year GARNet grant also covers for 3 years of Coordination of MASC. The new MASC Coordinator is based in the UK.
- The first Informatics Workshop (organised by MASC) was held in Nottingham, 15-16 April 2010 and the outcomes will be discussed at the 21st ICAR in Japan, 6-10 June 2010.
- The UK hosted the 20th ICAR in 2009 in Edinburgh
- BBSRC launched new strategic plan.
- A notable scientific breakthrough was provided by the publication of an article in Cell, where the discovery of the plant's thermometer was reported (Kumar and Wigge, Cell 2010).

United States
- The two newly elected members of the North American Arabidopsis Steering Committee (NAASC) are Dominique Bergmann (Stanford University) and Wolf Frommer (Carnegie Institution for Science). Joanna Friesner is the NAASC Coordinator and Julian Schroeder (U.S.A.) served as the NAASC Chair in the past year.
- A second Informatics Workshop (organised by NAASC) was held in Washington DC, 10-11 May 2010 and the outcomes will be discussed at the 21st ICAR in Japan, 6-10 June 2010
- Arabidopsis 2011 - The 22nd International Conference on Arabidopsis research will be held at the University of Wisconsin, Madison, from June 22-25, 2011.
- Breakthroughs involving US researchers and institutions include great contributions to the discovery of the ABA receptor and the decoding of the human epigenome.
- Philip Benfey (Duke University) and Jian-Kang Zhu (UC Irvine) were recently elected to the National Academy of Sciences.

Argentina

http://www.arabidopsis.org/info/2010_projects/Argentina.jsp
Contact: Jorge J. Casal
IFEVA, Faculty of Agronomy, University of Buenos Aires
Email address casal@ifeva.edu.ar

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

- PICT-1035. The function of mitochondria in copper homeostasis. Gonzalez, Daniel Héctor, Universidad Nacional del Litoral, Santa Fe.
- PICT-1542. L-Proline metabolism in Arabidopsis tissues that induce the hypersensitive response. Alvarez, Maria Elena, Universidad Nacional de Córdoba.
- PICT-1890. Programmed cell death during the development of the female gametophyte in *Arabidopsis thaliana*. Pagnussat, Gabriela Carolina Instituto de Investigaciones Biológicas, Mar del Plata.
- PICT-1061. Genetic architecture of shade-avoidance responses. Botto, Javier Francisco, Universidad de Buenos Aires.
- PICT-0558. Modulation of anti-herbivore defences in plants. Ballaré, Carlos Luis, Universidad de Buenos Aires.
- PICT-1748. Light regulation of early seedling vigour in plants. Casal, Jorge José, Universidad de Buenos Aires

Young investigator awards*:*

- PICT-2072. Function of Arabidopsis TCP transcription factors in leaf development. Schommer, Carla, Instituto de Biología Molecular y Celular de Rosario.
- PICT-1032. Molecular mechanisms of the action of transcription factors that regulate plant development. Viola, Ivana Lorena, Universidad Nacional del Litoral, Santa Fe.

New Grants from the Nacional Research Council of Argentina (CONICET), which support Arabidopsis research:

- PIP 112-200801-00237: Characterisation of starch synthase III in *Arabidopsis thaliana.* Busi, María Victoria, Instituto de Investigación Biotecnológicas, Chascomús.

The search for Arabidopsis in Patagonia

The analysis of natural genetic variation in Arabidopsis has provided key information to help our understanding of plant biology. Dr Javier Botto (botto@agro.uba.ar) has recently organized an expedition to the remote land of Patagonia in the search for local ecotypes of *Arabidopsis thaliana*. There are a couple of previous reports from botanists indicating the occurrence of *Arabidopsis thaliana* in Patagonia. Guided by this information, Dr Botto has identified spots of Arabidopsis close to the lakes located in the Andes in the South-West region of Argentina. He has collected seeds together with a full range of accurate environmental and ecological data (coordinates, altitude, exposition, light, soil sampling and plant community) and other descriptors of *Arabidopsis thaliana* populations (size, stage, flowering, pictures). These specimens may provide cues to identify the genes that help plants to cope with the extreme environmental conditions of this region of the planet.

Australia & New Zealand

http://www.arabidopsis.org/info/2010_projects/Australia.jsp
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http://www.anu.edu.au/bambi/people/academic/pogson.php
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Australia has a strong tradition in plant scientific research with most institutions across all states of Australia having some research involved Arabidopsis as a model system. Major areas of Arabidopsis research and functional genomics are Canberra, Melbourne and Perth. Major sites of plant science with foci on crops such as grains, grapes and legumes include Queensland, Tasmania, South Australia and NSW. Centres with a strong focus on Arabidopsis included Australian Research Council (ARC) Centre of Excellence in Plant Energy Biology (www.plantenergy.uwa.edu.au/) and CSIRO Plant Industry (www.pi.csiro.au), plus numerous researchers across all the Universities in New Zealand and Australia.

Increasing numbers of New Zealand plant scientists are incorporating *Arabidopsis thaliana* into their research, and several are using functional genomics approaches. Funding is principally available through the Royal Society of New Zealand's Marsden Fund and the New Zealand Foundation for Research, Science and Technology. In addition to the projects being conducted at the universities, research programs are carried out at the Government-owned Crown Research Institutes.

Key new developments during 2009 were:

Plant Phenomics (www.plantphenomics.org.au). The Canberra and Adelaide nodes were officially opened in 2009. The NCRIS funded National Facility will be available to researchers at the marginal cost of running the facility and several international collaborations are being established and encouraged. For more information contact Bob Furbank (Robert.Furbank@csiro.au) or Mark Tester (mark.tester@acpfg.com.au). More details can be found in the Phenomics Subcommittee section of this annual report.

SUBA (a SUBcellular location database for Arabidopsis proteins) brings together data from chimeric fluorescent fusion protein studies and mass spectrometry surveys of subcellular compartments with protein localisation information obtained from other literature references and bioinformatic prediction tools. The SUBA database provides a powerful means to assess protein subcellular localisation in Arabidopsis (http://www.suba.bcs.uwa.edu.au).

Anno-J: Interactive web-based genome browsing in Arabidopsis for large datasets in functional genomics Julian Tonti-Filippini and A. Harvey Millar (hmillar@cyllene.uwa.edu.au), ARC Centre of Excellence in Plant Energy Biology, M316. The University of Western Australia, Perth, WA, 6009, Australia. The rapid growth of new types of genome-aligned data at the DNA, RNA and protein levels requires a renaissance in web-based genome annotation browsers to provide useful data-mining tools for quickly exploring increasing complex data sets. Anno-J is a modern web-application for visualizing genome annotation data using Web 2.0 technologies for greatly enhanced style control, data syndication, data maintenance, user-interface and flexibility. Recent publications using Anno-J include: Lister *et al*. (2009) Nature (462): 296-7, Lister *et al*. (2008) Cell (133): 523-535.

Recent and Upcoming Conferences

- First International Plant Phenomics Symposium was held in Canberra in April 2009.
- OZBIO2010: an International Conference on "Molecules of life: from discovery to biotechnology" to take place in Melbourne 26 September to 1 October 2010. See http://www.asbmb.org.au/ozbio2010/
- XVIII International Botanical Congress, Melbourne 23rd-30th July 2011. See http://www.ibc2011.com/
- **Arabidopsis 2013** The 24th International Conference on Arabidopsis Research will be held in Australia. Tentative dates are 8th till 12th July, possible venue is tropical Cairns, in far north Australia, the gateway to the Great Barrier Reef.

