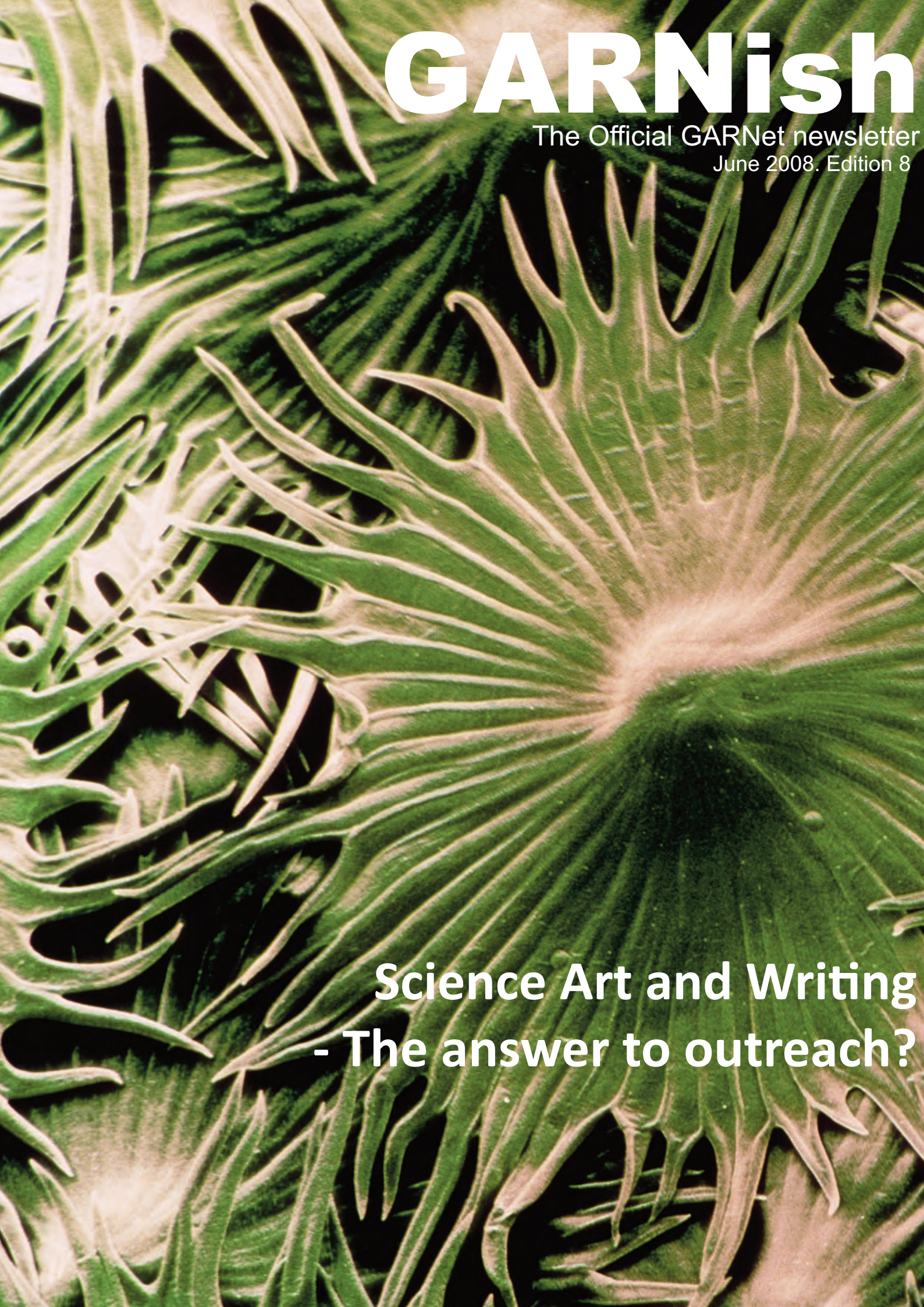


GARNish

The Official GARNet newsletter
June 2008. Edition 8

Science Art and Writing - The answer to outreach?

Editorial

Welcome to the 8th issue of GARNish. Since the last issue there have been a number of changes on the committee. We thank Claire Grierson, Julie Gray and Simon Turner for their help and support. Three new members have now been elected to the committee, myself (Durham University), Claire Halpin (University of Dundee) and Anna Amtmann (University of Glasgow).

With the push for multidisciplinary research, GARNet has been at the forefront of these developments and co-organised the first Mathematics in Plant Sciences Study Group in December http://cpib.info/workshop.shtml. This was a great success and will be followed up with another meeting in the new year. Coming up very fast it seems, is a joint Plant Symposium between the SEB and GARNet on the 8th -10th September 2008 at the Sutton Bonington Campus, University of Nottingham. The speaker list is impressive (see below) so all are encouraged to attend. Also the UK will be hosting the ICAR (International Conference for Arabidopsis Research) from 30th June to 4th July 2009 in Edinburgh, so another date for your diaries where we expect strong support from the UK community.

