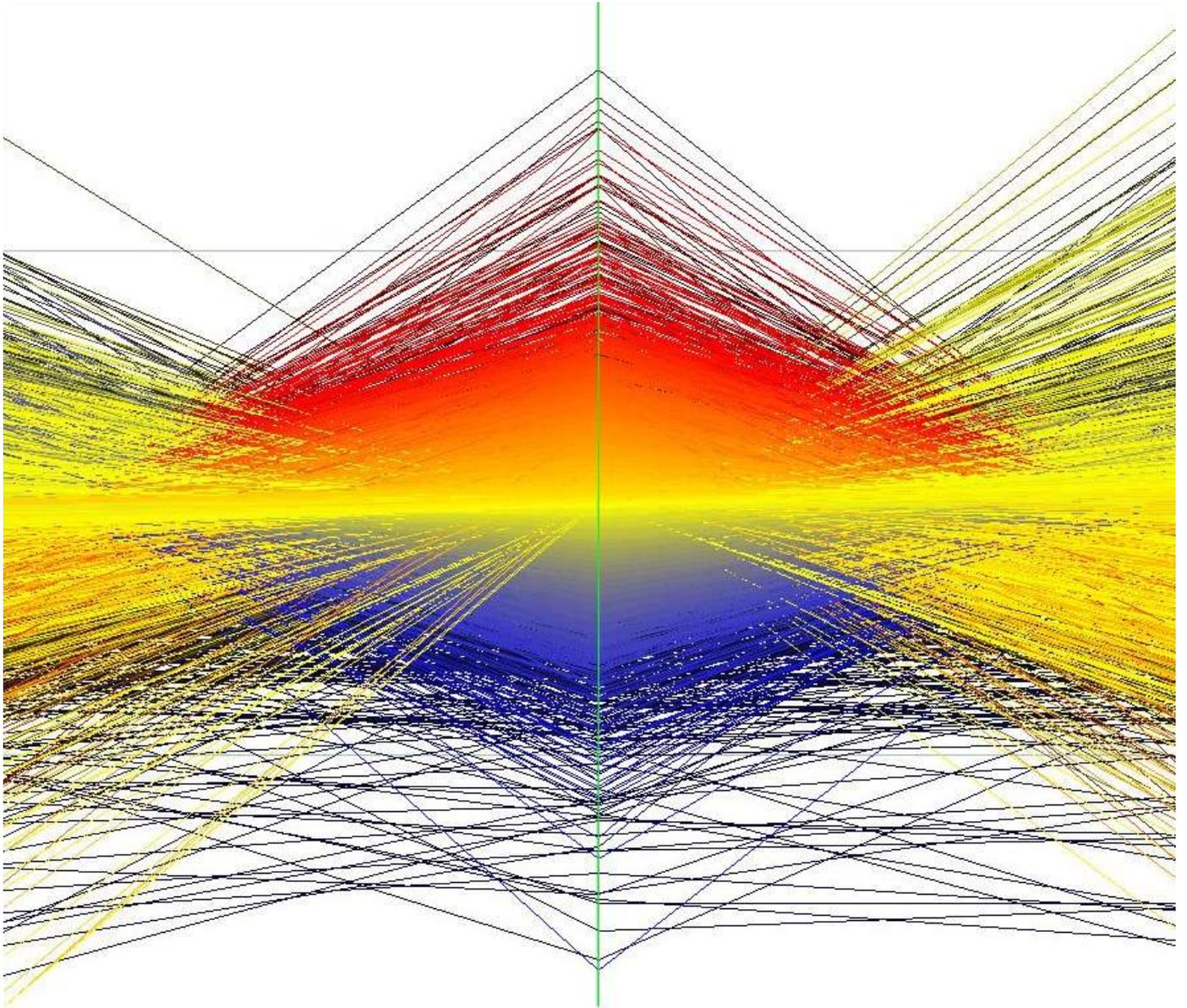


GARNish

The official GARNet newsletter



Systems Biology meets Arabidopsis

Also in this issue

PlaNet

Spotlight on WHRI and UWE

Barley Resources

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Many thanks to all who contributed to this issue of GARNish.

If you have any comments about GARNish or would like to contribute an article to the next issue please contact Ruth Bastow ruth@arabidopsis.info



Editorial

As this year draws to a close it would appear to be a good a time to reflect on the events of the past 12 months. 2005 has been an eventful and productive year for GARNet which began in April with a successful systems biology session at the SEB Plant Frontier meeting. The session included speakers from Madrid, Cambridge and Warwick and set the theme for the year, which saw GARNet become involved in numerous system events. These have included a 'Succeeding in Plant Systems Biology' Workshop in Edinburgh and a request from the BBSRC to submit a report on Systems Biology approaches to Arabidopsis research. More information on this report can be found opposite along with the dates for two town meetings, at which GARNet will be canvassing the opinions of the plant science community on the future of plant systems biology in the UK.

GARNet 2005 was held at the John Innes Centre in Norwich this year and was a great success both in terms of numbers that attended, at over 200 - the largest so far, and scientific content. For a full review of the meeting see below

GARNet has also begun to increase its interactions with other UK Plant communities this year, as was evident from the ABC forum. The Arabidopsis and Beyond to Crops forum was set up to improve current interactions and information exchange between Arabidopsis and Crop scientists. For further information on this and to see all the results of Arabidopsis surveys visit; http://garnet.arabidopsis.info/garnet_survey.htm

I hope you all have a happy Christmas and successful new year.

Hope to see you in 2006
Ruth

Would you like to learn about Cereals?



The small grain cereals network is able to support short exchanges between scientists from academic and commercial laboratories who wish to learn new techniques or share facilities. The scheme is funded by BBSRC and is targeted (but not limited) to young scientists (including postgraduate students). It also provides an ideal opportunity for scientists who are currently working on Arabidopsis or other model systems to develop new interests in cereals and other graminaceous crops.

Support of up to £500 per visit is available to cover travel and subsistence but not laboratory expenses. Applications should be made to Peter Shewry (email peter.shewry@bbsrc.ac.uk) and should comprise details of the applicant (including current position, up to one side of A4) and an estimate of costs.

GARNet 2005

written by Marc Knight, University of Oxford

This year's meeting was a very enjoyable and intense two days covering both advances in technologies and approaches to Arabidopsis research, as well as great strides towards answering some key fundamental biological questions. This meeting was strongly influenced by the need to consider and discuss crop science and systems biology. In this regard the meeting started appropriately with a presentation from Wayne Powell describing new opportunities for crop science research in the 21st century. This triggered a very robust and useful discussion at the meeting. One important point to emerge was the suggestion that the "ABC" from the ABC forum was too prescriptive as many other crop systems should be included in future planning, and suggested instead Arabidopsis and Beyond to Crops. Bob Pruitt's talk described one of those wonderful examples whereby textbook explanations of genetics which we hold dear can be proven wrong. The next two sessions covered exciting advances in post genomic technologies, both wet and in silico approaches. Andrew Bangham's description of a Grand Challenge to compute a model of Arabidopsis by 2017, was stimulating and generated an enthusiastic discussion. Richard Baldock described the Edinburgh mouse atlas, giving food for thought regarding how such a resource could be applied to Arabidopsis. The workshops on the first day were particularly useful in the current climate of plant research, one presenting new funding opportunities and approaches, the other new tools and resources, most notably handling of microarray data.

The second day focused more on presentations describing research aimed at understanding fundamental biological questions in Arabidopsis. The first session (response networks) detailed work on a novel hormone (Ottoline Leyser) and an interesting (and unexpected) role for phytochrome in root development (Frances Salisbury). The next session covered environmental interactions and included talks on UV light and ABA signalling (Ferenc Nagy and Nam-Hai Chua respectively). The final session covered gene regulation at several different levels including gene silencing and transcription or repression.

I very much enjoyed the meeting, and felt the enthusiasm around the place, during the sessions, workshops and poster sessions. I was very struck that this is one of the few occasions where the plant sciences community can get together and discuss important issues across disciplines and across experimental systems. In the face of the changing funding landscape, and new opportunities such as crop sciences and system biology initiatives, these types of meetings are invaluable. Here's to the next one!



Systems biology meets Arabidopsis

Systems biology has a grand vision – understanding all the components of a biological system and their interactions, across all relevant levels of organisation. In the plant context, the vision might translate into a whole-plant computer model that accounts for seed-to-seed development and environmental responses, starting from the scale of macromolecular and metabolic processes. GARNet's Advisory Committee is currently considering how this could best be approached in UK Arabidopsis research. BBSRC's strategy panel on Integrative and Systems Biology asked GARNet to produce a report that incorporates the community's views on this area for June 2006, with an interim report in January 2006. This article sets our questions (below) in context.

So what is Systems Biology?

The ISB panel has avoided an exclusive definition of Systems Biology, preferring to list the characteristics of a systems approach and noting that the balance among these will vary among projects:

- An integrative approach to the subject
- Large experimental data sets (we would add, of high quality)
- Predictive capability based on modelling
- A mix of inputs not only from across biology but also from the chemical, physical, engineering, mathematical and/or computational sciences.

The result is an iterative interaction between experiments and modelling. Informatics infrastructure underpins the approach as much as experimental methods. Scalability is a major advantage. Mathematical models make it possible to analyse and understand much larger data sets than the simple, logical models that are implicit in all scientific reasoning. Modelling from preliminary data is an excellent way to inform experimental design, to ensure that later experiments provide data that are suitable to test and extend the models.

These guidelines are broad enough to cover everything from data-led ("omics") projects that generate new hypotheses, to hypothesis-led projects that quantify and test current understanding. For example, the inference of preliminary network models from high-throughput data (not only transcriptomics – see Sachs et al. 2005) can be data-led, while the development of segmentation models for *Drosophila* was more hypothesis-led (von Dassow et al. 2000). In plant biology, examples would include Birnbaum et al. 2003 or Hirai et al. 2004, compared to Jonsson et al. 2005 or Locke et al. 2005, with Rolland-Lagan et al. 2003 between them. There is no dichotomy between these approaches: large data sets contribute to testing existing hypotheses and generate future hypothesis-led projects, perhaps on a broader scale than before.