Austria

http://www.arabidopsis.org/info/2010_projects/Austria.jsp
Contacts: Marie-Theres Hauser, BOKU-University of Natural Resources & Applied Life Science, Vienna
Ortrun Mittelsten Scheid, GMI-Gregor Mendel Institute of Molecular Plant Biology
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ortrun.mittelsten_scheid@gmi.oeaw.ac.at

Arabidopsis projects are undertaken at four institutions (BOKU-University of Natural Resources & Applied Life Science Vienna, GMI-Gregor Mendel Institute of Molecular Plant Biology, Faculty of Life Sciences, MFPL-Max F. Perutz Laboratories of the University Vienna and the Medical University Vienna, University of Salzburg) on:

Population genetics:
- Magnus Nordborg: (www.gmi.oeaw.ac.at/en/research/magnus-nordborg/)

Systems biology:
- Wolfram Weckwerth (www.univie.ac.at/mosys/wolfram_weckwerth.html)

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

Development, hormones and stress responses:
- Andreas Bachmair: (www.mfpl.ac.at/index.php?cid=702): ubiquitination and sumoylation
- Thomas Greb (www.gmi.oeaw.ac.at/tgreb.htm): vascular tissue development
- Marie-Theres Hauser (www.dagz.boku.ac.at/11135.html?&L=1): development, stress
- Claudia Jonak (www.gmi.oeaw.ac.at/cjonak.htm): stress signalling and adaptation
- Fritz Kragler (www.mfpl.ac.at/index.php?cid=52): proteins/RNA cell to cell transport
- Christian Luschnig (www.dagz.boku.ac.at/7968.html?&L=1): auxin, chromatin
- Irute Meskiene (www.mfpl.ac.at/index.php?cid=53): AP2C1/2 in stress adaptation
- Brigitte Poppenberger (www.mfpl.ac.at/index.php?cid=476): brassinosteroid biosynthesis
- Andrea Schnepf, Sabine Klepsch (www.boku.ac.at/marhizo/index.html): mathematical model, plant resource acquisition, root exudation, rooting patterns
- Tobias Sieberer (www.mfpl.ac.at/index.php?cid=592): development of the shoot apical meristem
- Markus Teige (www.mfpl.ac.at/ index.php?cid=55): targets of calcium-dependent protein kinases
- Andrea Pitzschke (www.fwf.ac.at/de/abstracts/abstract.asp?L=D&PROJ=P21851): stress
- Melinda Frances Anna Abas (www.fwf.ac.at/de/abstracts/abstract.asp?L=D&PROJ=P21533): PIN proteins

Epigenetics:
- Werner Aufsatz (www.gmi.oeaw.ac.at/waufsatz.htm): RNA mediated silencing, stress adaptation
- Antonius and Marjori Matzke (www.gmi.oeaw.ac.at/amatzke.htm): RdDM, nuclear architecture
- Ortrun Mittelsten Scheid (www.gmi.oeaw.ac.at/oms.htm): epigenetic changes in polyploids
- Hisashi Tamaru (www.gmi.oeaw.ac.at/htamaru.htm): chromatin during pollen development

Glycobiology:
- Georg Seifert (www.dapp.boku.ac.at/2238.html?&L=1): arabinogalactan proteins and PCD, cell wall biosynthesis
- Herta Steinkellner (www.dagz.boku.ac.at/11132.html?&L=1): “customised” N-glycosylation
- Richard Strasser (www.dagz.boku.ac.at/12349.html?&L=1): N-glycosylation, ER quality control
- Raimund Tenhaken (www.uni-salzburg.at/zbio/tenhaken): nucleotide sugar biosynthesis, cell wall polymers, PCD

Plant pathogen interactions:
- Gerhard Adam (www.dagz.boku.ac.at/11137.html?&L=1): role of mycotoxins in plant-pathogen interactions
- Holger Bohlmann (/www.dapp.boku.ac.at/2238.html?&L=1): plant-nematodes interaction, thionin processing
- Florian Grundler (www.dapp.boku.ac.at/2238.html): plant-nematode interactions
- Julia Hofmann (www.dapp.boku.ac.at/h953_einheit.html?&L=1):signal transduction, metabolomics, plant nematode-interactions
- Wieczorek Krzysztof (www.dapp.boku.ac.at/h953_einheit.html?&L=1): cell wall biosynthesis in plant-nematode interaction

RNA metabolism:
- Andrea Barta (www.mfpl.ac.at/index.php?cid=68): RNP complexes, spliceosome

Arabidopsis genomics tools and resources:
Public resources for Arabidopsis proteomics and metabolomics are provided by two subcommittees:

1. MASCP (Multinational Arabidopsis Steering Committee Proteomics, Chairman Wolfram Weckwerth, Department

MoSys, University of Vienna). This initiative is currently building a database integrator for functional proteomics studies in Arabidopsis. For more information see the 2010 MASCP report and the website: http://www.masc-proteomics.org/)

2. MASCM (Multinational Arabidopsis Steering Committee Metabolomics, Chairman Kazuki Saito, Plant Research Riken Yokohama, Co-chair Wolfram Weckwerth, Department MoSys, University of Vienna). Following a less active period, in 2010 the metabolomics group launched a new initiative to provide metabolomics resources to the larger Arabidopsis community. During 2010, the committee will revise the metabolomics-activities in Arabidopsis and will provide a platform for all interested researchers.

Current Research Consortia

- "Chromosome dynamics - unravelling the functions of chromosomal domains" is a multiorganismal project (Arabidopsis represented by Peter Schlögelhofer) with the focus on the interaction of kinetochore –microtubules, biochemistry of sister-chromatid cohesion, chromosome pairing and recombination (www.mfpl.ac.at/index.php?cid=647).
- "From regulatory complexity to biological function: Metabolic adjustment of plant development by regulatory bZIP factor networks"(www.zmbp.uni-tuebingen.de/PlantPhysiology/bzip/) a cooperative International Project funded by the German DFG, the Austrian FWF, the Dutch NWO, and the Spanish MEC.
- "Chloroplast Signals, COSI" (www.univie.ac.at/cosi) EC-funded Marie-Curie Initial Training Network (ITN) coordinated by the University of Vienna and investigating chloroplast signals and metabolic regulation in a network of 10 European Institutions including BayerBioScience as industrial partner.
- "Signalling to plant immunity responses" (PathoNet) is an ERANet PG project coordinated by Irute Meskiene with members from Austria, Germany and the United Kingdom (www.erapg.org/everyone/16790/18613/19533/19539).
- "Calcium Regulation of Plant Productivity" (CROPP) is an ERANet PG project with members from Austria, Germany, Israel and the United Kingdom (www.erapg.org/ everyo ne/16790/18613/19533/19537).
- "Alternative Splicing and Abiotic Stress" (PASAS) is an ERANet PG project with members from Austria, Israel and the United Kingdom (www.erapg.org/everyo ne/16790/18613/19533/19538).
- "Fusarium Metabolites and Detoxification Reactions" SFB-Project coordinated by Gerhard Adam from the BOKU-University of Natural Resources & Applied Life Sciences, Vienna.
- "Towards sustainable food and bioenergy security for society: Establishing an academic compound screening platform in Vienna to characterize and modulate Strigolactone synthesis in plants" WWTF-Project coordinated by Tobias Sieberer from the Max F. Perutz Laboratories (University Vienna and Medical University Vienna).

Conferences

- International Conference "Molecular Aspects of Plant Development" February 23-26, 2010, Vienna (http://www.vipca.at/mapd/home.html).
- Together with Germany and Switzerland, the Austria Arabidopsis Network is organizing a yearly, rotating, international conference on Arabidopsis functional genomics. The 7th Tri-National Arabidopsis Meeting will be held in Salzburg, from September 15-18, 2010 (www.tnam.org).
- **Arabidopsis 2012** – The 23th International Conference on Arabidopsis research will be held at the Hofburg Palace in Vienna, 3-7 July 2012. The local organising committee is: Magnus Nordborg, Marie-Theres Hauser and Wolfram Weckwerth.

Public Relations- Education

- GEN-AU Summer School: an educational program for high school students (www.summerschool.at/)
- "Dialog Gentechnik": a non-profit society dedicated to provide scientific information on molecular biology and different aspects of biotechnological applications (www.dialog-gentechnik.at/index.php)
- Vienna International PhD Programmes offer up to 4 years Arabidopsis research projects: www.univie.ac.at/vbc/PhD/, www.projects.mfpl.ac.at/mfpl-phd-selection/, www.phd-cellular-signaling.at/, www.projects.mfpl.ac.at/dk-rna-biology/

Major funding sources (government/public/private) for Arabidopsis functional genomics

- Basic and translational research: FWF (www.fwf.ac.at)
- Vienna region: WWTF (www.wwtf.at)
- Specific programs (GEN-AU) (www.gen-au.at/index.jsp?lang=en)
- Austrian Research Promotion Agency (FFG) (www.fff.co.at)

Belgium

http://www.arabidopsis.org/info/2010_projects/Belgium.jsp
Contact: Pierre Hilson
Department of Plant Systems Biology, VIB, Ghent University
Email: pierre.hilson@psb.ugent.be

Belgian Arabidopsis projects are funded via university, regional or federal level grants, but not within calls specifically targeting this model plant species or plants. In addition VIB, the Flanders Institute for Biotechnology, provides significant support to the Department of Plant Systems Biology (about 6 million Euro per year) in which about half the research activities are dedicated specifically to Arabidopsis studies.