Coming up in this issue, we have a brief evaluation of what is widely being recognized as the model crop, *Brachypodium distachyon*. It is hard to ignore the benefits of using this grass as it allows crop related research to be accessible to all UK plant laboratories. More impressive studies are emanating from CNAP, and the Artemisia research project using non-GM strategies to develop cost-effective quantities of artemisinin for treatment of drug-resistant malaria is yet another inspiring concept. NASC is continuing to lead the way in gene expression analysis and offers a Affymetrix service at a reasonable cost, which includes a freely accessible Genespring facility; notes on how to access this facility are included in the newsletter. Continuing our goal to publicise plant research in all UK institutions, the focus here is on Manchester and a synopsis from each of 13 labs is included. Finally, something I was keen to add to this scientific newsletter is how we can relate to junior education. In a climate of decreasing plant scientists in particular, we should be making every effort to engage budding young scientists. Here we have a highlight on the Science, Art and Writing (SAW) initiative and also a plug for the Plant Science Teaching Resource at www.gatsbyplants.leeds.ac.uk.

Finally I would like to thank Ruth for organizing and maintaining the high standards of another GARNish issue!
With best wishes

Patrick J. Hussey

Contents

Front cover image of Trichomes on a seabuckthorn leaf provided by Dr Jeremy Burgess/ Science Photo Library.
Many thanks to all who contributed to this issue, particularly Mike Bevan, Maggie Smallwood, Aurora Levesley, Neil Graham, Simon Turner, Anne Osborne, Jim Beynon and Patrick Hussey.
If you have any comments about GARNish or if you would like to contribute an article to the next issue please e-mail ruth@arabidopsis.info.

GARNet-SEB Plant Symposium 2008

The GARNet 2008 meeting will be held jointly with the SEB plant section at the University of Nottingham, Sutton Bonington Campus, 8-10th September. http://www.sebiology.org/meetings/Notts08/Plant.html

SEB and GARNet have put together an outstanding programme of world-renowned speakers for the symposium including:- Alistair Hetherington (University of Bristol), Tzyy-Jen Chiou (Academia Sinica, Taipei), Mark Aarts (Wageningen University), Ueli Grossniklaus (University of Zurich), George Coupland (MPI, Cologne), Caroline Dean (JIC), Ottoline Leyser (University of York), Nicholas Harberd (University of Oxford), Natasha Raikhel (UC Riverside) and John Schiefelbein (University of Michigan). For a full meeting programme visit http://www.sebiology.org/meetings/Notts08/programme.html

In addition to the plenary sessions there will be several evening workshops on a variety of topics including tools and resources, next generation sequencing, how to start a systems biology project and career development. NASC will also be hosting a hands on computer tutorial to help researchers get to grips with the newly implemented Genespring workgroup database, which enables the distribution and analysis of the data held in the NASCArrays database. This workshop will be limited to 40 attendees, so register early to book a place.

If you would like to talk at the meeting or present a poster to share your latest results and discoveries with the plant community, please submit an abstract at http://www.sebiology.org/meetings/Notts08/abstracts.html

With all this on offer what are you waiting for? Register now at http://www.sebiology.org/meetings/Notts08/Registration.html

News and Views

iPLANT – a "cyberinfrastructure" for plant science

http://iplantcollaborative.org/

The National Science Foundation (NSF) has funded a 5-year $50m project to develop a cyberinfrastructure for plant science. The project is based at University of Arizona and Cold Spring Harbor and is headed by Rich Jorgensen. The basic concept is to engage the plant science research community in a debate as to the nature of the software needed to support effective research and to deliver that informatic environment. A kick-off meeting was held at Cold Spring Harbor in April http://iplantcollaborative.org/meetings/34-meetings/116-cshl-april-2008. It was attended by Andrew Bangham (UEA), Jim Beynon (Warwick) and David Rand (Warwick and on iPLANT board) from the UK. iPLANT is currently soliciting "grand challenges" from the community that the consortium can assist in addressing. Scientists are encouraged to form multi-institute teams to put together such challenges and submit their proposals to the iPLANT board for consideration. Those that are successful will be invited to a workshop, at the Biosphere2 in Arizona, to develop the challenge with the iPLANT team. There is no money available for project-based research but the resources of iPLANT will be focussed on developing those tools and software solutions that the challenge demands. This represents a great opportunity for plant scientists to expand the effectiveness of informatics in their field and to solve data access and analysis problems, which they have been faced. We have an opportunity to influence the direction that iPLANT takes and, hence, it is worthwhile to engage with this process. Non US scientists are encouraged to participate in iPLANT. Those interested should view information provided at http://iplantcollaborative.org/.

Growth of a plant science teaching resource

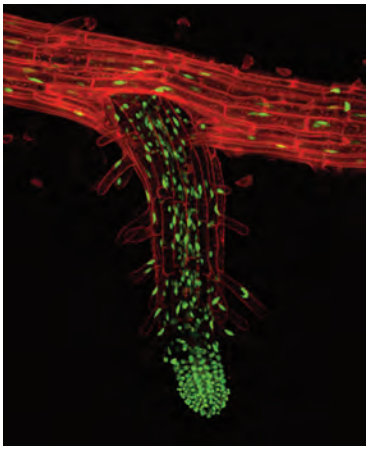
Article provided by Aurora Levesley

www.gatsbyplants.leeds.ac.uk

The Gatsby Plants Teaching Resource provides lecturers with quality teaching materials developed by plant science academics. Lecturers can download or link to copyright cleared video clips, films, images, lectures and practicals to use in their teaching. Resources currently available are:

Movies: These include time lapse photography of plant processes such as germination and tropic movements. Gatsby Plants has also co-produced its own 5 minute film in which Prof Enrico Coen, JIC tells the story of the Peloric form of *Linnaria vulgaris*, from its discovery and naming by Carl Linnaeus through to Prof Coen's own discovery of the gene responsible and his realisation that in Linnaria it is an epigenetic effect.