Systems Biology in Arabidopsis

Systems biology in any multicellular organism can face additional problems, for example the need to acquire data from specific cells or cell types. Arabidopsis will be harder to work with than yeast for many approaches, and including other plant species risks diluting the effort. Relatively few theoreticians are working on plant science questions and we have few models to start from. On the other hand, the limited cell movement and cell shape changes make development in Arabidopsis easier to model than in many animals.

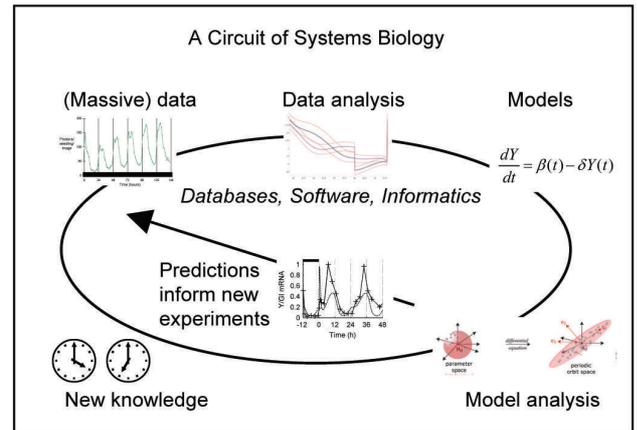
The Arabidopsis community has great strength to offer but our 200+ laboratories are dispersed around the UK. Systems biology has worked best when there is a close and continuous interaction between researchers with different backgrounds. BBSRC has funded three Centres for Integrative and Systems Biology (CISBs, in Newcastle, Imperial College and Manchester) to establish this type of joint research environment. Further institutions are now shortlisted for up to another three CISB awards, to be announced in early 2006. GARNet's report will provide input to "Phase 3" of systems biology funding (ca. £30M): this will not fund CISBs but might include coordinated activity across multiple locations.

Our questions to you

In addition to comments on the above, we are seeking input on these questions. Earlier versions have been circulated by email:

1. What concrete steps would most facilitate systems biology approaches in the UK Arabidopsis community? Examples might include: a national 4-year PhD programme with shared training and computing support; 'study group' events that allow plant scientists to present their research questions to theoreticians for preliminary analysis; a set of demonstrator projects that show what can be accomplished by the systems approach in plants; a 'virtual centre' that links interdisciplinary teams at different sites working on complementary topics.
2. Agreeing a single research goal might have significant advantages. What would be a suitable goal for a coordinated, national project? Examples might include: systems biology of the leaf, of the guard cell, of the auxin signalling pathway. For comparison, the systems biology centre in Cambridge proposes to have 100 researchers focussing on the Notch and wnt signalling pathways in *Drosophila*.
3. One aim of a large-scale systems biology project could be to collect a particular data set or to provide a particular resource in support of a national project, in addition to gathering researchers with the relevant expertise. Which data sets or resources would convince you to work in a new area, or which could you contribute to providing? Examples might include: a protein-protein interaction map, completion of the metabolic map, imaging of protein localisation throughout development, integrating biological databases, informatics that automates the link between data and models.
4. Which international or industrial partners would you be most interested to work with, and do you already have links to them in systems biology?

Please respond either to ruth@arabidopsis.info, to one of the committee members, or in person at one of the town meetings.



Town Meeting Dates

1. 27th January 14:30-16:30 at The Linnean Society London, after the New Phytologist 'Networks in Plant Biology' meeting. To register for this meeting see <http://www.newphytologist.org/networks/default.htm>
2. 5th April at the SEB Canterbury Meeting <http://www.sebiology.org.uk/>

References

1. von Dassow et al. (2000). Nature 406, 188-192.
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7. Rolland-Lagan et al. (2003). Nature 422, 161-163.

Arabidopsis Resources

PlaNet

A powerful portal for accessing plant genome data and analysis tools via web services

<http://www.eu-plant-genome.net>

written by Rebecca Ernst, GSF-National Research Center for Environment and Health, Institute for Bioinformatics (IBI/MIPS)

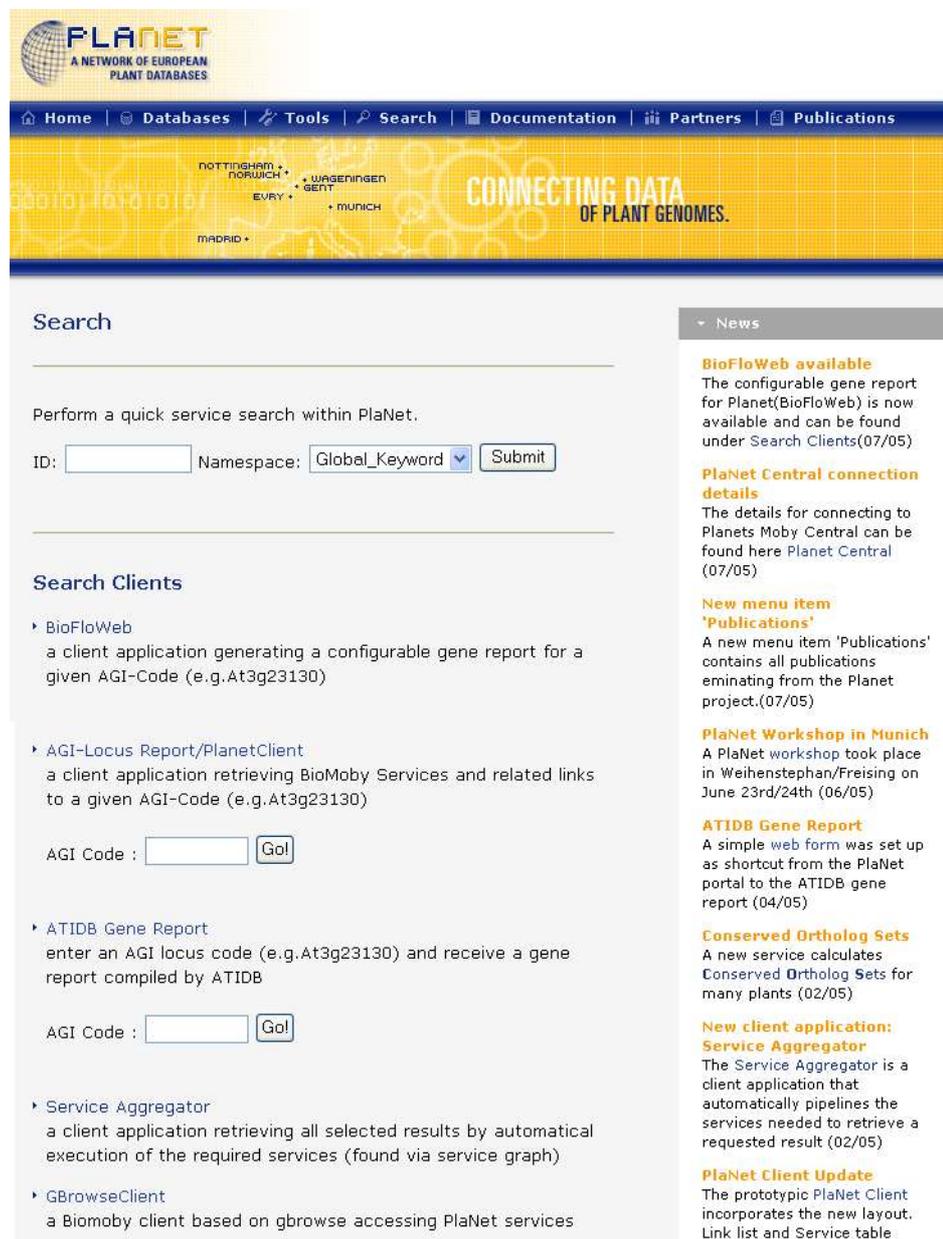
Every biologist working on plant genome data is familiar with the problem of data retrieval in on-line databases; databases are distributed, they require different inputs and formats and one has to know where to find them. To make the best use of all the data available therefore requires a considerable amount of knowledge, an ability to transform data types and copious amounts of copying and pasting. However, researchers often do not have the time to carry out lengthy data retrieval processes and can find it difficult to keep up to date with the ever increasing data mountain available via the web. This has created a situation in which numerous opportunities arise for researchers to run in to difficulties and frustrations when trying to retrieve data. To help scientists circumvent some of these problems PlaNet has created a number of web based services which aim to make current tasks, that are tedious to solve with on-line databases, easier and simpler.

PlaNet was launched in 2001 to develop and deliver a high level plant genome database for the systematic exploration of Arabidopsis and other plants. In contrast to many other data storage approaches, PlaNet doesn't use a data warehouse solution where all data are collated and curated in one big database. Instead it utilises web service technology (BioMoby); datasets remain distributed and are made accessible via web services. The advantages of this approach are obvious: the dataset is always up-to-date (data are retrieved from the local datasets on the fly), data remain with the specialists annotating it, resulting in little or no maintenance by external curators.

PlaNet has produced more than 130 web services that allow researchers to access all kinds of plant related data (esp. Arabidopsis) as well as analysis tools. The data accessed via this federate network, originates from databases located at the John Innes Centre, Norwich; NASC, Nottingham; Centro Nacional de Biotecnología, Madrid; Genoplante Info, Evry; VIB, Ghent; Plant Research International, Wageningen and MIPS, Neuherberg.

Included in the wide range of tools and data available via PlaNet are Arabidopsis sequences and annotations, stocks, Insertions, Protein-Protein Interactions (PPIs), literature, GO, Interpro Accessions, Expression data, mutants and phenotypes, synonyms, expressed sequence tags (ESTs), Blast (against Arabidopsis proteins), Transmembrane prediction, sequence and annotation data for Medicago, Maize and Rice, and many more.

To illustrate how PlaNet integrates all this data into easily accessible formats and aids researchers with data retrieval requests three commonly encountered problems along with their PlaNet solutions have been highlighted opposite.