Current Research Projects

- A Belgian national research project (IAP), coordinated by D. Inzé, focuses on the study of the molecular mechanisms regulating the development of plant roots and the interaction of roots with their environment. This program also involves T. Beeckman, G. Beemster, L. De Veylder, D. Van Der Straeten, J.-P. Verbelen, M. Boutry, X. Draye, N. Verbruggen and C. Périlleux. Malcolm Bennett (Univ. Nottingham, UK) is an international partner in this project.
- Other current Arabidopsis research topics in Belgium include systems biology of yield (D. Inzé), cell cycle regulation (L. De Veylder), root and leaf growth and development (T. Beeckman, G. Beemster, M. Van Lijsebettens), auxin (J. Friml), brassinosteroids (J. Russinova), phytohormone interactions (E. Benkova), oxidative stress and cell death (F. Van Breusegem), seed development (M. Nowack), evolutionary systems biology (S. Maere), genome annotation and evolution (Y. Van de Peer, P. Rouzé), functional genomics (P. Hilson), proteomics (G. De Jaegher), quantitative biology (M. Vuylsteke), tree biotechnology and bioenergy (W. Boerjan), gene regulation (A. Depicker), ethylene signaling (D. Van Der Straeten), cell biology (D. Geelen), hormone biology (E. Prinsen), membrane proteins (M. Boutry), salt stress and tolerance to heavy metal (N. Verbruggen), flowering (C. Périlleux) and plant pathogen interaction (B. Cammue).

Major funding sources for Arabidopsis functional genomics:

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework Programmes (www.cordis.lu/)
- Belgian Federal Science Policy Office (www.belspo.be)
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IWT; www.iwt.be)
- Research Foundation – Flanders (FWO; http://www.fwo.be/en/index.aspx)
- European ERA-Plant Genomics initiative (www.erapg.org)

Arabidopsis genomics tools and resources:

- The Department of Plant Systems Biology (PSB) continuously develops and disseminates an exhaustive collection of destination vectors, designed for the functional analysis of genes in plant cells and compatible with the recombinational cloning Gateway technology (www.psb.ugent.be/gateway).
- PSB also coordinates AGRON-OMICS, a functional genomics and systems biology project funded by the 6th European Framework Programme (www.agron-omics.be).

Canada

http://www.arabidopsis.org/info/2010_projects/Canada.jsp
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malcolm.campbell@utoronto.ca

As is the case elsewhere, Arabidopsis serves as an important model system for studies in basic plant biology in many Canadian laboratories, and is particularly relevant as a model for crop applications within the family *Cruciferae* (Rapeseed, Canola, Mustards). There exists no dedicated Arabidopsis funding channel or coordinating advocacy group within the Canadian 'Tri Council' family of funding agencies. Genome Canada (http://www.genomecanada.ca) has served as a funding NGO committed to advancing the development and application of genomics technologies, and has included plants as a major object of interest.

NSERC (Natural Sciences and Engineering Research Council) is one of three 'Tri-Council' funding agencies in Canada and serves as an important funding source for plant science research. This year (2009) was a year of challenge for many national economies globally, and Canada was no exception. Significant reductions to NSERC funding was announced in the 2009 budget – cuts that were not fully restored in the recent budget tabled by the Government of Canada in February 2010. There remains a growing emphasis on 'targeted' programs which link research and its applications, which have an effect on the scope of fundamental discovery-oriented research in the plant sciences. Furthermore, Genome Canada was not an object of new funding in the 2009-2010 Federal budgetary year, although the 2010 budget included a modest allocation of CDN$75Million to be earmarked for support to Technology Platforms, and to projects in the Forestry and Environment sectors. Taken together, funding opportunities for basic research in the plant sciences have been constrained.

As of late 2010, approximately 60 laboratory groups were listed as conducting research with Arabidopsis, as indicated by an Email poll for contributions to the MASC report. Of these, approximately 10 groups responded with updates to their contributions for the 2009 activity year. For reference, a comprehensive list of individual labs, their contact coordinates and major research thrusts were provided in the MASC report for 2007.

Individual Group updates for 2009

- Brian Ellis -Univ. Brit. Col. Current projects are focusing on the following research themes: 1) Reverse genetic analysis of transcription factors involved in secondary cell wall formation. 2) Development of growth kinetic profiling for precise non-destructive assessment of stages of development in flowering stems as they mature. 3) Reverse genetic and interaction analysis of the family of MAP kinases and identification of signaling complexes involving MAPKs and MAPKKs that help control cell wall biogenesis, cytoskeleton function and environmental stress responses.
- Maurice Moloney -SemBioSys Genetics, Calgary. Dr. Moloney, a long-established Arabidopsis and Brassica researcher in Canada, has been appointed as the new Chief Executive and Director at the Rothamsted Research Institute (Harpenden, Herts., United Kingdom) effective April 15 2010.
- George Haughn -Univ. Brit. Col. The Haughn group was co-recipient of major Genome Canada funding for a project entitled "Designing Oilseeds for Tomorrow's Market" – in collaboration with scientists and co-funding from the Genome Alberta and Genome Prairie organizations. This genome Canada project focuses on *B. napus* and has collaborated with the laboratories of Raju Datla and Raj Selveraj (Plant Biotechnology Institute, Saskatoon) to conduct a microarray analysis of the seed coat at three developmental stages in Wild Type, *ap2* (no differentiation of seed coat palisade and epidermis) and *tt16* (no differentiation of the endothelium) genetic backgrounds. Data arising from these studies are planned for release to the public later this year.

Facilities and Technology Availability

- The Canadian reverse genetic TILLING facility, **CAN-TILL** (http://www.botany.ubc.ca/can-till/) is being operated by the Haughn group at the University of British Columbia (Vancouver).
- The Bio-Array Resource (http://bar.utoronto.ca) continued to expand its collection of bioinformatic tools for exploring large-scale data sets from Arabidopsis. On the one hand, several cell-type-specific gene expression data sets were added to its popular eFP Browser, including several root cell-type-specific sets from Brady *et al.* (2007), Dinneny *et al.* (2008), and Gifford *et al*. (2008), as well as pollen germination and shoot apical meristem data sets from Qin *et al.* (2009) and Yadav *et al.* (2009), respectively. The eFP Browser also is now able to display At-TAX data from the Weigel Lab. In addition, the BAR introduced its ePlant for exploring data sets covering kilometre to nanometre scales (from sequence variation to protein 3D structure). Part of the ePlant effort predicted protein structures for approximately 75% of the Arabidopsis proteome.

Major Funding Sources:

- NSERC (http://www.nserc.ca)
- Genome Canada and associated five regional Genome centres (http://www.genomecanada.ca)
- Agriculture Canada (http://www.agr.ca)

Researchers in Canada are highly supportive of the maintenance and functional expansion of internationally coordinated sample and information repositories. Chief among these have been TAIR (Stanford Univ.), the ABRC (Ohio State Univ.) and the European Arabidopsis Stock Centre (the NASC) based in Nottingham, UK. These resources are deemed to be an invaluable clearinghouse and coordinating presence that serves the global Arabidopsis research community. Their continued funding, by whatever national or international means, has been a topic of interest and concern in Canada, as it has elsewhere. Canadian researchers understand the value of these resources – both in terms of their individual research programs, as well as the role of these organizations in supporting the global Arabidopsis community. Ongoing support to all three centres is strongly supported among the majority of Canadian Arabidopsis researchers.

China

http://www.arabidopsis.org/info/2010_projects/China.jsp
Contact: Wei-Cai Yang
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences
Email: wcyang@genetics.ac.cn

The funding climate continued to improve in China during 2009. The National Science Foundation of China (NSFC) granted 12 key projects to research laboratories using Arabidopsis as a model system. In addition, many plant laboratories received grants from the National Transgenic Crop Development initiative, which was lunched in 2008.

NSFC major projects related to Arabidopsis in 2009:

- The role of C27 gene in disease resistance in plants. Dr. Yule Liu, Tsinghua University
- Identification and functional analysis of histone demethylase genes in plants. Dr. Xiaofeng Cao, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences
- Molecular mechanism controlling pollen wall formation in Arabidopsis. Dr. Zhongnan Yang, Shanghai Normal University
- Trimeric G-protein signaling and its role in chloroplast development in plants. Dr. Jirong Huang, Shanghai School for Biological Sciences, Chinese Academy of Sciences
- Genetic and molecular control on crosstalk between brassinosteroid and abscisic acid in plants. Dr. Xuelu Wang, Fudan University
- Molecular mechanism of hormonal control on somatic embryogenesis in plants. Dr. Xiansheng Zhang, Shandong Agricultural University
- Molecular mechanism of strigolactone, auxin and light signaling on flowering time and morphogenesis in plants. Dr. Hongquan Yang, Shanghai Jiaotong Univeristy
- The role of polar auxin transport on phototropism and root development in plants. Dr. Yingtang Lv, Wuhan University
- The role of TCP transcription factors in brassinolide biosynthesis and signaling in Arabidopsis. Dr. Jia Li, Lanzhou University
- Molecular mechanism of abscisic acid controlled ethylene biosynthesis in plants. Dr. Rongfeng Huang, Chinese Academy of Agricultural Sciences.
- Metabolome study on the intermediates during strigolactone biosynthesis in rice. Dr. Cunyu Yan, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences.
- Two-dimensional GC-MS analysis of plant hormones. Dr. Yafeng Guan, Dalian Institute of Physical Chemistry, Chinese Academy of Sciences

France

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

National Research Agency (ANR) - newly funded Arabidopsis research projects (2009)

Plant Genomics programme:
The plant genomics research theme is expected to provide new knowledge concerning the diversity of genes that are important targets related to a) various productivity challenges and opportunities (plants for food and feed, plants for agro-fuels), b) environmental concerns and c) improved and safer food ingredients and products. Most of the newly funded projects are devoted to crop plants. This year only two are dealing with Arabidopsis:

- **GeneTOP** : Gene Targeting Optimisation in Plants. Fabien NOGUE (IJPB INRA, Versailles)
- **SingleMeiosis** : Identification of the whole set of meiotic recombination events in a single meiosis of *Arabidopsis thaliana*. Christine MEZARD (INRA, Versailles)

The non-thematic 'Blanc' programme:
The Blanc programme is a bottom-up, blue-sky call for proposal in all research fields. It aims to give significant impetus to ambitious projects, internationally competitive, focusing on pioneer objectives, and in breach of traditional research paths.