Gatsby Plants Summer School lectures: These are research led lectures aimed at level 1 and delivered by internationally recognised researchers. For example, find out how 'Grasses Bite Back' against herbivores in this lecture by Prof Sue Hartley, University of Sussex. In 'From Genes to Greens to Vaccines' Prof Julian Ma, St. George's Hospital Medical School, addresses the problems of infectious diseases in the developing world and queries how medicines can be delivered in the future.



Arabidopsis thaliana. Lateral root emergence from the main root. Cell walls (red) and nuclei (green) are marked. Contributed by Dr John Runions to the Gatsby Plants Teaching Resource © Dr John Runions, Oxford Brookes University.

Practicals: As well as a diverse range of practical protocols, the Teaching Resource also offers 'The Virtual Plant Pathology Lab' developed by Dr Victor Galea, University of Queensland. This media rich computer-based practical uses real life case studies to teach the principles of plant disease case management.

Plant News: Lecturers can search the Plant News database with its links to current news articles, video and audio reports from leading journals and the media. As well as being a useful research resource, we hope this will help lecturers to keep their teaching topical.

The Teaching Resource welcomes submissions from the plant science community and offers lecturers and researchers a platform to showcase their work. If you would like to suggest or submit a resource then please contact Aurora Levesley (a.levesley@leeds.ac.uk) or Juliet Jopson (s.j.jopson@leeds.ac.uk).

To view the Gatsby Plants Teaching Resource please register at: http://www.gatsbyplants.leeds.ac.uk

The project is funded by the Gatsby Charitable Foundation.

Brachypodium distachyon genomics: bridging the gulf to grass genomes.

Written by Mary Byrne, Philippe Vain, John Snape, Fiona Corke, Melanie Febrer, John Wright and Michael Bevan
John Innes Centre, Norwich Research Park, Colney Lane, Norwich. NR4 7UH

Members of the grass family are among the most significant crop and pasture plants in the world and in the UK, wheat, barley and forage grasses such as Lolium and Festuca are of primary importance in agriculture. The potential of grasses such as *Miscanthus giganteus* for sustainable energy production further increases the economic and social importance of the grass family. Because of this fundamental importance, research focussed on identifying genes and genetic variation associated with important agronomic traits is a high priority. However, there are significant barriers to this work: gene isolation and characterisation is relatively slow and complex, and these species are relatively difficult experimental subjects. Consequently there is a gap in our capabilities to apply the powerful approaches of modern biology to key crop species relevant to the UK economy.

This situation can be contrasted with the resources and capabilities enjoyed by researchers working with Arabidopsis. By establishing a community focus on a single system for plant research, major progress in understanding the mechanisms involved in growth, development and environmental responses has been accomplished in a remarkably short time. Much of the knowledge generated in Arabidopsis is directly relevant to understanding gene function in grasses, but there are significant differences, such as in seed and flower development, pathogen responses and cell wall composition, that suggest in-depth focussed research carried out in a grass species could be more directly relevant to grass and cereal crop improvement. Rice has been proposed as a model system for grass research, but due to its relatively long life cycle, tropical physiology and acutely demanding growth conditions in the UK, it has not “taken off” as much as perhaps was hoped (1). Moreover, a model system that is more closely related to wheat, barley and forage grasses than rice would also be more relevant.

Pioneering work by Draper and colleagues (2) showed that *Brachypodium distachyon*, a member of the Pooideae subfamily of grasses that includes wheat, barley and forage grasses, was also a promising candidate species for biological research in temperate grasses. Its small size, rapid generation time and abundant seed set were reminiscent of these advantageous features of Arabidopsis (Figure 1). Furthermore its undemanding growth conditions and high density cultivation will facilitate introduction into many labs in the UK. Current estimates suggest that Brachypodium and wheat shared a common ancestor between 25-35 mya (3). The International Brachypodium Initiative (www.brachypodium.org) was established in 2006 to develop community resources for research in Brachypodium. The main project involves a collaboration between the John Innes Centre, the USDA and the DOE Joint Genome Laboratory to sequence the genome of the community standard line Bd21 using a whole genome shotgun strategy. The sequence assemblies are supported by a physical map of BACs and a genetic map, funded by the BBSRC. Both physical maps of BACs and genetic map have recently been completed, and the 8x final coverage of the genome is on target for completion during June 2008. An automated FGENESH annotation of the 4x genome assemblies is available at www.modelcrop.org, which also describes alignments with wheat and barley transcriptome assemblies. Integration of the physical map with the 4x checkpoint sequence assembly revealed 13 supercontigs spanning 303 Mb. Fluorescent In Situ Hybridisation (FISH) analyses, carried out in a collaboration with Robert Hasterok in Poland, are anchoring these sequences to the 10 chromosome arms of the diploid Bd21. Deep transcriptome sequencing using GS-FLX and EST sequencing, also underway at the JGI, will be the basis for a high quality annotation of the genome. The first resource made from the genome sequence, available in early 2009, will be an Affymetrix 5µm combination chip with exon probes and a tiling array with 49 nt resolution. This can be used to study gene expression and chromatin modification and to map genome deletions.

Figure 1. Comparison of Arabidopsis (left) and Brachypodium (right).