The screenshot shows the PlaNet homepage with a navigation bar (Home, Databases, Tools, Search, Documentation, Partners, Publications) and a banner with the text 'CONNECTING DATA OF PLANT GENOMES.' Below the banner is a search section with a text input field for 'ID', a dropdown menu for 'Namespace' (set to 'Global_Keyword'), and a 'Submit' button. Below the search section is a 'Search Clients' section listing several services:

- BioFloWeb**: a client application generating a configurable gene report for a given AGI-Code (e.g. At3g23130)
- AGI-Locus Report/PlanetClient**: a client application retrieving BioMoby Services and related links to a given AGI-Code (e.g. At3g23130)
- ATIDB Gene Report**: enter an AGI locus code (e.g. At3g23130) and receive a gene report compiled by ATIDB
- Service Aggregator**: a client application retrieving all selected results by automatical execution of the required services (found via service graph)
- GBrowseClient**: a Biomoby client based on gbrowse accessing PlaNet services

On the right side of the screenshot, there is a 'News' section with several articles:

- BioFloWeb available**: The configurable gene report for Planet(BioFloWeb) is now available and can be found under Search Clients(07/05)
- PlaNet Central connection details**: The details for connecting to Planets Moby Central can be found here Planet Central (07/05)
- New menu item 'Publications'**: A new menu item 'Publications' contains all publications emanating from the Planet project.(07/05)
- PlaNet Workshop in Munich**: A PlaNet workshop took place in Weihenstephan/Freising on June 23rd/24th (06/05)
- ATIDB Gene Report**: A simple web form was set up as shortcut from the PlaNet portal to the ATIDB gene report (04/05)
- Conserved Ortholog Sets**: A new service calculates Conserved Ortholog Sets for many plants (02/05)
- New client application: Service Aggregator**: The Service Aggregator is a client application that automatically pipelines the services needed to retrieve a requested result (02/05)
- PlaNet Client Update**: The prototypic PlaNet Client incorporates the new layout. Link list and Service table



Screenshot of the PlaNet homepage

PlaNet offers several different mechanisms/clients to make use of the intergrated PlaNet datasets including BioFlow-see overleaf, AGI Locus Report - provides all information on given AGI code, ATIDB - Genome browser for Arabidopsis, Service Aggregator - Creates pipeline for information retrieval on AGI code, GBrowse Client - Generic genome browser and Cos Marker Analysis - Finds conserved orthologs from defined genome sets.

Arabidopsis Resources

PlaNet continued

Common data retrieval requests

Scenario 1

A researcher working on Arabidopsis wants to know everything about his/her favorite gene (e.g. At3g19100). To retrieve all the current and up to date data on one locus would normally require several searches at different databases but by using the BioFlow web interfaces at PlaNet, scientists can carry out this task in one step.

Users simply enter the AGI code in the BioFloWeb interface (e.g. At3g19100 below left) and select the output categories of interest (e.g. Gene structure and Gene Function above left). The BioFloWeb client then retrieves all the relevant data from the numerous databases associated with the PlaNet network and generates a gene report (below right). For example the report shown below (right) consists of data that has been gathered from six different PlaNet partners (as indicated by bubbles) and incorporated into one simple format that can be easily read.



This tool allows you to search for information about an *Arabidopsis thaliana* gene. It displays a gene report containing data provided by PlaNet BioMoby web services.

This site is under construction : what you see is a static prototype. The dynamic application will be available soon.

AGI code	At3g19100
Select one or more workflows	<input type="checkbox"/> Names
	<input checked="" type="checkbox"/> Gene Structure
	<input checked="" type="checkbox"/> Gene Function
	<input type="checkbox"/> Functional Genomics
	<input type="checkbox"/> Expression
	<input type="checkbox"/> Sequences
	<input type="checkbox"/> Links
<input type="checkbox"/> My personal workflow 1	
Add a personal workflow	<input type="text"/> <input type="button" value="Browse..."/>
Select a profile	<input type="radio"/> light (no detail, no link)
	<input checked="" type="radio"/> optimal
	<input type="radio"/> full (all raw information)

BioFlow Query Page

Scenario 2

A researcher working on Medicago would like to identify all genes on a single contig.

This type of request would require a substantial amount data analyses and a comparative genomics approach in which sequences related to the contig would need to be identified, blasted against a database of Arabidopsis proteins and the Gene Ontology (GO) Accessions and Interpro Accessions for these genes retrieved.

Researchers can make use of Taverna to streamline this type of multi-step sequence analysis. Taverna is a workflow composition tool allowing for the definition of inputs and outputs and creation of workflows in between. Taverna makes it possible to set up complex workflows that can be carried out by a computer in a matter of minutes but would take months to complete if executed manually via websites and online databases. For example to achieve the Medicago cross-species comparison one would define the Medicago contig as input and GO- and Interpro Accessions as outputs and then sequentially select the intermediate steps from a list of 'services' on the Taverna webpage and connect them all together to generate the workflow illustrated (opposite).

Scenario 3

A researcher wants to know if his/her gene of unknown function in tomato has any related sequences that could help in understanding the role of this gene.

At present this request is achieved by a weekly search of all plant databases. By using Taverna this tedious task can be circumvented as once a workflow is built it can be saved and run whenever needed.

To find out more about any of the services outlined above please visit the following websites

PlaNet

<http://www.eu-plant-genome.net/>

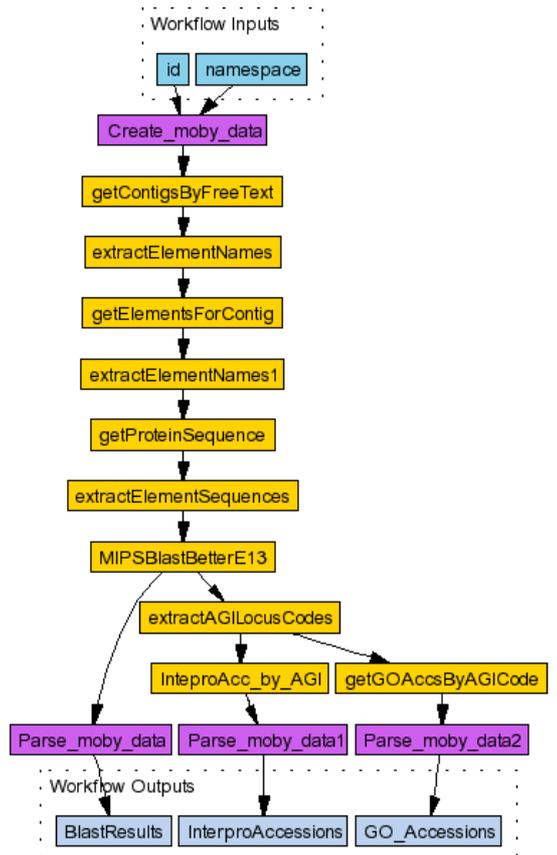
Taverna

<http://taverna.sourceforge.net/>



Results	
Gene Structure	
Transcript Coordinates	MAIDB2 start:6605616, stop:6608915, direction + AtEnsembl start:6605581, stop:6609301, direction:+
Exon Graphical Overview	gff image here
Exon Number	10
Alternate Transcripts	At3g19100.1
Size	3721
Gene Function	
GO Terms	GO:0009507 component, chloroplast GO:0006468 process, protein amino acid phosphorylation GO:0004672 function, protein kinase activity GO:0004713 function, protein-tyrosine kinase activity GO:0004674 function, protein serine/threonine kinase activity GO:0005524 function, ATP binding GO:0014301 GO:0005509 GO:0004723
Interpro Terms	IPR002048 IPR000719 IPR000887 IPR010440 IPR000246 IPR008271
Phytoprot Clusters	1 2 3 8
Localization Prediction	CHLOROPLAST (predicted by TargetP) None (predicted by PredotarP)
Protein-protein Interactions	No result

BioFlow Results Page



UK Plant Science

There are over 350 plant research groups in the UK, in 42 institutions scattered from Aberdeen to Exeter. Many of these groups are international leaders in their field. To promote the breadth of plant science throughout the UK and increase awareness of the different types of research being undertaken, GARNish is focusing on geographic areas and institutions across the UK. In the last issue of GARNish we focused on activities at York and in this issue we continue our tour in Warwick and the University of the West of England.

Warwick-HRI



Warwick HRI (WHRI) was formed on 1st April 2004 following the integration of Horticulture Research International's (HRI) sites at Wellesbourne and Kirton with The University of Warwick. As a devolved department of The University of Warwick, WHRI is dedicated to undertaking world-class horticultural research and development (R&D) and transferring the results to industry. A wide range of basic and strategic research is undertaken at WHRI by multidisciplinary teams of world-class scientists as outlined below.

Name Dave Astley
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 Research Area Warwick HRI Genetic Resources Unit



Research Activities

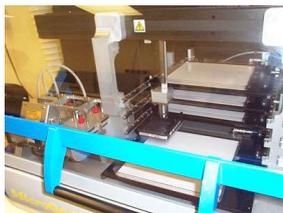
The Warwick HRI Genetic Resources Unit (HRIGRU) is involved in the conservation of a variety of vegetable crops and their wild relatives. The Unit has facilitated the global distribution of over 25 years worth of collected material for use in a wide range of disciplines. HRIGRU collaborates in 5 European crop working groups (Allium, Brassica, Leafy Vegetables, Vegetable Solanaceae & Umbellifers) and manages 2 European crop databases for Allium and the Umbellifers. GRU is also involved in an international initiative to develop models for 'A European Genebank Integration System' (AEGIS), the aim of which is to ensure conservation and continuing use of existing crop genetic diversity in Europe. In addition to these 'traditional' collections the unit has also supported the development of new tools in the form of Diversity Fixed Foundation Sets (DFFS). The core conservation and documentation elements of the Unit are funded through a Defra project.

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 Research Area Comparative genomics and genetics (GRC)

Research Activities

Brassica researchers at WHRI are interested in a wide variety of traits from seed germination to novel oils and to ensure they make the best possible progress in their studies the Genomic Resource Centre provides a range of tools and resources. For example, the centre is generating physical and genetic maps of Brassicae and via screening with common markers provides the prerequisite links to move from traits to genes and to link different genetic maps together. In order to isolate genes of interest the centre employs a fine mapping approach; BAC end sequencing and BAC pool screening generate tiling paths across identified QTL, whilst subsequent shotgun sequencing of selected BACs identifies candidate genes. However, this type of method can be complicated by the triplicated nature of the Brassica diploid species and becomes even further entangled in the amphidiploids. Consequently the GRC is carrying out comparative genomics studies looking at paralogous loci within Brassica oleracea and how their collinearity with Arabidopsis is maintained. This has provided researchers with important insights into the role transposons may play in polyploid genomes.