- PANACEA: Plasmalemma lipids and signalisation of biotic interactions in plants. Sébastien MONGRAND (CNRS Bordeaux)
- CHEMIGENA: Genetic analysis of a pathway limiting Arabidopsis root growth in response to phosphate limitation. Thierry DESNOS (CEA Cadarache)
- EPIMOBILE: Assessing the impact of DNA methylation loss on genome stability: a quantitative genetics perspective. Vincent COLOT (ENS Paris)
- PetalSize: Molecular genetics study of petal morphogenesis. Mohammed BENDAHMANE (ENS Lyon)
- PPR-Rf: Fonctional characterization of the PPR-Rf sub-family in *Arabidopsis thaliana*. Hakim MIREAU (INRA Versailles)
- Quantirex: Identification of key *Arabidopsis* genes involved in quantitative resistance to *Xanthomonas campestris* by QTL analysis and association genetics. Dominique ROBY (CNRS Toulouse)
- TransN: Post-translational regulations of the root nitrate transporter NRT2.1. Alain GOJON (INRA Montpellier)
- 2Complex: Functional Natural Variation at 2 levels of Complexity: plant growth and cis-regulation. Olivier LOUDET (INRA Versailles)

Noteworthy breakthroughs published in 2009:

- Bikard *et al*. (2009) Divergent Evolution of Duplicate Genes Leads to Genetic Incompatibilities within *A. thaliana*. Science (323): 623-626
- Teixeira *et al.* (2009) A Role for RNAi in the Selective Correction of DNA Methylation Defects. Science (323): 1600 - 1604
- Matsuno *et al*. (2009) Evolution of a novel phenolic pathway for pollen development. Science (325): 1688-1692
- d'Erfurth *et al*. (2009) Turning meiosis into mitosis. PLoS Biol (7): e1000124

Germany

http://www.arabidopsis.org/portals/masc/countries/Germany.jsp
Contact: Klaus Harter, AFGN Coordinator, ZMBP, University of Tübingen
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AFGN (Arabidopsis Functional Genomics Network)– a success story

AFGN was founded in 2001 as a DFG-funded basic research programme and will end in October 2010. From the start AFGN has been organized in close coordination with the NSF Arabidopsis 2010 Project, including joint international reviewing processes. AFGN was an extraordinary success, not only with respect to science but also from an educational point of view.

During the 9 years of funding, DFG invested more than 18 million Euro to support over 50 different research groups, involving 80 research projects. Whilst the research of the first two funding periods (2001 to 2007) focussed on the collection of basic functional genomics data, research of the last period (2007 to 2010) used these achievements to progress to the functional genomics analysis of biological processes. In addition, the program also supported the development of tools, technologies, and new resources to address unmet needs.

- The most prominent resource - created in collaboration with colleagues from Japan, Switzerland, the UK and the US - is the AtGenExpress transcriptome data set. DFG and the Max-Planck Society conjointly invested more than 700.000 Euro in 2003/2004 to generate a gene expression profiling database, covering 280 data sets derived from more than 500 Arabidopsis RNA samples. These data form the “hard fact” backbone of popular web-based tools such as Genenvestigator, MapMan and the Arabidopsis eFP browser, and are also widely used by computer scientists to develop novel bioinformatics tools.
- In the course of the AFGN programme more than 120 PhD students and postdoctoral researchers have been educated in functional genomics in Germany. Furthermore, together with the 2010 Arabidopsis Project, AFGN implemented the collaborative AFGN-2010 Young Researcher Exchange Programme. The programme provided funding to young scientists for 1-3 month research visits to the US and *vice versa*. 8 PhD students from the German side applied successfully for this programme and carried out functional genomics research in their US host laboratory.

AFGN has been successful as a driving force and strategic tool for the implementation of basic science in Arabidopsis functional genomics in Germany. Furthermore, the AFGN programme has succeeded in disseminating the functional genomics approach in plant science, and its achievements have also come to the attention of non-plant scientists.

Tri-National Arabidopsis Meeting

Together with colleagues from Austria and Switzerland, AFGN has initiated a yearly international conference on Arabidopsis functional genomics, the Tri-National Arabidopsis Meeting (TNAM). Cities like Cologne, Lutherstadt-Wittenberg, Neuchatel, Tübingen, Vienna and Zürich have officiated as excellent hosts for the meeting. In 2010, the 7th meeting will be held in Salzburg, Austria. This conference is predominantly funded by DFG, is attended by around 200 scientists, prevailingly young scientists and is well known for its convivial and very productive scientific atmosphere. DFG is currently looking into ways to continue funding this conference beyond 2010.

AFGN-related Arabidopsis tools and resources:

AFGN: http://www.uni-tuebingen.de/plantphys/AFGN/AFGNHome2.html
AFGN-2010-YREP: http://www.uni-tuebingen.de/plantphys/AFGN/yrep.htm

Israel

http://www.arabidopsis.org/portals/masc/countries/Israel.jsp
Contact: Danny Chamovitz
Tel Aviv University, Tel Aviv
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In 2009, ~40 research articles employing Arabidopsis as an experimental system were published from research groups in Israel. These included diverse subjects such as bioinformatics and systems biology, metabolic engineering, photosynthesis and molecular development. The major centres of Arabidopsis research are in The Hebrew University of Jerusalem (Faculty of Agriculture), Tel Aviv University, the Weizmann Institute of Science, and the Ben Gurion University of the Negev (Sde Boker Campus).

Funding for basic research in decline:
In a further effort to encourage projects more immediately related to agriculture (and thus curtail basic research, primarily involving Arabidopsis), *BARD* (*The United States - Israel Binational Agricultural Research and Development Fund)* announced that no more than 25% of awards could go to "proposals whose outcomes are expected to have application in more than seven years", or in other words for Arabidopsis-based research. This comes one year after BARD cancelled their "Model System and Functional Biology in the Service of Agriculture" panel, the panel that funded the majority of Arabidopsis research. The Israel Science Foundation remains the major source of funding for basic research employing Arabidopsis.

New Arabidopsis public resources:
@CoEX, The Arabidopsis Co-Expression database, based on Atias et al (BMC Syst Biol *3*, 86), http://ibis.tau.ac.il/AthMod/.

Newly opened facilities:
The Manna Center for Plant Biosciences was opened at Tel Aviv University. This modern plant, primarily Arabidopsis, growth and analyses facility was funded by a $1,000,000 donation from an anonymous donor.

Italy

http://www.arabidopsis.org/portals/masc/countries/Italy.jsp
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Newly awarded Arabidopsis projects:

- Several Italian groups have been awarded National Research grants (PRIN) by the Italian Ministry of University and Scientific Research (MIUR, (http://www.miur.it) as part of its institutional activities. PRIN grants for the year 2009-2011 have been awarded to S.Sabatini/P.Costantino and Altamura M.M, A. Carpaneto, F. Cervone. The group of G. De Lorenzo and F. Cervone have been awarded two grants from the Italian Ministry of Forestry and Agriculture and one from the CRUI-British Council (to S. Ferrari). In addition, the groups of M.Cardarelli/P. Costantino (La Sapienza University and CNR, Rome) and the groups of M.M. Altamura (La Sapienza University, Rome) are involved in a COST action FA0903 on Harnessing Plant Reproduction of Crop Improvement.
- A new collaboration between the Italian groups of G.Serino/P. Costantino and G. Frugis with Q. Xie and LJ. Qu (Chinese Academy of Sciences) has been selected by the Italian Ministry of Foreign Affairs as one of the significant research projects within the frame of the Executive Programme of Scientific and Technological Cooperation between Italy and China. C. Tonelli and M. Galbiati have also established a new laser micro-dissection facility for plant tissues at Fondazione Filarete (www.fondazionefilarete.com).