Highly efficient *Agrobacterium tumefaciens* - mediated transformation methods have recently been developed that include the community standard line Bd21 (4). The flanking sequences of 2,500 T-DNA insertion lines are currently being sequenced to assess the feasibility and utility of developing larger populations for systematic reverse genetics. Vectors tailored for gene expression and efficient gene transfer are also being built. Forward genetic resources are being created, including a fast- neutron mutagenized population (Figure 2) that has already yielded several morphological mutants. Therefore several of the key resources that have been so important in driving the success of Arabidopsis as a biological system could be developed at a larger scale to become useful community resources for research in many areas of temperate grass biology.

Brachypodium distachyon genomics: bridging the gulf to grass genomes.

Figure 2. *Brachypodium* mutants identified in a fast-neutron mutagenised population. Wild-type Bd21 on left.

Grass genomes are thought to have evolved from a monophyletic ancestor, reflected in the exceptional conservation of large- scale features seen among grass genomes (5). The huge differences in genome size in the grasses are caused by the differential accumulation of repeat sequences in intergenic space (6), by genome polyploidization (7). These factors suggest that conserved gene order may be useful for establishing a first approximation of gene order and identity in wheat, barley and forage grasses using Brachypodium gene order as a template. While little will initially be learnt about non-genic repeat regions, this approach will be reasonably accurate: for any region of the Brachypodium genome approximately 70% of wheat genes in the collinear region have the same order. Furthermore the high degree of sequence similarity between wheat, barley, forage grasses and Brachypodium genes permits accurate assignment of orthologous relationships. In turn, these relationships provide a reasonably good predictive power for comparing gene functions between wheat, barley and Brachypodium. In a paradigmatic study, this strategy has been used for targeting gene discovery in wheat (8). It also promises to be useful in large-scale ordering of BAC clones in physical mapping projects in these three species. Systematic physical mapping of the wheat and barley genomes will soon be initiated in an EC- funded project called Triticeae Genome. The progress made in Brachypodium genomics and functional genomics described here establishes new possibilities for UK researchers to develop research programmes in a model grass species closely related to a major crop and forage plants. This sets the stage for achieving, through concerted community effort, competitive and creative research programmes focussed on food and energy production (e.g. Figure 3) from our major crops.

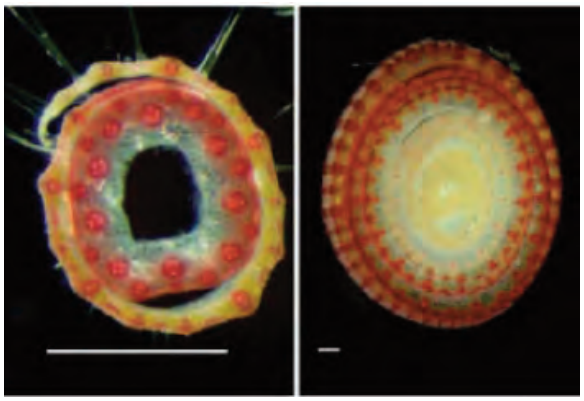


Figure 3. Stems of Brachypodium (left) and Miscanthus (right) stained to reveal lignin. Scale = 1mm

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Fast Track Breeding of *Artemisia annua*:

Cheaper anti-malarial treatment for the developing world

Written by Dianna Bowles, Maggie Smallwood and Ian Graham,
Centre for Novel Agricultural Products, Department of Biology, University of York, PO Box 373, YO10 5YW

Introduction

Artemisia annua is the sole source of the sesquiterpene lactone, artemisinin, the leading active for treatment of drug-resistant malaria. In the face of increasing resistance to older generations of anti-malarial drugs, over 70 countries have adopted artemisinin combination therapies (ACTs) as their first line treatment. However, the cost of ACTs is a major obstacle to their widespread deployment in the developing world, and artemisinin is a significant element in this cost.

The principal reason for artemisinin's high production cost is the low yield in *A. annua*. The best varieties cultivated under ideal conditions produce around 1% dry weight in their leaf tissue. The plant remains nearer to a weed than a domesticated crop, with commercial cultivars often only one generation removed from the wild varieties.

Application of modern fast track breeding methods founded in genomics offers a rapid route to increasing yield thus decreasing costs of artemisinin production and making ACTs accessible to more of those who need them.

Figure 1 *Artemisia annua* growing in East Africa

Technologies and materials

Over recent years a number of high throughput genomic tools have been developed in the model plants, Arabidopsis and rice, to a stage where they can be applied to more exotic species, such as *A. annua*, where knowledge of both genetics and physiology is limited. These tools allow high throughput screening of large populations of plants at both the genetic and the trait level. For instance developments in mass spectrometry now allow quantitative analysis of hundreds of secondary metabolites in crude plant extracts within a few minutes, enabling a high throughput screening for levels of artemisinin and other compounds.

High throughput reverse genetic screens using techniques such as heteroduplex mapping (also known as TILLING) enable detection of rare alleles or induced mutations in target genes that are predicted to impact on yield. Pyro-sequencing of cDNA libraries can provide 400,000 reads of genes that are expressed in specific tissues such as glandular trichomes, where artemisinin is thought to be synthesised and stored. In addition to sequence information, the redundancy inherent in this technology provides information on the relative expression levels of thousands of genes in parallel. Importantly for a breeding program, single nucleotide polymorphisms (SNPs) can be identified in the more abundantly expressed genes providing ideal genetic markers for traits of interest.