WHRI has also developed a large collection of Brassica species over the years (see Dave Astley) and the centre is developing genomic based approaches to exploit the diversity present in these collections for crop improvement.



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 Research Area Host-pathogen interactions

Research Activities

Plants are constantly exposed to attack by an array of diverse pathogens which can cause infection and disease, resulting in large yield losses. To combat this continual threat plant breeders have either incorporated naturally occurring resistance genes into commercially important varieties or have applied chemicals to prevent diseases from developing.

Work in the Beynon lab is focused on obtaining a fundamental understanding of the mechanism of plant resistance and the methods used by the pathogen to overcome that resistance. The knowledge gained from this research will reveal new routes of resistance, provide novel sources of genetic material for plant breeders to utilise, and identify new targets for the development of novel agrochemicals. Previously Jim's group have cloned both plant resistance genes and the pathogen genes that trigger the resistance responses and have shown how they are involved in an evolutionary "arms race" whereby the genes in both the plant and pathogen rapidly alter protein sequences to detect or avoid being detected. Currently Jim's group is involved in sequencing the genome of the downy mildew pathogen that invades Arabidopsis and aims to discover how this pathogen uses its arsenal of proteins to overcome its host resistance mechanisms.



Focus on Warwick-HRI



Name Vicky Buchanan-Wollaston
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 Research Area Signalling networks in plant senescence
 Research Activities

Senescence in green plants is a complex and highly regulated process that occurs as part of plant development or can be prematurely induced by stress. The identification of key regulatory genes and pathways involved in the control of senescence will provide plant breeders with tools to improve yield, stress-resistance and also post-harvest quality which will benefit growers, suppliers and consumers.

Multiple signalling pathways regulate gene expression during plant developmental senescence and there is much crosstalk with pathways involved in stress responses. To help us gain a better understanding of these pathways and their interactions Vicky's laboratory is carrying out a functional analysis of senescence regulatory genes in Arabidopsis via microarray analysis of knock out and overexpression mutants. This work has shown that of the >150 regulatory genes that exhibit enhanced expression during senescence a small number appear to have important roles in controlling senescence. To investigate the role of these key regulators in the senescence regulatory network researchers are carrying out yeast two hybrid analyses and identifying upstream activators/repressors via yeast one hybrid analysis of cloned promoters. The group is also investigating genetic and environmental factors that affect post harvest quality losses in broccoli and other vegetable brassicae.



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 Research Area Insect biology and decision support
 Research Activities

Rosemary's main focus is the modelling of interactions between insects and the environment and the development of Integrated Pest Management strategies for the pests of field crops. The group currently works on brassicas, carrots, alliums, lettuce and narcissus and has particular expertise in dealing with phytophagous flies, aphids, caterpillars and thrips. Researchers are particularly interested in non-insecticidal methods of pest control for conventional and organic production including companion planting, trap cropping, repellents, biological control with predators and parasitoids, host plant resistance, physical methods of control such as crop covers, cultural methods of control such as rotation and crop isolation. Rosemary also has a keen interest in decision support systems for agriculture and leads a Defra-funded project on MORPH, the software developed at Warwick HRI to transfer crop protection and crop production models to the horticultural industry.



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 Research Area Digital imaging and ornamental plant quality
 Research Activities

Objective measurement of plant quality is important for monitoring and grading glasshouse ornamental crops during production. To aid this process researchers at WHRI are developing statistical and biometric methods for automated collection and analysis of ornamental plant data. Current projects include a Horticultural Research Council funded endeavour to model the quality of bedding plants both at the point of sale and during subsequent garden life. As part of this project, Rodney's group are developing methods for extracting quantitative information on plant quality and plant growth from digital images using image analysis techniques such as neural network methods. It is anticipated that this work will eventually lead to automated systems for plant quality grading and assessment. In collaboration with the Computing Department at the University of Warwick work is also being undertaken to develop a visual systems for plant growth and quality analysis.



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 Research Area Seed science and seedling establishment
 Research Activities

The quality of seeds, their dormancy status and how they perform in the field directly affects crop production efficiency and the structure of natural plant communities. Despite this, little is known about how seed vigour or dormancy is determined at the molecular level or how they interact with the soil environment to determine seedling emergence patterns. Research in Bill's group is therefore focussed in three areas.

1. Quantifying and modelling the interaction of biotic and environmental constraints on seed dormancy, germination and seedling establishment.
2. Investigating the molecular basis of physiological seed dormancy.
3. Understanding the causes of variation in seed vigour and its effect on crop establishment.

Focus on Warwick-HRI

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 Research Area Weed Ecology & Management

Research Activities

Weeds remain a major constraint to field vegetable cropping systems, impacting on yield, quality and harvesting. As the number of available selective herbicides declines and environmental pressures for reduced pesticide inputs increase, there is greater emphasis on improved targeting of herbicides, reduced application rates and finding sustainable cost-effective non-chemical alternatives. There is also the additional challenge that many problematic weeds are increasingly valued for their own benefits to biodiversity and are therefore viewed as desirable components of the agro ecosystem. The research programme at Warwick HRI reflects the challenges posed by conventional and organic production systems and environmental concerns. Research in Andrea's group is focused on understanding the underlying biology and ecology of weed populations. The knowledge gained for this work is incorporated into simulation models, which will enable researchers and growers to take a longer-term view of weed management. Current projects in the laboratory include understanding how the seeds of both crops and weeds respond relative to one another in the seedbed. It is hoped that this work will provide information on seedbed husbandry that favours the emergence of crop at the expense of the weeds. Other work in the group is centred on brassica and includes the development of novel mechanical weeding technologies and the use of weeds to help reduce other brassica pests.



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 Research Area Crop Improvement in Brassicas and salad crops

Research Activities

Quantitative trait loci (QTL) underly many traits of interest in modern plant breeding. These include pest and disease resistance, quality traits and nutrient uptake and assimilation. Paul's work is targeted at the development of tools and strategies for the utilisation of QTL in plant breeding. Particular emphasis is given to the development and utilisation of strategic resources for crop improvement, including mapping populations and linkage maps for brassica and lettuce, identification of QTL and linked molecular markers. In collaboration with industry, strategies for marker assisted selection and deployment of quantitative traits are under development. Current research is focussed on quantitative resistance to pests and diseases, especially downy mildew of lettuce and; improved shelf life of brassicas, and nitrate accumulation in lettuce.



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 Research Area Molecular and population biology of plant-parasite symbioses

Research Activities

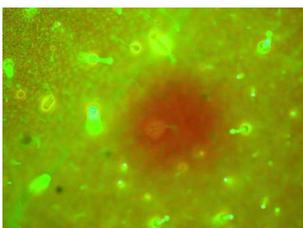
Innate immunity in wild plant species will provide a unique resource for understanding how to achieve sustainable disease control in crops through research that is rooted in molecular and evolutionary biology. Arabidopsis is the forerunner among wild plants in providing molecular knowledge from natural variation in race specific disease resistance, as well as from species level (non-host) resistance to economically important crop pathogens. Since 1990, Eric has been fostering the widespread use of an oomycete *Hyaloperonospora parasitica* (downy mildew), as a model for understanding the molecular biology of host/parasite interactions in Arabidopsis. This work has often involved comparative studies with other model pathogens (bacterial, fungal and viral), and was instrumental in laying the foundation for Peronospora genomics in the UK. He is currently pursuing projects with Mahmut Tör on the "Janus faced" interplay of membrane and cytoplasmic receptor-like genes that mediate resistance or susceptibility to different downy mildew isolates. Eric has also been using *Albugo candida* (white rust) from other wild and cultivated crucifers for molecular genetic dissection of species level resistance in Arabidopsis. In 2005 he launched a career ambition to develop Arabidopsis-oomycete symbioses as a model for the emerging field of molecular epidemiology.



Name Yiguo Hong
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 Research Area Plant-Pathogen interactions

Research Activities

Plants have evolved pathogen-inducible resistance mechanisms against infection, including RNA silencing and hypersensitive response (HR). RNA silencing is a sequence specific RNA degradation mechanism that operates in plants, animals, and fungi. In plants, RNA silencing protects the host against virus infection, regulates host gene expression, and controls development. RNA silencing is non-cell autonomous. In contrast the HR is often elicited by pathogen-specific avirulence determinants. In order to withstand these different defence responses, pathogens have evolved to encode defence-suppressing proteins, such as silencing suppressors. Using viruses as a tool, research in Yiguo's group aims (1) to reveal mechanisms of cell-to-cell spread of mobile silencing signals; (2) to identify and characterise novel silencing suppressors that may be used to study plant development; (3) to identify novel virus-encoded HR suppressors. The group is also interested in development of novel approaches for in planta detection of protein-protein interactions and production of pharmaceutical proteins in crops.



Focus on Warwick-HRI



Name Stephen Jackson
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 Research Area Molecular Control of Flowering and Plant Development.

Research Activities

Steve is interested in the molecular basis of the control of flowering, especially how it is regulated by daylength (or photoperiod). To gain a better understanding of this process researchers have isolated a number of flowering mutants, by screening Arabidopsis T-DNA populations for altered flowering time under different photoperiods, and are now analysing individual mutants to characterise them further. Other aspects of flowering regulation under investigation by the group include the vernalisation response, and what controls the juvenile phase, in crop plants such as Lavender, Antirrhinum and Brassica species.

Steve's laboratory are also studying a developmental mutant called lilliput (lpt) which resembles wild type at the cotyledon stage but subsequently develops as a dwarf. The mutant can not be rescued by exogenous gibberellic acid (GA), is not affected in response to auxin or ethylene, but does exhibit an enhanced response to abscisic acid (ABA) in germination and root growth assays. The group are currently trying to ascertain if the LPT gene is involved in the response to a factor that affects sensitivity to ABA.