Outreach conferences:

- C. Tonelli was also the organizer of the 5th conference on the future of Science, held in Venice on September 20-22.

Relevant Arabidopsis genomics tools and resources:

- Several useful engineered Arabidopsis lines have been created, among which: *afb1-3opr3* double mutants defective in auxin perception and jasmonic acid biosyntheis (by M. Cardarelli, CNR, Rome), and plants overexpressing active and inactive polygalacturonases from *A.niger*, as well as plants overexpressing the *MEI* genes (by the group of F. Cervone and G. de Lorenzo).
- New GFP-tagged lines for HD-Zip II transcription factor genes, as well as new single and double mutants for HD-Zip II transcription factor genes have been generated in I. Ruberti's laboratory.
- Novel tissue- and cell- specific promoters have been generated by C. Tonelli and M. Galbiati (University of Milan).

Major funding sources for Arabidopsis functional genomics:

The groups of P. Costantino (La Sapienza University, Rome) and I. Ruberti (CNR, Rome) have been involved in an ERA-PG project on MULTI-STRESS. New Arabidopsis-related functional genomics initiatives have not been initiated this year in Italy.

Highlights of groundbreaking Arabidopsis journal articles:

- The group of P.Vittoriosos/P. Costantino (La Sapienza, Rome) have provided evidence in a paper published this year in Plant Journal for a regulatory function of the DOF transcription factor DAG1 in the PhyB signal transduction pathway that regulates GA and ABA metabolic genes during seed germination. In particular, DAG1 negatively regulates GA biosynthesis, by directly binding the AtGA3ox1 promoter. DAG1 is to date the only transcription factor whose direct binding to a GA metabolic genes in the PhyB/PIL5 signaling in seed germination has been demonstrated. The group of M.Trovato/P.Costantino has recently published in *Physiol. Plantarum* a paper showing the importance of the proline in Arabidopsis flower transition.
- The development of a new technique to measure calcium permeation in cation channels has published a paper in Plant Journal by the group of A.Carpaneto.
- The group of F. Cervone/G. de Lorenzo (La Sapienza, Rome) has shed light on the molecular recognition between pathogen-derived polygalacturonases (PGs) and plant polygalacturonase-inhibiting proteins (PGIPs), a key event for the activation of the plant immune response. In particular, this work leaded to the identification of unique hotspots for this particular interaction. In a broader view, it contributes to the validation of a combined approach to the study of pattern-recognition receptor or resistance gene product, which can be of general utility in cases where structural information on an interaction is available. This work has been published in PNAS.

Awards to Arabidopsis researchers:

- Eleonora Cominelli from the group of C.Tonelli (University of Milan) has been awarded a prize from the region of Lombardia for the project "DAMP-dehydration avoidance mechanisms in plants".

Japan

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

Developing research platforms for 'omics' analysis including genome sequencing, metabolomics, transcriptomics and proteomics- is a major aim of Institute laboratories in Japan. Major Arabidopsis metabolomics research in Japan is carried out at the RIKEN Plant Science Center and at the Kazusa DNA Research Institute. These two institutes serve as analytical platforms for plant metabolome analysis. RIKEN groups include the Plant Science Center (PSC), the BioResource Center (BRC) and the Bioinformatics and Systems Engineering division (BASE). Several universities are also active in Arabidopsis metabolomics collaborating mainly with these platform institutes. Transcriptome analysis based on tiling array and high-throughput sequencers are predominantly carried out at RIKEN PSC and at the National Institute of Basic Biology (NIBB). Proteome analyses are performed at RIKEN PSC and at the Nara Institute of Science and Technology (NAIST).

1. The RIKEN PSC (http://www.psc.riken.jp/english/index.html) has established the following platforms; (1) Metabolome platform by using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito), (2) Hormonomics platform (systematic analysis of plant hormones) (Hitoshi Sakakibara, Yuji Kamiya), (3) Transcriptomics by using tiling array in collaboration with RIKEN BASE (http://omicspace.riken.jp/gps/) (Motoaki Seki), (4) Proteomics analysis (Ken Shirasu) (5) Phenotype analysis of *Ds*-tagged lines, and Full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (Minami Matsui), (6) Collection and phenome analysis of Ds- or T-DNA tagged mutants for nuclear–encoded chloroplast protein genes (Kazuo Shinozaki). The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/, Plant J 61:529-542, 2009) provides easy access to all-inclusive knowledge data, including the information of Arabidopsis knockout mutant resources and their phenotypes for nuclear-encoded chloroplast protein. Special issue on -omics and bioinformatics was published in PCP, http://pcp.oxfordjournals.org/content/vol50/issue7/. RIKEN PSC established the Arabidopsis MS/MS spectral tag database (*Plant J.,* 57: 555–577, 2009), widely-targeted metabolomics technology (*Plant Cell Physiol*., 50: 37-47, 2009), and Arabidopsis metabolome expression database AtMetExpress (*Plant Physiol*., 152: 566-578 2010). RIKEN PSC (Ken Shirasu) and Keiko University (Yasushi Ishihama) have developed a high-throughput shotgun phosphoproteomics tool for plants and phosphorylation site databases (http://phosphoproteome.psc.database.riken.jp, http://phosphoproteome.psc.database.riken.jp and http://pepbase.iab.keio.ac.jp http://pepbase.iab.keio.ac.jp/) including MS/MS spectra. A new project started to identify novel small ORFs in Arabidopsis genome for the discovery new functions of small polypeptides (Kosuke Hanada, supported by BRAIN).
2. RIKEN BRC, Experimental Plant Division (M. Kobayashi, kobayasi@rtc.riken.jp) preserves and distributes plant seeds, cDNA clones and cultured cell lines including transposon-tagged mutants, FOX lines, Arabidopsis full-length cDNA clones and Arabidopsis T87 cells via the National BioResource Project. More than 1,300 laboratories and groups in the world have already received materials from RIKEN BRC (http://www.brc.riken.go.jp/lab/epd/Eng/).
3. RIKEN BASE (Tetsuro Toyoda) (http://www.base.riken.jp/) (1) Japan's national integrated database project covering Arabidopsis omics information resources, (2) PosMed (Positional Medline) for Arabidopsis genes is an intelligent search engine integrating genome information and literature http://omicspace.riken.jp/PosMed/search?objectSet=gene&species=At) http://pcp.oxfordjournals.org/cgi/content/full/50/7/1249
4. Kazusa DNA Research Institute (Daisuke Shibata). New releases of the KaPPA-View4 viewer (http://kpv.kazusa.or.jp/kpv4/) for integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, MassBase (http://webs2.kazusa.or.jp/massbase/), the co-expressed gene search tools KAGIANA (http://pmnedo.kazusa.or.jp/kagiana/index.html) and Cop (http://webs2.kazusa.or.jp/kagiana/cop/), and the regulatory network research RnR (http://webs2.kazusa.or.jp/kagiana/rnr/).
5. National Institute of Advanced Industrial Science and Technology (AIST) (Masaru Ohme-Takagi). Functional analysis of transcription factors using novel gene silencing system named CRES-T (Chimeric REpressor gene Silencing Technology) in Arabidopsis and rice. Identification of the master and licensing factors that regulate metabolic pathway, environmental stress response and growth (http://unit.aist.go.jp/rigb/gf-gre/, ttp://www.cres-t.org/).
6. New 5-year project supported by the Grant-in-Aid of MEXT: Consortium for the systematic analysis of plant responses to high CO_2 based on molecular physiology and ecology. (PI: Ichiro Terashima, The Univ of Tokyo)

Arabidopsis genomics tools and resources

- RIKEN resources and tools

Resources from RIKEN BRC (http://www.brc.riken.go.jp/lab/epd/Eng/)
The Chloroplast Function Database (http://rarge.psc.riken.jp/chloroplast/)
Arabidopsis MS/MS spectral tag (MS2T) viewer (http://prime.psc.riken.jp/lcms/ms2tview/ms2tview.html)
Arabidopsis metabolome expression database AtMetExpress (http://prime.psc.riken.jp/lcms/AtMetExpress/)
Widely targeted metabolomics (http://prime.psc.riken.jp/?action=wide_index)
Annotation of metabolites by NMR from 13C-HSQC peaks (http://prime.psc.riken.jp/?action=nmr_search)
Omicspace of RIKEN BASE (http://omicspace.riken.jp/gps)

- Kazusa tools

The KaPPA-View4 viewer (http://kpv.kazusa.or.jp/kpv4/)
MassBase (http://webs2.kazusa.or.jp/massbase/)
KAGIANA (http://pmnedo.kazusa.or.jp/kagiana/index.html)
Cop (http://webs2.kazusa.or.jp/kagiana/cop/)
The regulatory network research RnR (http://webs2.kazusa.or.jp/kagiana/rnr/).