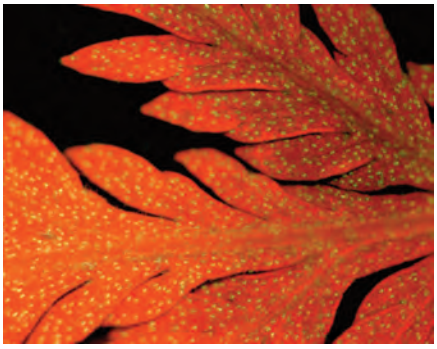

Figure 2 Artemisinin is thought to be synthesised and stored in glandular trichomes which are distributed over the aerial tissues of *A. annua*

Through selective combination of the different high throughput approaches to screening both natural and induced variation in large populations of *A. annua* it is possible to rapidly identify individuals that carry beneficial genes and select against those that carry deleterious ones.

Although modern technology offers a data-rich environment for engineering yield in *A. annua*, the plant presents its own specific set of problems. For instance, the levels of artemisinin in the leaf tissue of any individual plant may vary from 0 to 2% of dry weight depending on the age of the individual leaf, the developmental status of the plant and the environment in which it is growing. Although artemisinin concentration in leaf tissue is highly heritable[2], development of standardised growth conditions and leaf harvesting protocols together with robust internal controls is essential for high throughput screening of metabolites, and selection of individuals rich in artemisinin.

Parameters affecting yield

Three traits are thought to control the yield of artemisinin per hectare in *A. annua*:
- leaf biomass, trichome abundance and artemisinin level in the trichome.

Both flowering and plant architecture impinge on yield of leaf tissue. *A. annua* is a short day plant and premature flowering induced by short days in the tropics can reduce biomass yield. Under good growing conditions, *A. annua* accumulates an annual biomass comparable with commercial tree plantations but unfortunately at least three quarters of this is stem tissue whilst only the dried leaf tissue is suitable for extraction of artemisinin. Bushy plants with several stems arising near the base have a higher leaf:stem ratio than other architectures and it has been speculated that reduced apical dominance and dwarfing might increase leaf yield. Genes that control both flowering and architecture are well conserved across the plant kingdom, and *A. annua* homologues of these well known genes are relatively easy to identify, enabling their use in reverse genetic approaches to increase leaf yield.

Figure 3 *A. annua exhibits a range of architectures*

Fast Track Breeding of *Artemisia annua*:

Cheaper anti-malarial treatment for the developing world

By contrast, genes that control initiation and development of glandular trichomes remain poorly characterised. Although genetic control of the non-glandular trichomes of Arabidopsis has been studied extensively[5], it is not clear that the same genes control secretory structures[4] and therefore forward rather than reverse genetic approaches may be more productive.

A range of options exist to manipulate metabolism within the trichome to increase accumulation of artemisinin. *A. annua* produces other secondary metabolites at significant levels[1,3,6], and it is possible that knocking down key enzymes in these pathways might release precursors for synthesis of artemisinin as well as storage space in the sub-cuticular cavity. Both the cytosolic and the plastidial pathways to isoprenoid precursors are highly regulated and increasing expression of critical enzymes or removing feedback inhibition could also increase flux into artemisinin. It is also possible that there are global regulators that could increase expression of genes in the committed pathway to artemisinin synthesis.

Fast track breeding

The aim of the CNAP Artemisia Research project is to create a cost-effective plant product that will improve artemisinin cost and availability. Several lines of investigation are being pursued in parallel. These include forward and reverse screens of EMS-treated *A. annua* populations using high throughput mass spectrometry and heteroduplex mapping. This is complemented by development of a genetic map and QTL analysis. The genetic analyses will not only enable introgression of mutations identified in the EMS-treated population into a desirable genetic background but also represent an independent route to higher yield varieties. Variation present in natural populations is also being studied by linkage disequilibrium and association studies. The programme is supported by a workstream aimed at discovering genes that control traits of interest in *A. annua* for use in reverse genetics. Although transgenics are being used as a research tool, the project has adopted a non-GM strategy to creation of new varieties in order to minimise the regulatory burden the novel varieties will face.

Figure 4 *Sectored leaf from EMS-treated A. annua*

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Conference Diary

17-22 August - XVI FESPB Congress Tampere, Finland
http://www.fespb2008.org/

17-22 August - GRC - CO_2 Assimilation in Plants, New England, USA
http://www.grc.org/programs.aspx?year=2008&program=co2

7-12 September - GRC - Salt and Water Stress in Plants, Big Sky Resort, MT, USA
http://www.grc.org/programs.aspx?year=2008&program=salt

8-10 September - GARNet-SEB Plant Symposium, University of Nottingham, UK
http://www.sebiology.org/meetings/Notts08/Plant.html

15-18 September - Plant Modelling Summer School, University of Nottingham
http://cpib.info/meeting/index.shtml

17-20 September - 19th New Phyologist. Symposium - Physiological sculpture of plants, Timberline Lodge, Oregon, USA
http://www.newphytologist.org/physiologica

28 June - 1 July 2009 - SEB Main Meeting, Glasgow, UK
http://www.sebiology.org/meetings/

30 June - 4 July 2009 - ICAR 2009, EICC, Edinburgh, UK

Plant Modelling Summer School

University of Nottingham
15-18 September 2008

Co-organised by
CPIB GARNet CISBE
STEMN SIGNET

Target audience:

Open to all - plant biology postdoctoral researchers and PhD students are particularly encouraged to attend

Aims:

- To introduce modelling and quantitative approaches to biology
- To encourage experimental design which generates data suitable for modelling

Programme:

Day 1: Introduction to biological data and modelling
(Dr Nick Monk, Dr Markus Owen, Nottingham)
Day 2: Inferring cellular networks and model parameters from data
(Dr Barbel Finkenstadt, Warwick)
Day 3: Dynamic modelling and iterative model refinement
(Dr Carl Troein, Edinburgh)
Day 4: Multicellular modelling
(Dr Henrik Jönsson, Lund)

Registration is FREE but places are limited

Deadline: 1st August 2008

For further details visit www.cpib.ac.uk

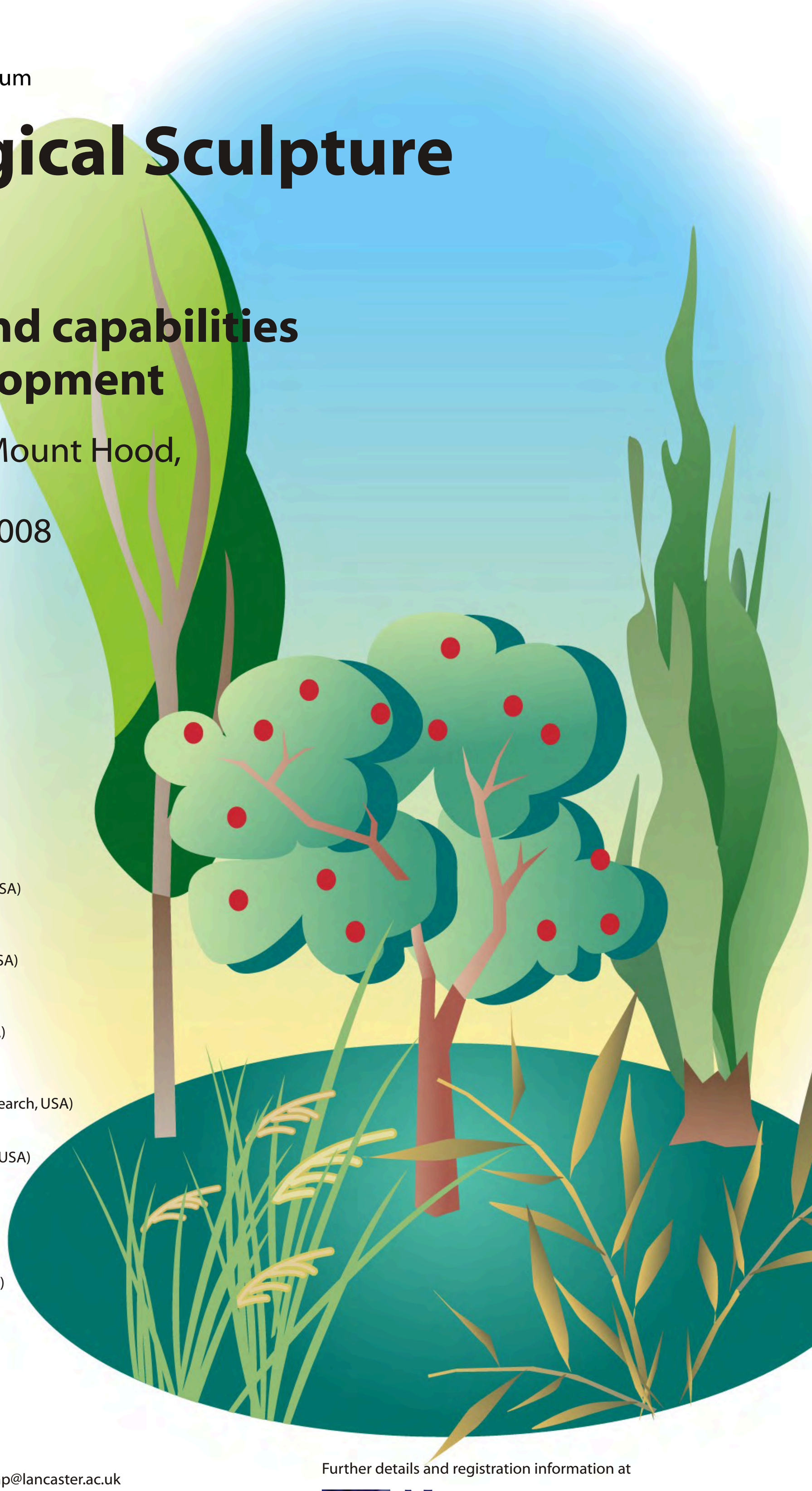
EPSRC Engineering and Physical Sciences Research Council
bbsrc biotechnology and biological sciences research council
STEMN
signet
CPIB.ac.uk The Centre for Plant Integrative Biology
csbe centre for systems biology at edinburgh