Name Roy Kennedy
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 Research Area Measuring and predicting population change in fungal pathogens

Research Activities

The development of fungal plant pathogens in agri-ecosystems is determined both by genetic interactions and the environment. An ability to 'forecast' changes in pathogen population relative to these variables is therefore essential if we are to effectively and reliably combat pathogen infection. To assist breeders in this area Roy's work is centred on investigating the epidemiology of these interactions at the crop and molecular level. The group has a particular interest in oomycete pathogens and are currently developing modelling based approaches for the prediction of pathogen population changes. These models will provide a better understanding of pathogen host interactions, allowing researchers to improve conservation strategies of important R genes within cropping systems and assist with the rationalisation of chemical disease control. Other aspects of the group's work include the development of rapid detection systems for plant pathogenic spores. The use of these systems within transmission models for important crop pathogens is also being investigated.



Name Graham Seymour
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 Research Area Fruit ripening

and

Name Ken Manning
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 Research Area Fruit quality

Research Activities

Fleshy fruits are of high economic value and provide a substantial part of the daily intake of vitamins and minerals whether they are consumed in a fresh or processed condition. The fruit ripening group at WHRI are investigating the role of key regulator genes which have been conserved during the evolution of dry and fleshy fruits. One of these is the gene at the Colourless non-ripening (Cnr) locus. Cnr belongs to a small class of single gene mutations in tomato (including rin, and nor) that have pleiotropic effects resulting in the reduction or almost complete abolition of ripening. The Cnr gene has now been cloned and the mutation is the result of an epigenetic change in a ripening specific transcription factor (Manning et al, submitted for publication). Work is underway to investigate its role in the ripening regulatory network. In addition to these studies the group are working with Jim Giovannoni at Cornell to investigate if the strawberry orthologues of the tomato RIN and NOR genes can modulate ripening in this non-climacteric fruit. Graham Seymour is also spearheading the UK Solanaceae Research Community contribution to the International effort to sequence the tomato genome, in collaboration with Gerard Bishop at Imperial College and Glenn Bryan at Scottish Crop Research Institute.

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Focus on Warwick-HRI



Name Andrea Massiah
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Research Area Environmental and genetic control of flowering and bulbing in horticultural crops

Research Activities

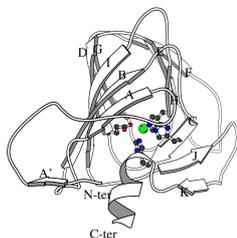
The juvenile phase of plant development can be defined as the period after germination in which the plant is incapable of responding to environmental stimuli that would otherwise promote flowering, such as photoperiod or temperature. Using a combination of physiological, molecular and genetic approaches in *Antirrhinum* and *Brassica oleracea*, Andrea aims to gain a better understanding of the environmental and genetic factors that regulate the juvenile phase. The information obtained from this work will feed in to the production of tools and resources for more predictable manipulation of flowering in horticultural crops.

Andrea is also investigating the regulation of bulb initiation in the long-day onion (*Allium cepa*). This process is similar at the physiological level to photoperiodic induction of flowering in *Arabidopsis thaliana* allowing researchers to transfer the knowledge gained in this model to their studies of the genetic basis of photoperiodic bulb initiation in onion. Alliums are amongst the most widely grown vegetables in the world and this work will be vital for the development of new varieties that can be grown at different latitudes.

Name Richard Napier
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Research Area Hormone perception

Research Activities

Plant hormones induce a wide variety of responses at low concentrations with great specificity. Work in Richard's group is focused on how these molecules are recognised and how specificity is conferred. Researchers at WHRI have worked with auxin, and in particular ABP1, for some years and along with collaborators in 2002 revealed the structural detail of how auxin is bound by this protein. Taking this understanding of ligand binding forward, the group is now developing quantitative sensors for plant hormones. To aid their work the group have generated plant protein display libraries to identify putative novel plant hormone binding domains. Richard is also collaborating with Andrew Thompson's group at WHRI on ABA binding and biochemistry.



Name Dave Pink
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Research Area Genetics and crop improvement

Research Activities

Dave's main research interest is the development of tools, resources and information to facilitate the improvement of quantitative traits of agronomic interest through the exploitation of natural allelic variation. This is achieved by the development of mapping populations and linkage maps which are used to carry out QTL analysis for a range of traits. Current targets include: Resistance to *Xanthomonas campestris* pv *campestris*; Resistance to *Brevicoryne brassicae*; Improving shelf life of broccoli and other brassica vegetables. Significant effort is also being put in to developing a Diversity Fixed Foundation Set of 14 wild C genome brassica species from accessions maintained by the WHRI Genetic Resources unit as a resource for brassica crop improvement.



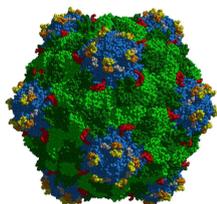
Name Claudine Porta
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Website <http://www2.warwick.ac.uk/fac/sci/hri2/about/staff/cporta/>
Research Area Expression of foreign genes in horticultural crops

Research Activities

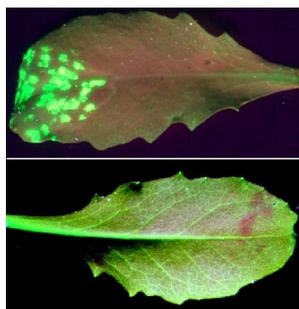
Foreign peptides or proteins can be expressed in plants via the generation of chimeric viruses and their exploitation as episomal vectors. Cowpea mosaic virus (CPMV), which consists of an icosahedral capsid and single-stranded RNA genome, is particularly suited to this type of approach since it can be genetically engineered for the expression of heterologous sequences by two approaches.

Firstly it is possible to graft peptides within defined, surface-exposed regions of either of the two capsid proteins (shown in green and blue on the figure, with the positions that are amenable to insertions highlighted). This method can be used to develop presentation vectors in which peptides derived from animal pathogens are displayed on the viral coat proteins for use as antigenic epitopes in the development of novel vaccines

Alternatively a foreign gene can be slotted into the viral genome where it will be amplified as the virus replicates; differential modes of expression allow the production of either free or coat protein-fused products. This technique can be used to biomanufacture high value proteins such as those with therapeutic applications.

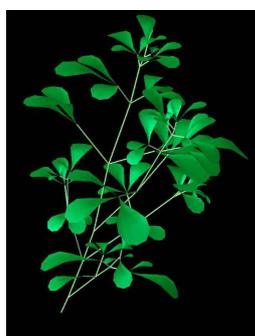


Focus on Warwick-HRI



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 Research Area Plant-virus interactions
 Research Activities

Plants defend themselves against viral infection via number of mechanisms including RNA silencing; an evolutionary conserved sequence-specific RNA degradation mechanism. Viruses are able to withstand this response, by deploying structurally diverse suppressors of RNA silencing which interfere with different stages of the RNA silencing pathway. To gain an insight into the mechanisms of virus-induced RNA silencing development and the role of viral RNA silencing suppressors in both Arabidopsis and Nicotiana, researchers in Ryabov's group have designed a novel viral vector system based on the Turnip crinkle virus genome. These RNA based vectors are being used to investigate the requirements of RNA silencing initiation and its spread within plants as well as the effect of the expression of structurally different RNA silencing suppressors on viral cell-to-cell and long-distance movement.



Name Dave Skirvin
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 Research Area Effect of plant structure on insect searching and biocontrol
 Research Activities

The architecture and interconnections of a plant canopy play a major role in determining the searching patterns of predatory insects and their success as biological control agents. Researchers in Dave's group are investigating how the canopy structure influences the insect's ability to progress through the canopy by using three dimensional models of plant canopy structure (virtual plants) linked to simulations of insect movement. Researchers aim to identify particular characteristics/types of canopy structure that influence insect motion. This will work provide information for the development of biological control strategies for specific canopy types leading to more robust and sustainable biological control schemes.



Name Graham Teakle
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 Research Area Brassica genetics and diversity
 Research Activities

Brassicacae are closely related species that encompass a number of oilseed, vegetable and condiment crops. Despite the extensive range of genetic diversity displayed by this group breeding has resulted in many crop types having a restricted genetic base. To ensure that the best use is made of the available diversity Graham's group, working closely with others in the Brassica Genomics and Crop Improvement teams at WHRI, are developing and curating a combination of diversity core collections, called Diversity Fixed Foundation Sets (DFFS), and mapping populations. Molecular tools, including genetic markers and their associated linkage maps, are being used to characterise this diversity and enable its interpretation within the context of genomic sequence information. These resources, partly being developed within the Defra-funded Oilseed Rape Genetic Improvement Network (OREGIN), underpin a range of trait-based brassica research. Graham's group are currently working with others in the areas of mineral/water use efficiency, juvenility and the control of the floral transition.



Name Brian Thomas
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 Research Area Environmental control of plant and crop development
 Research Activities

The properties of plants, including those that contribute to their economic and societal value, are determined by the interaction between their genotype and the environment. One of the most important environmental determinants is light, which exerts specific effects on plant development either directly through light quantity and quality or in a complex manner through photoperiodism. Brian's interests include understanding the mechanisms by which light regulates development and how this information can be applied to enhance crop performance and quality. Current research includes a multidisciplinary study of the control of juvenility in Antirrhinum where flowering is photoperiod-sensitive. The goal of this research is to provide physiological information and genetic markers that will aid in the reliable scheduling of high quality flower and vegetable crops with minimal waste. A second interest is in the genetic components of daylength induction of bulbing in Allium species and how these relate to known to the well-characterised components of photoperiodic regulation of flowering.