Major funding sources for Arabidopsis functional genomics

- RIKEN and Kazusa projects are supported by MEXT and Chiba prefecture, respectively.
- Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT), www.jsps.go.jp/english/e- grants/grants.html
- CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
- Program of Promotion of Basic Research Activities for Innovative Biosciences (www.brain.go.jp/welcome-e.html)

Awards to Arabidopsis researchers:

Dr. Kiyotaka Okada (NIBB) received the BSJ Award of the Botanical Society of Japan, and Dr. Nobuharu Goto, former director of Sendai Arabidopsis Seed Stock Center (SASSC), received a Special Award from The Botanical Society of Japan for his devoted service to the research community (September 2009). Drs. Kazuo Shinozaki (RIKEN) and Kazuko Yamaguchi-Shinozaki (The Univ. of Tokyo) received the JSPP award from Japanese Society of Plant Physiologists (March 2009).

Arabidopsis Conferences:

Japan will host the 21st International Conference on Arabidopsis Research (ICAR2010, http://arabidopsis2010.psc.riken.jp/) on June 6-10, 2010 in Pacifico Yokohama, Yokohama, Japan. ICAR 2010 will highlight recent advances in Arabidopsis research and its translation to research in crops and trees.

The Netherlands

http://www.arabidopsis.org/portals/masc/countries/Netherlands.jsp
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New Arabidopsis Programmes:
For Arabidopsis research in the Netherlands, 2009 was a relatively quiet year. The new programmes, the Centre for BioSystems Genomics 2012 (CBSG2012) and the Netherlands Proteomics Centre 2 (NPC2), both with substantial components of Arabidopsis research, have started and are beginning to bear fruit in terms of publications. CBSG2012 is predominantly oriented towards crop plants with a contribution for Arabidopsis research and translation of results into applications in crops. NPC2 is organized around proteomics technology and is devoted predominantly towards animal systems, with an Arabidopsis contribution aimed at the isolation of membrane receptor and transcription factor complexes and networks. One NWO-VENI innovation grant was awarded to an Arabidopsis project of a junior scientist.

Scientific Highlights for the Netherlands:
Overall Dutch Arabidopsis scientists have published 70 papers in the past year including a number of highlights shown below:

- Kaufmann K *et al*. (2009) Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biol (7): e1000090
- Immink RG *et al.* (2009) SEPALLATA3: the 'glue' for MADS box transcription factor complex formation. Genome Biol (10): R24
- Fu J *et al*. (2009) System-wide molecular evidence for phenotypic buffering in Arabidopsis. Nat Genet (41): 166-7
- Tessadori F *et al.* (2009) Phytochrome B and histone deacetylase 6 control light-induced chromatin compaction in Arabidopsis thaliana. PLoS Genet (5): e1000638

Spain

http://www.arabidopsis.org/portals/masc/countries/Spain.jsp
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Major established Arabidopsis centres and programmes:

- Centro de Biotecnología y Genómica Vegetal UPM-INIA, Madrid
- Centro de Investigación en Agrogenómica (CRAG; IRTA-CSIC-UAB)
- Centro Nacional de Biotecnología-CSIC-Madrid, Spain
- Instituto de Biología Molecular y Celular de Plantas UPV-CSIC Valencia
- Additional research activities on Arabidopsis functional genomics are being carried out in several universities and research centres of the CSIC, most importantly, Universidad de Elche, Alicante; Universidad de Malaga; IRNASE-CSIC, Sevilla and Instituto de Instituto de Bioquímica Vegetal y Fotosíntesis-CSIC, Sevilla

Scientific Highlights from Spain:

The two most important results from Spanish teams have been the identification of the chemical nature of the active Jasmonate (Fonseca S, Chini A, Hamberg M, *et al.* Nature Chemical (5): 344-350; Roberto Solano team) and the contributon to the identification and functional and structural characterisation of ABA receptor (Santiago J, Dupeux F, Round A *et al*. Nature (462): 665; Park SY, Fung P, Nishimura N *et al*. Science, (324): 1068; Fujii H, Chinnusamy V, Rodrigues A, *et al*, Nature (462): 660 -PL, Rodriguez team, IBMCP, Valencia).

Recent efforts to establish international Arabidopsis functional genomics collaborations

These are possible in the context of the TRILATERAL French German Spanish programme on plant genomics.

Arabidopsis genomics tools and resources:

- A collection of 1000 transgenic lines, each expressing a different TF under the control of an estradiol inducible promoter (XVE) is being prepared and will be made available through the NASC stock centre (TRANSPLANTA Programme).
- A tilling facility for *Landsberg erecta* ecotype has been now operative for 2 years (http://www.cnb.csic.es/; Carlos Alonso Blanco)

Major funding sources for Arabidopsis functional genomics:

Arabidopsis research is mostly funded by the Ministry of Science and Innovation. Overall, 30-45 project are funded with an average amount of 200,000 Euro/3 years.

United Kingdom

http://www.arabidopsis.org/portals/masc/countries/United_Kingdom.jsp
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Irene Lavagi, MASC Coordinator/GARNet Email: i.lavagi@warwick.ac.uk
Warwick HRI, University of Warwick

Arabidopsis Research in the UK

Over 300 research groups in the UK utilise the model plant Arabidopsis in their studies. Many of these groups are leaders in their field producing world-class research and publications in high impact journals. Arabidopsis research is largely project-focused, with work based in individual laboratories, multi-institutional collaborations or national Centres and Institutes; the UK also hosts one of the two international Arabidopsis stock centres; NASC.

UK Funding News

- The Biotechnology and Biological Science Research Council (BBSRC) is the major funder of Arabidopsis research in the UK. In early 2010 BBSRC launched its new strategy after a community wide consultation. The new plan sets out BBSRC's high-level priorities and aspirations over the next 5 years, and articulates BBSRC's vision to lead world-class 21st century bioscience, promote innovation and help realise benefits for society within and beyond the UK. The new strategic plan highlights three priority areas for particular focus, food security; bioenergy and industrial biotechnology; and basic bioscience underpinning. Of these three core areas, two are relevant to plant science and Arabidopsis research, placing plant science at the core of the BBSRC remit. Arabidopsis researchers can apply for support from BBSRC through responsive mode funding.
- In July 2009 in partnership with the East of England Development Agency and local authorities BBSRC launched the Genome Analysis Centre (TGAC), which will conduct, whole genome sequencing and other applications of sequencing, develop new high throughput sequencing technologies and develop a centre of excellence for bioinformatics associated with genome sequencing.
- BBSRC also launched its Crop Improvement Research and Technology Club (CIRC) in 2010. CIRC is a £6M, 5-year partnership between BBSRC, The Scottish Government and a consortium of leading companies, aimed at supporting innovative and excellent research to underpin the development of improved crop varieties that deliver increased productivity and consistent, high quality end products.
- The Technology Strategy Board (TSB) announced a call for New Approaches to Crop Protection in 2009. This collaborative call between industry and research provided £13M to help crop growers respond to the dual challenges of increasing the productivity of crops while reducing the environmental impact of crop production.

UK Arabidopsis Research Network

- In December 2009 GARNet (the network of Arabidopsis UK researchers) was awarded a five year grant from BBSRC to continue its coordination activities, ensure that the full impact of the excellent UK plant science base is realised by acting as an information hub, provide a point of contact for researchers and funding agencies, promote interactions between fundamental and applied plant science and to increase opportunities for UK plant science at the international level.
- GARNet represents UK Arabidopsis researchers via a committee of 12 elected members and two ex-officio members, Prof Sean May and Dr Sabina Leonelli. Each year new members are elected to the GARNet committee as others rotate off. In December 2009 Juliet Coates, Ian Moore and Nicholas Smirnoff were elected to the committee for a three year term to join the current committee of Anna Amntmann, Jim Beynon, Alessandra Devoto, Claire Halpin, Patrick Hussey, Stefan Kepinski, Andrew Millar and Robert Sablowski
- Alex Webb was elected as the new chair of GARNet and began his role on the 1st January 2010.

MASC Coordinator funded by UK

BBSRC funds to support the MASC coordinator for three years were awarded to Prof Jim Beynon and Dr Ruth Bastow at Warwick HRI during the autumn of 2009. Dr Irene Lavagi has been appointed as the MASC coordinator from December 2009 – December 2012.