19th New Phytologist Symposium

Physiological Sculpture of Plants:

new visions and capabilities for crop development

Timberline Lodge, Mount Hood,
Oregon, USA
17–20 September 2008



Invited speakers

Tom Adams (Monsanto, USA)
Richard Amasino (Univ. of Wisconsin, USA)
Jeffrey Bennetzen (Univ. of Georgia, USA)
Luca Comai (UC-Davis, USA)
Deborah Delmer (Rockefeller Foundation, USA)
Rebecca Doerge (Purdue Univ., USA)
Richard Flavell (Ceres Inc., USA)
Robert Goldberg (UC-Los Angeles, USA)
Neal Gutterson (Mendel Biotechnologies, USA)
Robert Horsch (Gates Foundation, USA)
Rich Jorgensen (Univ. of Arizona, USA)
Harry Klee (Univ. of Florida, USA)
Erik Legg (Syngenta Biotechnology Inc., USA)
Rob Martienssen (CSHL, NY, USA)
Susan McCouch (Cornell Univ., USA)
Daniel Rokhsar (US Dept. of Energy, USA)
Chris Somerville (Carnegie Inst. of Plant Research, USA)
Brian Staskawicz (UC-Berkeley, USA)
Scott Tingey (Dupont Corporation, USA)
Michael Thomashow (Michigan State Univ., USA)
John Willis (Duke Univ., USA)

Organisation

Steven Strauss (Oregon State University, USA)
Richard Amasino (Univ. of Wisconsin, USA)
Richard Flavell (Ceres Inc., USA)
Richard Jorgensen (Univ. of Arizona, USA)
Harry Klee (Univ. of Florida, USA)
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Further details and registration information at

New Phytologist

www.newphytologist.org

Physiological sculpture of plants logo by Gretchen Bracher. Print & Design supplied by APPS, www.promotional-goods.org.uk

Arabidopsis Resources

The FREE Genespring Workgroup at NASC

http://affy.arabidopsis.info/workgroup.html
Written by Neil Graham - Nottingham Arabidopsis Stock Centre

The NASC Affymetrix service (http://affy.arabidopsis.info) was established in early 2002 to provide a transcriptomics service for the Arabidopsis community. The service has subsequently expanded to provide a service for all Affymetrix arrays (including other plants, animal, yeast, tiling arrays) and has performed over 3000 hybridisations. As part of the conditions of using the service all Arabidopsis data must be made public through the NASCArrays database, which also includes Arabidopsis data donated by other groups. This MIAME compliant database allows both access to the MAS5 normalised data and has additional tools to download and analyse the data (e.g. spot history, digital northern).
To further advance the analysis of Arabidopsis array data, we now have a freely accessible Genespring facility at NASC for the whole Arabidopsis community.

Genespring Workgroup

NASC has a BBSRC grant to implement and develop Genespring Workgroup to maximise the distribution and analysis of data in the NASCArrays database. Genespring Workgroup is a database solution developed by Agilent Technologies that can manage and analyse array based data. This will allow users to download the raw data (.CEL files) and fully analyse all the data sets with a very rich set of tools.

Accessing Genespring Workgroup

The workgroup can be accessed in three ways: a web based viewer; the Genespring viewer; or the full Genespring suite of tools remotely linked to our central database (if you already own Genespring).
The **web based viewer** allows users to view the data (e.g physical position, line graph, pathway) and detailed information about the experiments, including sample details and normalisation methods. The expression profiles of single genes can also be analysed. This is mainly a 'quick look' route to the data.

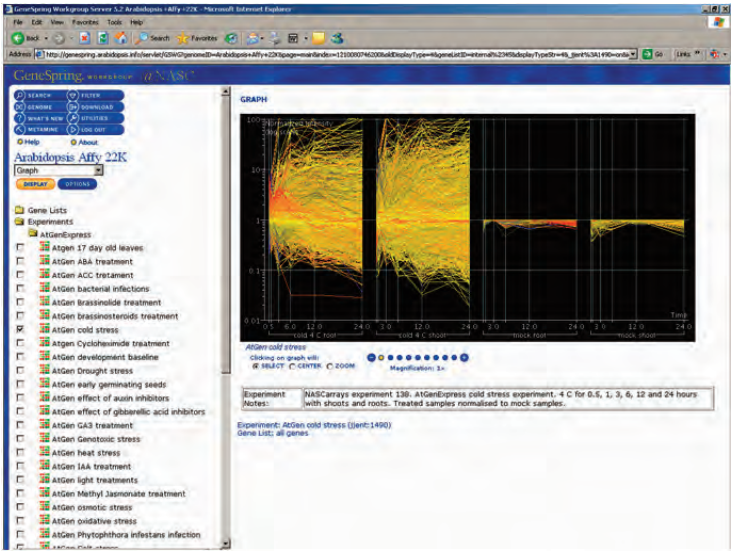


Figure 1 Web viewer main view

The **Genespring viewer (recommended)** allows more detailed analysis of the data. The data can be viewed in multiple ways (e.g line graphs, scatter plots, box plots, pathways) and detailed experiment and sample information can be shown. Expression profiles and GO ontologies of single and multiple genes can all be analysed in a user friendly and powerful manner. Detailed annotation and expression values can be downloaded for single, multiple and all genes on the array. The raw data in the form of .CEL files can be downloaded using both the web based and Genespring viewers.
FREE access to the workgroup for readers of this article. **username = garnish, password = garnish**

Experiments available

Currently the database has experiments performed on the ATH1, AG and Wheat Genome arrays. In total there are 44 experiments and 1151 samples available for analysis (May 1st 2008), with more being added. This includes many of the AtGenExpress experiments such as developmental stages, hormone treatments, abiotic and biotic stresses.