Focus on Warwick-HRI

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 Research Area Genetic control of traits related to water use
 Research Activities



Water is the most important factor limiting crop production on a global scale and water resources are increasingly under pressure due to global climate change, competition from diverse users and the desire to protect the environment. Andrew's research is driven by the need to generate crop varieties with improved water-use efficiency. By using QTL and candidate gene approaches the group aims to generate crop that are suited to production with reduced water inputs. For example the group are using the genetic resources of Brassica oleracea and Arabidopsis thaliana, together with comparative genetic analysis, to define QTL that contribute to crop water-use efficiency. Other researchers are exploring the genetic control of traits related to water capture in the genus Solanum, employing genetic resources available in Solanum lycopersicum (cultivated tomato) and its sexually compatible wild-relatives. Additional studies are also being carried out to assess the role of Abscisic acid (ABA) in water use. ABA is known to mediate plant responses to water deficit. By manipulating the biosynthesis of this hormone in both photosynthetic and non-photosynthetic tissues Andrew's laboratory hope to gain a better understanding of the physiological roles of ABA and assess the impact of increased ABA synthesis on crop production.

Name Mahmut Tör
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 Research Area Plant-pathogen interaction
 Research Activities



Understanding the molecular events involved in host-pathogen interactions could help to find new ways to intervene in the infection process and thus help protect the host. Membrane bound receptor proteins in insects, mammals and plants are key players that sense the invasion of pathogens and activate the innate immune system of the organism. Several classes of membrane associated proteins including receptor-like proteins (RLPs), receptor-like kinases (RLKs) and polygalacturonase inhibiting proteins (PGIPs) are involved in defense signalling. Work in Mahmut's group is focused on understanding the communication between plants and their pathogens. Currently, research is being undertaken in the following areas: a) identification of a ligand for a receptor-like protein that confers resistance and susceptibility to the downy mildew (*Hyaloperonospora parasitica*); b) elucidating the mechanism of transmission of the recognition signal from the extracellular to the intracellular space (endocytosis/conformational changes); c) revealing downstream signalling

Name Joana Vicente
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 Research Area Plant Pathology, bacteriology and plant breeding
 Research Activities



Joana Vicente's research has involved the study of the pathogenic and genetic diversity of *Xanthomonas campestris* pv. *campestris* (the cause of black rot of crucifers) and other *X. campestris* pathovars including pv. *raphani* (the cause of a leaf spot disease of brassicas, radish, ornamental crucifers and tomato). Race specific and potential broad spectrum sources of resistance to black rot have been identified and the inheritance of resistance in Brassica oleracea, *B. napus* and *B. carinata* has been studied. Joana Vicente's current work is aimed at breeding and understanding the inheritance of resistance to bacteria and oomycete pathogens. The main goals are to study broad spectrum resistance to black rot in *B. rapa*, to transfer this resistance to *B. oleracea* and to study and deploy broad spectrum resistance to downy mildew (caused by *Hyaloperonospora parasitica*) in *B. oleracea*. Joana Vicente is also the curator of a large collection of bacterial isolates.

Name John Walsh
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 Research Area Plant – Virus Interactions
 Research Activities



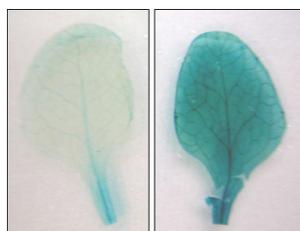
John's research group studies the mechanisms of plant resistance to viruses, virus-virus interactions and the co-evolution of viruses and wild plants. The laboratory is particularly interested in interactions between Turnip mosaic virus (TuMV) and Brassica/Arabidopsis. Using a variety of brassica sources of resistance to TuMV that exhibit a wide range of responses and a collection of TuMV isolates/genotypes from a range of plant species, the Walsh group is characterising and isolating a number of the resistance and virulence genes in this relationship. The group is also studying the interactions between different TuMV genotypes and how these are mediated by the plant. Work in this area is divided into two main projects, 1) the use of mild isolates of viruses to protect plants against severe isolates and 2) investigation of the plant mechanisms that control the exclusion of one viral genotype in viral mixtures. Additional research is also being carried out on the relative fitness of TuMV isolates from wild plants growing in different wild brassica communities around the UK and the co-adaptation of TuMV isolates to plants from the different wild communities using brassica microarrays.

Focus on Warwick-HRI



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 Research Area Biological disease control and microbial interactions
 Research Activities

There are increasing environmental concerns over the widespread use of chemical pesticides and alternative, more sustainable methods of disease control are therefore being sought. Work within John's group has focussed on understanding and developing microbial inoculants, including biological disease control agents and plant growth promoters, as well as other control methods such as disease suppressive growing systems and composts. Implicit in this work is a need to understand the biology and aetiology of the target pathogens and their control agents, their interactions, and the influence of the physical and chemical environment where the control is aimed. Studies of microbial population dynamics and interactions in a number of non-biocontrol based systems are also a feature of the groups' work.



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Name Philip White
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 Research Area Plant Mineral Nutrition
 Research Activities

Plants require at least 17 elements to complete their life cycle. Fourteen of these elements are acquired primarily from the soil solution. These include six macronutrients (N, K, P, S, Mg, Ca) and eight micronutrients (B, Cl, Cu, Fe, Mn, Mo, Ni, Zn). Research in Philip's laboratory aims to optimise the delivery of these minerals to crops in order to increase efficiency, safeguard quality and protect the environment. This work addresses topics from genes to the harvest. It incorporates classical genetic, molecular-biological, physiological, agronomic and modelling techniques. The group primarily focuses on (i) the management of phosphorus fertilisation, (ii) the biofortification of crops with beneficial elements and (iii) the development of safer crops that accumulate less of radioactive and toxic elements.

Name Doreen Winstanley
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 Website <http://www2.warwick.ac.uk/fac/sci/hri2/about/staff/dwinstanley/>
 Research Area Insect virology: baculoviruses and aphid pathogenic viruses.
 Research Activities



The focus of this group is insect virology, in particular baculoviruses and aphid pathogenic viruses. The emphasis is on their genome structure, molecular biology and potential for pest and disease control. A new aphid pathogenic virus has been isolated from rosy apple aphid closely related to the pea aphid virus (APV) and a survey is being conducted of aphid pathogenic viruses in important aphid pests of outdoor crucifer and lettuce crops. The focus has been on pathogenic viruses of the cabbage aphid (*Brevicoryne brassicae*), currant lettuce aphid (*Nasonovia ribisnigri*) and the peach potato aphid (*Myzus persicae*). To date one new virus has been identified in *Brevicoryne brassicae*. The effect of these viruses on the fecundity of the aphids and on their influence on plant virus transmission by aphids will be investigated.

ERA PG Update

The ERA Net in Plant Genomics is close to announcing its first call and the final documents are being prepared. Essential features of the call are a common peer review process and a clear and transparent procedure. Applications are to be welcomed under broad and inclusive themes, open to participation by all countries able to provide evidence of available budget. The call will be split into two sub calls in order to take into consideration the desire of the existing European trilateral partnership between France, Germany and Spain to expand their Public Private Partnership activities. The titles of the two sub calls will be;

Sub Call A; Broad call for publicly funded research in Plant Genomics

Sub Call B; Trilateral partnership and beyond; the future of Public Private Partnership in Europe.

There will be a pre announcement on the 15th December 2005, which will give further details of the topics and contributing partners, and this will provide an opportunity for applicants to informally register their interests. The deadline for pre proposals is expected to be 1st February 2006.

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Spotlight on UWE



The Centre for Research in Plant Science (CRISPS) is part of the University of the West England (UWE) Genomics Research Institute, which houses state-of-the-art equipment for post-genomics research and is well placed to meet the demands of 'systems biology' approaches to plant science. Studies at CRISPS cover a wide range of activities and encompass researchers from several academic areas and research groups within the Faculty of Applied Sciences. Research spans the spectrum of plant science, from laboratory investigations to field and environmental studies as outlined below.

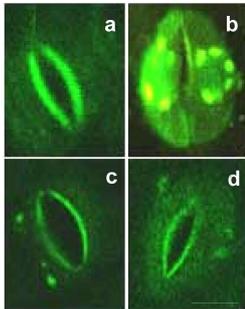
Abscisic acid signalling



Drought stress of plants is a major threat to agricultural yield and productivity. The plant hormone abscisic acid (ABA), synthesised in response to water deficit, induces cellular responses leading to tolerance towards such stress. Research at UWE is involved in elucidating some of the key cellular processes which occur in response to ABA - this includes perception of ABA at the plasma membrane, induction of stomatal closure, as well as activation of specific genes and proteins such as MAP kinases in specialised guard cells.

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Dr Radhika Desikan
e-mail Radhika.Desikan@uwe.ac.uk

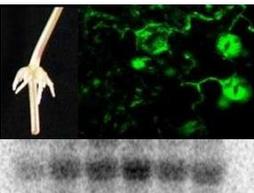
Reactive oxygen species and free radicals



For many years the role of free radicals had been considered to be only destructive, but it is now apparent that reactive oxygen species and nitric oxide are key signalling molecules orchestrating cellular responses to pathogen challenge and other stresses in addition to regulating growth and development. Work at CRISPS is focused on understanding the role of hydrogen peroxide, superoxide and nitric oxide in the control of normal cellular physiology and in disease states.

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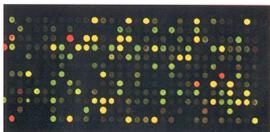
Auxin signalling



Hormones regulate plant development and influence numerous day to day activities within the plant. For example, auxin controls a wide range of functions from phyllotaxy to regulation of stomatal aperture. Researchers at CRISPS are studying the role of this key hormone in guard cells, in particular the interaction of auxin with ABA and reactive oxygen signals. In addition, work is being carried out into the role of the auxin-binding protein, ABP1, in auxin perception and the identification of auxin-activated protein kinases.

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Plants and Radioactivity



CRISPS members carry out research focused on anthropogenic radionuclides in the soil-plant system. Studies based on angiosperm phylogenies are being used to predict radionuclide uptake by plants. Studies with soil amendments and plant management systems are being used to develop phytoremediation systems, and genomic/proteomic technologies are being applied to understand plant responses to radioactivity.

Dr Neil Willey
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Biofuels



Declining resources and the need for farming diversification present opportunities for the development and utilisation of biofuels. CRISPS staff and collaborators are researching novel production methods and applications for biofuels, using both micro-algal production and farm-based systems.