UK Meetings

- In the summer of 2009 the UK hosted the 20th International Conference on Arabidopsis Research (ICAR) in Edinburgh. Over 900 delegates from across the globe attended an informative and enjoyable meeting.
- In April 2010 the UK hosted the first of two workshops to assess the future of Arabidopsis/ plant biology data management and handling. The second workshop was held in the US in May. The outcomes of these meeting will be presented at the 21st International Conference on Arabidopsis Research (ICAR) in Yokohama in June and a final report will be posted on the MASC website and sent to policy makers and funding agencies.

Notable Research Breakthroughs in the UK

- Kumar SV, Wigge PA (2010) H2A.Z-containing nucleosomes mediate the thermosensory response in Arabidopsis. Cell (140): 136-47
- Etchells JP, Turner SR (2010) The PXY-CLE41 receptor ligand pair defines a multifunctional pathway that controls the rate and orientation of vascular cell division. Development (137): 767-7
- Mosher RA, Melnyk CW, Studholme DJ, Baulcombe DC (2009) Uniparental expression of PolIV-dependent siRNAs in developing endosperm of Arabidopsis. Nature (460): 283-6
- Kover *et al* (2009) A multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in Arabidopsis thaliana. PLoS Genet (5): e1000551

United States

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

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North American Arabidopsis Steering Committee (NAASC)

NAASC (www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp) is composed primarily of US researchers and represents Arabidopsis researchers in the United States, Canada and Mexico. NAASC provides North American representation to the MASC and serves as the main organizing and fundraising body for the ICAR when it is held in North America and raises funds to support young North American scientists to participate in foreign ICARs.

1. Annual elections replace two members that rotate off the committee each year. Julian Schroeder and Caren Chang conclude their four year term at the 2010 International Conference on Arabidopsis Research.
2. Continuing committee members include George Haughn, Scott Poethig, Mark Estelle, Jane Glazebrook, Xinnian Dong and Blake Meyers. Newly elected committee members in 2010 are Dominique Bergmann (Stanford University) and Wolf Frommer (Carnegie Institution for Science).
3. Following four years as MASC Coordinator, Joanna Friesner assumed the role of NAASC Coordinator in 2010.
4. Scott Poethig received NSF funding to support participants of the 2009 ICAR in Scotland. Those funds, combined with remaining NSF funds from 2008, supported full funding for 9 participants including under-represented minority undergraduate/graduate students, postdoctoral scholars, and faculty at minority serving institutions or historically black colleges/universities. Also supported were travel grants to 14 graduate students, postdocs, and young faculty, and 12 invited U.S. speakers.
5. Committee service: Caren Chang and Scott Poethig continue to serve on the ABRC advisory committee while Julian Schroeder serves on both the ABRC and TAIR advisory committees

The International Conference on Arabidopsis Research (ICAR) Returns to Madison

The ICAR is currently on a 3 year conference site rotation: North America, Europe, and Asia/Pacific Rim. The 22nd ICAR will be held back in the US at the University of Wisconsin, Madison, from June 22-25, 2011. The lead organizers from NAASC are Mark Estelle (UC San Diego) and Jane Glazebrook (University of Minnesota) with assistance from the NAASC Coordinator, Joanna Friesner.

Reduction in TAIR Funding and Workshops to Address Bioinformatics in the Arabidopsis Community

1. The Arabidopsis Information Resource (TAIR) is a vital resource to the Arabidopsis Community. It maintains the Arabidopsis genome sequence and updates gene annotations regularly. It is also the portal to ordering stocks from ABRC and it acts as a central information point for the worldwide community including functional genomics projects, the Multinational Arabidopsis Steering Committee, and the annual Arabidopsis conference. TAIR's previous 5 year NSF grant ended in 2009 and its recent renewal was for reduced funding that will severely affect its existence. The renewal provides level funding for one year (September 2009 - August 2010) followed by steeply decreasing budgets (75%, 50% and 25% of the current year) for the remaining three years. A Nature article, with community comments, was published last fall entitled 'Plant genetics database at risk as funds run dry.' Published online 18 November 2009, Nature (462): 258-259. In order to address the bioinformatics needs of the community and discuss approaches for long-term funding of databases, including TAIR, two community workshops are scheduled for the first half of 2010 (see below).
2. In recent years, international projects have generated vast volume of data and resources, contributing to our understanding of the fundamental processes in plant biology. As sequencing technologies continue to improve and the cost decreases, genomics is generating massive amounts of new data in the public domain in a wide variety of data formats. An international, coordinated effort is needed to manage the vast datasets and infrastructure and effectively leverage these data and resources. NAASC is organizing one of a pair of workshops on the long-term informatics and database needs of the Arabidopsis community. The first workshop, organized by MASC in the UK in April, 2010, will provide a forum for open discussions about the current and future informatics needs of the community. The second workshop, organized by NAASC in the US in May, 2010, will discuss informatics, databases and infrastructure technologies as well as examples of approaches used from other model communities. One goal of the US workshop is to discuss long-term bioinformatics storage including sustaining support for TAIR. Outcomes of the workshops will be presented to the community at the Arabidopsis conference in Japan (June 6-10, 2010). Reports from the workshop will be posted at the MASC pages publicly online at TAIR.

   US and UK organizers of the Bioinformatics workshops plan to present their findings as part of a larger community discussion during a workshop at the 2010 ICAR in Japan.

New Online AT2010 Project Resource at TAIR

http://arabidopsis.org/portals/masc/2010_resources.jsp

Cataloging of publicly-available data and resources generated by NSF-funded AT2010 projects began in 2006 by the MASC Coordinator (Joanna Friesner). The goal was to provide a service to the community by developing a centralized resource listing project websites, databases, investigator contact information, and most importantly, the availability to the community of data and physical resources. The desired outcomes of this resource are increased sharing of knowledge and resources and leveraging of the gains achieved through 2010 project funding.

The Coordinator, assisted by other Arabidopsis resource experts, culled information from public sources and followed-up with investigators by email and phone conversations as needed. Responses, if received, were used to update the table. Those involved diligently tried to ensure the accuracy of their information. However, there are bound to be omissions and inaccuracies, which we hope to correct through community input. Information on corrections and additions to the online resource can be found at the TAIR URL above. Information to populate the table came from these sources:

- NSF award abstract pages
- Project websites
- TAIR
- ABRC
- Feedback from project PIs obtained through contacts by TAIR and the MASC Coordinator

AT2010 Project Update and Special Session at 2010 ICAR

1. January 12, 2010 was the final call for proposals to the National Science Foundation (NSF)-sponsored 2010 project which aims to determine a function for all genes in *Arabidopsis thaliana*. Since its inception the project has funded proposals in two main areas: proposals that address gene function directly and proposals that develop enabling tools and resources for functional genomics research. Since the first awards were granted in 2001, 150 awards encompassing 120 diverse projects have been funded (through fiscal year 2009). During the project, two U.S. and one European community workshops were held to evaluate the success and course of the project and to strategize for future Arabidopsis genomics funding. The results of these workshops (2020 Vision for Biology: The Role of Plants in Addressing Grand Challenges in Biology; EU 2020 European Vision for Plant Science, and Mid-course Evaluation of 2010 Program) can be found at TAIR (http://arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp).
2. Special 2010 Session: The 21st ICAR will include a session to honor the NSF AT2010 and related genome-oriented projects. This session will feature speakers who have been funded by the 2010 project as well as representatives of GARNet (UK), RIKEN (Japan) and AFGN (Germany). Invited speakers for this session will be Mary Lou Guerinot (US), Rick Vierstra (US), Andrew Millar (UK), Kazuo Shinozaki (Japan), and Klaus Harter (Germany).

Several Notable Research Breakthroughs Involving United States Researchers

The Human Epigenome- Decoded- a Time Magazine 'top scientific discovery'

Humans and plants share many things, including a propensity to methylate their DNA. Changes in DNA methylation have been associated with a variety of heritable "epimutations" in Arabidopsis, and are common cause of cancer in humans. The first comprehensive pictures of genomic patterns of DNA methylation in any organism were provided for Arabidopsis by the Jacobsen and Ecker labs. This year, the Ecker lab used the approach they developed for Arabidopsis to catalogue genome-wide DNA methylation in a human embryonic stem cell and a fetal fibroblast cell line. Remarkably, DNA methylation profiles differed significantly between these cell lines; furthermore, the embryonic stem cell line had a significant amount of non-CG methylation--a type previously thought to be extremely rare in humans (1). This study was the first of its kind for humans and was cited at the one of the "top ten scientific discoveries" of 2009 by Time magazine (2).

References:

(1) Lister R, Pelizzola M, Dowen RH, Hawkins RD, Hon G, Tonti-Filippini J, Nery JR, Lee L, Ye Z, Ngo QM, Edsall L, Antosiewicz-Bourget J, Stewart R, Ruotti V, Millar AH, Thomson JA, Ren B and Ecker JR (2009) Human DNA methylomes at base resolution show widespread epigenomic differences. Nature (462): 315-322

(2) www.time.com/time/specials/packages/article/0,28804,1945379_1944416_1944418,00.html

ABA Receptors- a Science Magazine 'scientific breakthrough of the year (2009)'

Receptors for the plant hormone abscisic acid (ABA) have long been sought. In 2009 international groups of researchers from the US and Europe led by Sean Cutler and Erwin Grill identified a new class of ABA receptors that encode START domain proteins, presently named "PYR/RCAR" proteins (1,2). Functional biochemical, genetic, proteomic and structural analyses together provide strong evidence that this family of PYR/RCAR proteins encode the long sought major ABA receptors that control ABA-induced abiotic stress resistance and developmental responses (1-7). The discovery of this ABA receptor family was named as one of the top 'scientific breakthroughs of the year' by Science magazine (December 18, 2009, Vol 326, p. 1600.) For more information on this breakthrough, please see the research highlights section of the MASC report.

References:
1) Ma Y, Szostkiewicz I, Korte A, Moes D, Yang Y, et al. (2009) Regulators of PP2C phosphatase activity function as abscisic acid sensors. Science (324): 1064–68
(2) Park SY, Fung P, Nishimura N, Jensen DR, Fujii H, et al. (2009) Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. Science (324): 1068–71
(3) Miyazono K, Miyakawa T, Sawano Y, Kubota K, Kang HJ, et al. (2009) Structural basis of abscisic acid signalling. Nature (462): 609-14
(4) Nishimura N, Hitomi K, Arvai AS, Rambo RP, Hitomi C, et al. (2009). Structural mechanism of abscisic acid binding and signaling by dimeric PYR1. Science (326): 1373-9
(5) Melcher K, Ng LM, Zhou XE, Soon FF, Xu Y, et al. (2009) A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. Nature (462): 602-8
(6) Santiago J, Dupeux F, Round A, Antoni R, Park SY, et al. (2009) The abscisic acid receptor PYR1 in complex with abscisic acid. Nature (462): 665-8
(7) Yin P, Fan H, Hao Q, Yuan X, Wu D, et al. (2009) Structural insights into the mechanism of abscisic acid signaling by PYL proteins. Nat. Struct. Mol. Biol. (16): 1230-6

National Academy of Science Newly elected members

Philip Benfey (Duke University) and Jian-Kang Zhu (UC Irvine) were recently elected to the National Academy of Science

Analysis and Recommendations

As the 2010 project draws to a close, it is timely to reflect on progress in Arabidopsis research over the last decade before looking forward. There has been a dramatic series of developments both in understanding the molecular mechanisms of basic plant processes and in the application of new technologies to biological problems. Some of these developments have occurred more quickly that perhaps expected, while some significant challenges remain, and new ones have emerged. There have been important new discoveries in the area of plant hormone perception, transport and mode of action, and the identification of novel roles for strigolactones. Small RNAs have emerged as incredibly important regulators of gene expression, and our understanding of epigenetic mechanisms has moved forward impressively. The basis of plant defence mechanisms against a range of biotic and abiotic stresses has become clearer, and this knowledge is gradually being translated into crop protection strategies. The genetic control of organogenesis, and its integration with hormone signalling systems, is another high point, with new insight into the evolution of molecular mechanisms.

Technological advances have also been rapid. Next Generation sequencing and new chip-based genomics tools are transforming the way we can investigate genome structure, organization and function. The 'omics' approaches have become common, and we are also getting to grips with transcriptomic, proteomic and metabolomic processes at the single cell level. The more traditional genetics approaches such as forward and reverse genetics have been facilitated by the production of very large numbers of insertional and activation tag lines. Advances in imaging techniques, such as spinning disc confocal and total internal reflectance microscopy, in combination with new fluorescent tags, are providing new insights at the cell biological level. A strength of the ethos associated with Arabidopsis research has always been the willingness of individuals to contribute materials and technologies to the wider community. Bioinformatics support and the seed and DNA resource centres have played a central role in keeping the wheels of Arabidopsis research rolling, and it is important to find sustainable funding routes for these. This point is highlighted by the partial loss of funding for TAIR in 2010.

So, as ever of course, the nature of plant research is changing, and we can see how this has happened over these last 10 years. Attention is less focused on the role of individual genes and proteins (though this information is still crucial), and more towards the question of integration. The function of a gene in an organism is the product of its regulatory system, its partners and its downstream responses. This is systems biology. How do proteins interact, how is their coordinated expression regulated, how does gene expression link with metabolic pathways, with compartmentation, with environmental responses, with development? These are some of the big questions for the next decade – we need to build the big picture. And can we make use of this information to inform crop breeding strategies, to feed the world and help provide it with a sustainable supply of energy in a changing environment? How does gene relate to phenotype in the field, where plants experience a plethora of stresses and other inputs from the environment? New imaging techniques are emerging for the computational description of plant phenotype, at both lab level and, potentially, in the field. This area of phenomics will ultimately help provide the link between genotype, environment and phenotype.

So what does the next decade hold for Arabidopsis research? Is there still a place for it, with pressures to develop crops with higher yields? If so, what approaches will emerge?

We would argue that Arabidopsis, as a reference organism, holds a very important place in plant science research. This report illustrates the volume of research activity and output, particularly in understanding molecular mechanisms, that is not readily obtainable using other species. This is particularly true if one aims to adopt an integrative Systems Biology approach to unravelling the link between genotype and phenotype. If one wants to develop new organisms for industrial purposes using a 'Synthetic Biology' strategy, it is essential to have the required building blocks (genes, regulators) and to understand how they interact to produce the desired outcome. Predictive mathematical modelling approaches will become increasingly important, as complex interactions become too difficult to assimilate outside of a computer. Biologists have generated models for decades, but the use of computational tools will doubtless become more important.

This leads to another feature of how things are changing – an increased multidisciplinarity in approach. Biologists are interacting more that ever with mathematicians, engineers, physicists and chemists in order to achieve their scientific goals. And many mathematicians and physical scientists welcome this new interaction, as biological problems are typically complex and challenging. Biological systems also offer new approaches to solving engineering problems, so it works both ways. Arabidopsis, with its genetic and other resources and offering a high level of understanding of an increasing number of molecular mechanisms, is the ideal plant species in which to take forward this type of research. The techniques and biological information will certainly be of value in crop development, through the provision of molecular markers, candidate genes, interaction models and predictive tools for the more intractable crop species.

The new approaches outlined are data rich, and this presents significant problems of data management and interpretation. Experiments using cell biological and phenomics imaging, omics technologies and NextGen sequencing generate massive amounts of data, and of different types (ie in different

formats). The volume generated is approaching that produced by even cosmologists, and is set to overtake them in the coming decade. For example, the Bejing Genomics Institute has recently announced the purchase of 128 Illumina NextGen DNA sequencing machines, with the combined potential of generating 25,600 Gigabases of sequence data in a single run. It is very easy to see how the current information overload could become completely out of hand very quickly, if not managed effectively. How will the data be stored, transmitted around the world and interpreted? If each of these criteria is not satisfied, the investment in producing the data will be of limited value. To begin to address this, MASC and NAASC are hosting two workshops on the future of plant biology data management and handling during Spring 2010; one in Nottingham, UK and the other in Washington DC, USA, with a view to producing a report to inform policy makers and funding agencies. The outcome of these workshops will be presented and discussed at the International Arabidopsis Conference in Yokohama.

A number of recommendations for the scientific community were published by MASC in its 2009 report, and these are still valid. They included working towards homozygous mutant lines for all genes; a detailed analysis of their expression patterns and epigenetic control the large scale analysis of proteins and metabolites and their functions; the genomic analysis of wild accessions of Arabidopsis for a better understanding of genome evolution and adaptation; and the development of modelling tools. New recommendations for the coming year are as follows.

1. The continued elaboration of a systems approach to plant biology, incorporating diverse data sets and using computational techniques to integrate data and predict plant function.
2. The development of resources for i) association mapping, ii) ecological genetics and iii) field experiments. Such resources include plant populations, appropriate and accessible statistical methods, good field sites, and sharing of knowledge.
3. The development of an international policy to maintain bioinformatics and biological material resource centres, through sustainable funding models.
4. The development of strategies to store, maintain, distribute and interpret the very large amounts of data that will be generated experimentally in the coming years.
5. The effective translation of basic plant knowledge and tools, generated in Arabidopsis research, to crops in order to address the major global challenges of food and energy security in the face of climate change.

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The 2010 MASC report, and previous reports, are available online at:

TAIR, The Arabidopsis Information Resource
http://www.arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp
NASC, The European Arabidopsis Stock Centre
http://arabidopsis.info/progreports.html

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