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Temperate Forest Research



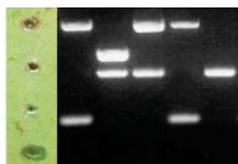
CRISPS has amassed a considerable experience in many aspects of conservation and management of biological resources, with a specific focus on biodiversity and plant resources in the UK. Current research focuses on the effects of air pollution on plants and plant communities.

Dr Katy Ling
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Spotlight on UWE

Host-Pathogen Interactions

There is a substantial research effort within CRIPS to investigate the interactions between plants and microbial pathogens. Areas under investigation include;



Molecular Genetics of Plant Pathogenic Bacteria

The molecular basis of pathogenicity and host plant specificity for pathogens of pea (*Pisum sativum*) and bean (*Phaseolus* spp.) are being studied at UWE, with special reference to avirulence and virulence genes and their genomic context in pathogenicity islands.

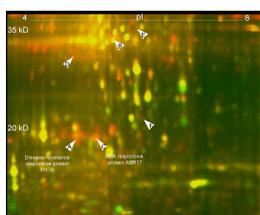
Dr Dawn Arnold
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Downy mildews

Downy mildew fungi are amongst the most important diseases of crop plants, accounting for approximately 17% of global fungicide sales. These pathogens belong to the kingdom Straminipila, and are distinct phylogenetically from the other fungi (kingdom Mycota). For this reason, control with chemicals designed primarily for fungi of the Mycota has never proved completely effective. CRIPS researchers are working to understand the fundamental biology of this host-pathogen interaction with the aim to develop novel and effective strategies to control downy mildew infection.

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Detecting disease in crops

Crop losses due to disease can be devastating and there is a clear need to develop environmentally-sustainable approaches to disease management. With funding from organisations such as Defra and the British Potato Council, CRIPS has established novel collaborations with sensor scientists to detect post-harvest spoilage at its earliest stage, as well as statutory organisms in order to exclude non-indigenous pathogens. Current work is combining proteomic and biosensor approaches to detect early stage infections both in the field and during storage.

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To learn more about the research activities of CRIPS visit <http://science.uwe.ac.uk/research/homePage.aspx?pagelD=crispHome> or contact CRIPS Director - Professor Steven Neil, e-mail Steven.Neill@uwe.ac.uk or CRIPS Deputy Director Dawn Arnold, e-mail Dawn.Arnold@uwe.ac.uk

Open invitation to attend the U.K. CONSULTATION

“PLANTS FOR THE FUTURE” TECHNOLOGY PLATFORM

13th December 2005, 11am-4.30pm.

The Royal College of Surgeons,
The Strand, London, WC2A.



A Strategic Research Agenda for plant science in Europe has recently been established with input from scientists, industry and other stakeholders. This and related Agendas for other fields of research are very useful documents for policy makers, for example in devising Framework 7 work programmes. Consequently the articulation of a common research agenda is of primary importance to all plant scientists and the industries and social stakeholders who will benefit from the research. The Strategic research Agenda has now been published and can be downloaded from <http://www.epsoweb.org/Catalog/TP/index.htm>. The purpose of this meeting is to bring together a range of interested parties from UK academia, industry, funding bodies and other stakeholders to review and get further input to the proposed long term Strategic Research Agenda for plant science, to identify UK-based activities which complement the proposed research and to seek support in pressing for funding and implementation at the EU level. There are 20 places remaining at this important meeting, at which Prof Julia Goodfellow, Dr Tina Barsby and others will speak. We do hope you will be able to come and contribute to discussions and planning future directions in plant science. If you would like to attend please respond to debra.darling@bbsrc.ac.uk by Dec 2.

With best wishes

Simon Bright, Technology Platform
Chris Lamb, Technology Platform
Mike Bevan, European Plant Science Organisation

Crop Resources

Barley Genetics and Genomics

An Ideal Translational Tool for the products of Arabidopsis Research.

<http://germinate.scri.ac.uk/barley/>

written by David Marshall (SCRI)

Barley (*Hordeum vulgare*), an inbreeding simple diploid member of the grass family, Poaceae. Barley is the fifth largest cultivated cereal crop in the world (530,000 km²). Each year the UK produces around 6 million tonnes of barley. Roughly 1 million tonnes are exported, 2 million tonnes are used in the brewing and distilling industry with 3 million tonnes being used for animal feed. A combination of good soils an ideal climate and long day-length in the summer mean that Scottish barley yields are amongst the highest in the world. Barley is able to grow in more extreme environments than many of the other temperate cereals and is a simple diploid with a long history of exploitation as a tool in genetic studies.

Historically barley was the model species for mutation studies with a wide range of mutants characterised and mapped. At least 50 barley mapping populations are available using parents from cultivated and exotic germplasm from around the world. This valuable resource is now been supplemented by a series of molecular tools generated through rapid developments in genomics. Though the genetics and genomics resources available in crop plants, have lagged behind the tools and resources in Arabidopsis, that situation is rapidly changing. A combination of comparative sequence and genome analysis, together with the powerful array of genomics tools that are now available, make barley the ideal major cereal model for the proof of concept transfer of new discoveries in Arabidopsis into agronomically valuable germplasm. A typical informatics-led route to exploiting these barley resources based on initial gene discovery in Arabidopsis would be as follows:

The screenshot shows the SCRI Bioinformatics Portal homepage. At the top, there is a search bar and navigation links. The main content area is divided into several sections:

- LATEST NEWS:** Includes links for Legal Documentation, seed mutagenesis, mutagenesis, Cell Isolation, and PCR and Heteroduplex formation.
- POPULAR:** Lists Cell Digestion, PCR and Heteroduplex formation, seed mutagenesis, A structured mutant population for forward and reverse genetics in Barley (Hordeum vulgare L.), and Cell Isolation.
- MAIN MENU:** A vertical list of blue buttons for Home, Collaborations, Protocols, Databases, References, Information for Visitors, Links, Search, The Team, and CONTACTS.
- Introduction:** A central article titled 'Introduction' written by Administrator on Wednesday, 22 June 2005. It welcomes visitors to the BARLEY MUTAGENESIS web pages and describes a reverse genetics tool that screens 8600 EMS mutagenised lines of cv. Optic to identify mutants in one or more genes of interest. It notes that the service is free to UK academics and available to non-UK academics and commercial partners.
- LOGIN FORM:** A section for user authentication with fields for Username and Password, a Remember me checkbox, and a Login button. It also includes links for 'Forgotten your password?' and 'WHO'S ONLINE' (showing 1 guest online).
- Images:** Two photographs of barley plants are shown: one is a close-up of a green barley spike, and the other is a whole green barley plant.

Step 1: Reciprocal Blast search of a characterised Arabidopsis gene against the public assembly of barley ESTs. In parallel to this search against the barley sequence data a search against the current gene models from the rice genome portal at TIGR will help benchmark the search and ensure that the likely orthologues of the target gene are in the proportion of the barley genome covered by the available EST sequence resource.

Step 2: Given a successful outcome of the initial search, annotation information for identified barley sequences can be found in either the Harvest or BarleyBase databases or through search for homology in the TIGR barley Gene Index.

Step 3: Given suitable EST coverage, then a reasonable prediction of the intron/exon structure of the gene can be made from the alignment of the barley data against rice at the Gramene database or through undertaking your own analysis using one of the series of available tools such as Spidey from NCBI. This may provide valuable information on which to base primer design. It is also possible at this stage to obtain full length genomic sequence from the classic barley BAC library in the North American cultivar Morex.

Step 4: If the target sequence is matched by one the 22K probe sets on the Affymetrix Barley1 GeneChip, then expression patterns can be studied in the growing volume of Affymetrix data at the BarleyBase repository at Iowa State. If an obvious rice orthologue is available from step 1, then it may be profitable to carry out a parallel search of rice expression resources, e.g. the Rice MPSS database of the University of Delaware.

Crop Resources

Barley Genetics and Genomics continued

Step 5: Further analysis of the potential barley orthologues is then possible through the exploitation of barley functional genomics tools. The SCRI Barley TILLING, resource developed with funding from SEERAD and the BBSRC, is now a well established route for the generation of mutants in target barley genes. In addition, VIGS vectors for cereals are now available and their utility has been recently demonstrated in barley.

Step 6: Further characterisation is possible by utilisation of the established protocols for barley transformation that now exist. Though at present these are still restricted to a number of key genotypes, the available methods include a microspore protocol which enables homozygosity to be achieved in the initial transformed generation.

Step 7: The target gene can also be mapped in barley through the extensive range of mapping families and molecular markers resources which now include a large number of SNP markers.

Step 8: SCRI has the capability to estimate most economically important phenotypes in barley and thus can assess the effect of the target gene under the widely different genetic background of today's highly adapted barley cultivars.

The international barley germplasm resources in Europe alone exceed 180,000 accessions, including *Hordeum spontaneum* (the wild ancestor of cultivated barley which still grows extensively in the Middle East) and landrace material. These extensive germplasm collections are valuable resource for breeding and genetics. SCRI in combination with a number of academic and industrial partners has just started a large new LINK project to genotype elite lines with an extensive range of SNP markers from a functional map. This project together with other work at SCRI and a recently funded Barley USDA CAP Project will provide valuable resources for LD and Association Analysis in barley.

In this short article it is only possible to give a flavour of the resources available in barley. Members of the SCRI Barley team are happy to provide support and guidance for Arabidopsis researchers wishing to access and exploit these barley resources and are happy to make our extensive barley resources and experience available to the wider UK Plant Sciences community through collaboration. Our online barley resources, including UK relevant maps and genotype information, are currently being extensively updated and will be available through our barley portal (<http://germinate.scri.ac.uk/barley/>).

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Genes, Genomics & Breeding Programme
Scottish Crop Research Institute.
On behalf of the SCRI Barley Team which is supported by the Scottish Executive Environment and Rural Affairs Department as well as the BBSRC, the EU and other sponsors.



Useful Links

Barleyworld. This site is maintained by Dr Pat Hayes at the University of Oregon and contains links to an extensive variety of barley resources. He will even sell you a Barley hat!
<http://www.barleyworld.org/>

Washington State University. Dr Andy Kleinhofs at Washington State University maintains a number of value online barley resources.
<http://barleygenomics.wsu.edu/databases/databases.html>

WWW Links to Barley Information and Resources

Mutants and Germplasm Resources

1. The European Barley database. This database, maintained at IPK Gatersleben was the result of an extensive project to integrate information on European barley germplasm resources.
<http://barley.ipk-gatersleben.de/genres/>
2. The Barley Core collection. The International Barley Core Collection (BCC) is a selected and limited set of accessions. It optimally represents the genetic diversity of cultivated barley and the wild species of *Hordeum*. This collection and support information is maintained at a number of sites including this one in Japan
<http://earth.lab.nig.ac.jp/~dclust/cgi-bin/BCC/>
3. The UK National Cereal Germplasm Collection. The UK national barley collection is maintained at the John Innes Centre as a part of this collection. The Primary contact is Dr Mike Ambrose.
http://www.jic.ac.uk/GERMPLAS/bbsrc_ce/index.htm
4. The Classic Barley Mutant Database. This collection of barley mutants, many with detailed pictures, contains about 10000 accessions resulting from a joint Scandinavian mutation research programme. The project was initiated in 1928 and was largely developed and maintained by Dr. Udda Lundqvist.
<http://www.ngb.se/Cereal/>
5. The SCRI Mutant Database. This database supports an ongoing project at SCRI to record phenotype and image information from a large barley mutant population developed at SCRI in the cultivar Optic.
<http://germinate.scri.sari.ac.uk/barley/>

Barley Sequence and Genomics Resources

6. The Harvest Database. The Harvest database is maintained by Dr Tim Close at the University of California, Riverside. It is available as a downloadable database to run on local PCs. It contains virtually all of the Barley ESTs in the public domain together with a number of assemblies including those used in the design of the Affymetrix Barley1 GeneChip.
<http://harvest.ucr.edu/>
7. TIGR Barley Gene Index. This assembly of the Barley ESTs and gene sequences is a valuable resource as the result of the quality of annotation and links with other plant sequence data.
http://www.tigr.org/tigr-scripts/tgi/T_index.cgi?species=barley
8. The Barley Morex BAC library. The Morex barley BAC library was developed by Dr Rod Wing as a collaboration with a number of barley groups around the world. Filter sets of this library are held at a number of laboratories around the world, including SCRI
<http://www.agronomy.ucdavis.edu/Dubcovsky/BAC-library/ITMlbac/Andris.html>

Barley Mapping Resources

9. Barley Resources at GrainGenes. The USDA GrainGenes database maintained by groups at Cornell and Albany, CA is the main repository in the US for map, QTL and genomics information on small grain cereals. It contains information on an extensive set of barley maps (largely US) and other molecular resources.
<http://wheat.pw.usda.gov/GG2/germplasm.shtml#barley>
10. Barley Physical Mapping. A number of projects are now underway which will make a major contribution to the generation of a barley physical map. eg. Dr Tim Close of the University of California, Riverside leads a project which is making a major contribution to the generation of a barley physical map through the anchoring of barley gene sequences to clone sin the Morex BAC library.
[http://www1.agric.gov.ab.ca/\\$department/deptdocs.nsf/all/fcd10194/](http://www1.agric.gov.ab.ca/$department/deptdocs.nsf/all/fcd10194/)
<http://phymap.ucdavis.edu:8080/barley/>

Barley Functional Genomics Resources

11. The SCRI Barley TILLING Portal. Through the support of the BBSRC and SEERAD, SCRI currently runs a barley TILLING service based on a large population developed from the cultivar Optic.
<http://germinate.scri.sari.ac.uk/barley/>
12. VIGS in Barley. The utility of Viral Induced Gene Silencing has recently been demonstrated in barley by Dr Christophe Lacombe's group at SCRI.
<http://www.plantphysiol.org/cgi/content/abstract/138/4/2155>
13. BarleyBase. The BarleyBase at Iowa state is maintained by Dr Roger Wise and Dr Julie Dickerson as a repository for datasets from the Affymetrix Barley1 GeneChip. It also contains annotation information and a number of analysis and visualisation tools.
<http://www.barleybase.org/>
14. Barley Transformation. A number of protocols for barley transformation exist. e.g. Hensel G, Kumlehn J (2004) Genetic transformation of barley (*Hordeum vulgare* L.) by co-culture of immature embryos with *Agrobacterium*. In IS Curtis, ed, *Transgenic Crops of the World: Essential Protocols*. Kluwer Academic Publishers, Dordrecht, The Netherlands, pp 35–45. In the UK the Defra funded BRAC project provides transformation capability to UK researchers.
<http://www.bract.org/>

Rice and Comparative Information

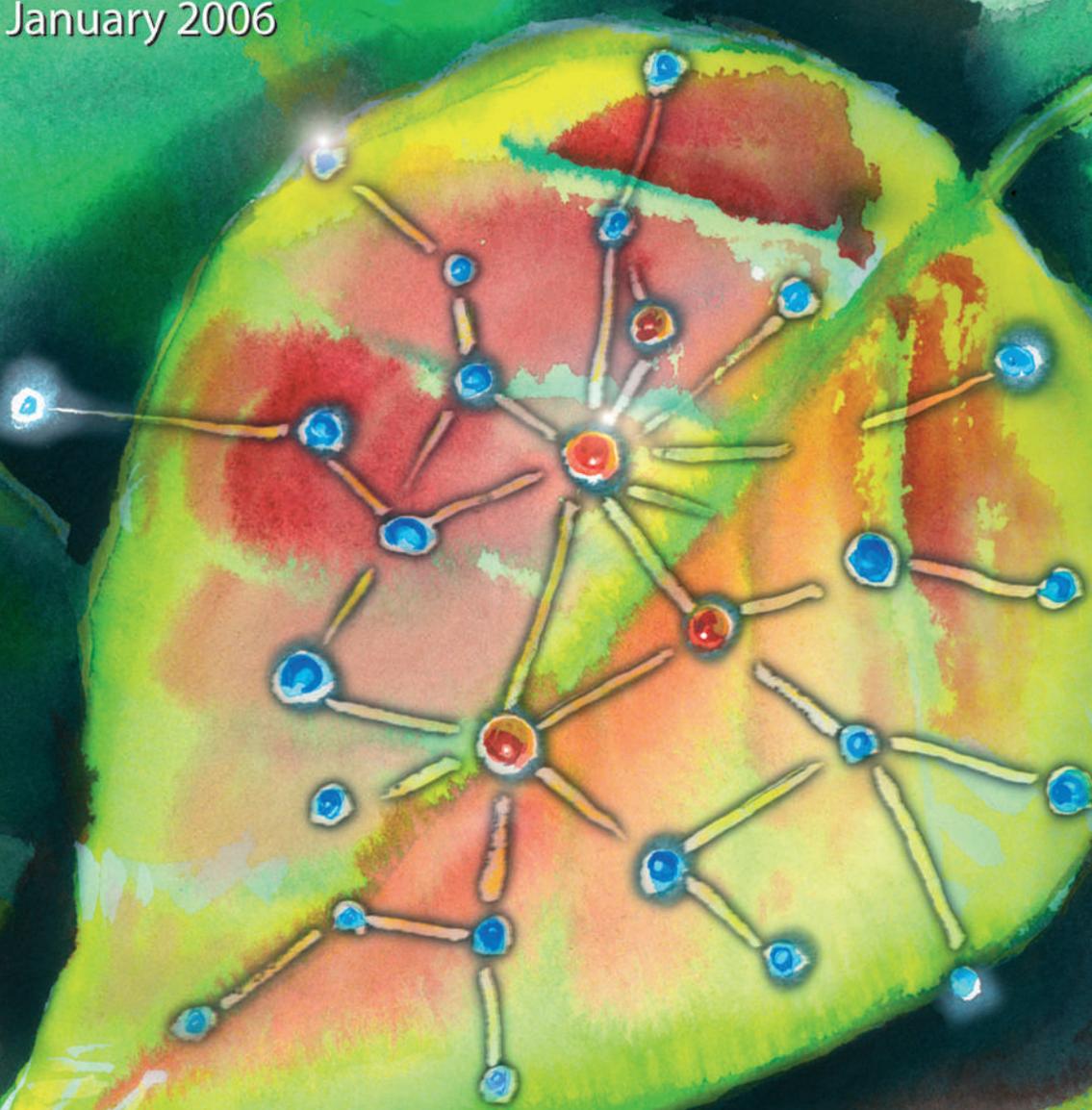
15. The Gramene Rice and Comparative Cereal Database. The Gramene database is a joint project between CSHL and Cornell. It is a valuable a rice and comparative cereal resource.
<http://www.gramene.org/>
16. The Rice MPSS Database at the University of Delaware. This database together with the parallel Arabidopsis resource is maintained by Dr Blake Myers. The Massively Parallel Signature Sequencing approach gives an extremely sensitive indication of gene expression over a wide range of tissues and treatments.
<http://mpss.udel.edu/rice/>
17. TIGR Rice Genome Annotation Site. This site provides a set of valuable tools for the comparative analysis of rice and other cereals.
<http://www.tigr.org/tdb/e2k1/osa1/>

15th New Phytologist Symposium

Networks in plant biology

The Linnean Society, London, UK

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Andrew Bangham (*University of East Anglia, Norwich, UK*)
Hamid Bolouri (*Institute for Systems Biology, Seattle, WA, USA*)
Juliette Colinas (*Duke University, Durham, NC, USA*)
David Fell (*Oxford Brookes University, UK*)
Claire Grierson (*University of Bristol, UK*)
Jane Memmott (*University of Bristol, UK*)
Andrew Millar (*University of Edinburgh, UK*)
Nick Monk (*University of Sheffield, UK*)
Lee Sweetlove (*University of Oxford, UK*)
John Turner (*University of East Anglia, Norwich, UK*)
Ian Woodward (*University of Sheffield, UK*)

Organization

Alistair Hetherington (*Lancaster University, UK*)
Ian Woodward (*University of Sheffield, UK*)
Claire Grierson (*University of Bristol, UK*)
Andrew Millar (*University of Edinburgh, UK*)
Holly Slater (*New Phytologist, Lancaster, UK*)

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