Figure 2 Gene Information Page

Using the web based viewer

The web based viewer is accessed from http://genespring.arabidopsis.info.
After logging-on you then select which genome you would like to use (Arabidopsis Affy 22k for ATH1, Arabidopsis Genome for AG and Wheat Affy Genome for Wheat Genome experiments). The main web viewer page is divided into 2 areas (see figure 1). The main window displays the data and the left-hand side contains the experiments, gene lists, clustering results, pathways and other definitions or organisational data.
To view a specific experiment, first click on the experiments folder to see all available experiments and then click on the required experiment.
Experiment viewing options can be changed by selecting display from the drop-down menu. Clicking on an individual gene in the main view window will select that gene and clicking on the gene name will then display detailed gene information, including expression levels in each sample and GO annotation (see figure 2).

Arabidopsis Resources

The FREE Genespring Workgroup at NASC

Links to a range of databases for further information include AtEnsembl, spot history gene swinger, and Genbank. Genes with a very similar expression pattern can be viewed by clicking on “display similar genes”. To find a gene of interest select “annotated data” from the drop down menu. This will list all the individually selectable genes on the array (inc. Affy ID and AGI code).

Using the Genespring viewer (recommended)

The Genespring viewer must be downloaded from the web viewer log-in page and installed locally on a windows system. On starting the viewer you must select which genome to use. The main view will be familiar from the full Genespring programme (see figure 3). On the left-hand side are folders containing experiments, gene lists, analysis results, pathways for example. The main browser window displays the experiment and results. An experiment is opened by selecting it from within the experiments folder. Double clicking on any gene from the browser window will open the gene information window, which displays signal values, gene annotation and links to external databases. Information about individual genes can be found by selecting edit > advanced find genes. This can then be searched using AGI code, Affy ID, keyword and more (the Wheat experiments can also be searched using AGI codes as we have annotated the Wheat genes with potential Arabidopsis homologues). From the results of the search individual genes can be selected or new gene lists generated. New lists can also be generated by pasting a list of AGI codes or Affy IDs. To do this, generate a list of codes in notepad or word and copy the list to the clipboard. In Genespring viewer, select edit > paste > paste gene list and the new gene list will be saved in the gene lists folder. Further information on gene lists can be viewed by double clicking on the gene lists in the gene list folder. This will open the gene list window which displays information about the individual genes and further analysis options. The“similar list” tab displays the gene lists which have significant number of overlapping genes with the current list. The GO ontology browser groups the genes in the list based on their GO ontologies (biological process, cellular component and molecular function) and displays the results as either an interactive pie chart or as a table (see figure 4). In the table display, the list can be limited to most significant ontologies by selecting a p value cut-off. There are also tools (select tools) for finding similar samples and similar genes using correlation scores. With these tools, a sample or gene of interest is selected and compared to all or a subset of samples or genes.

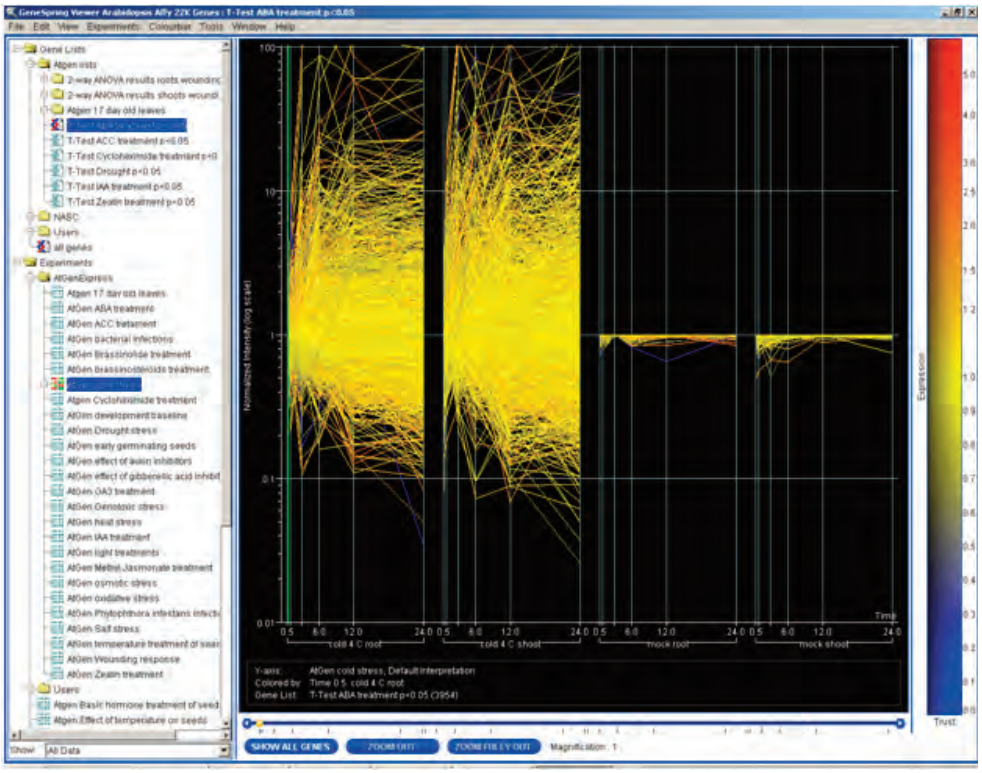


Figure 3 Genespring viewer main view

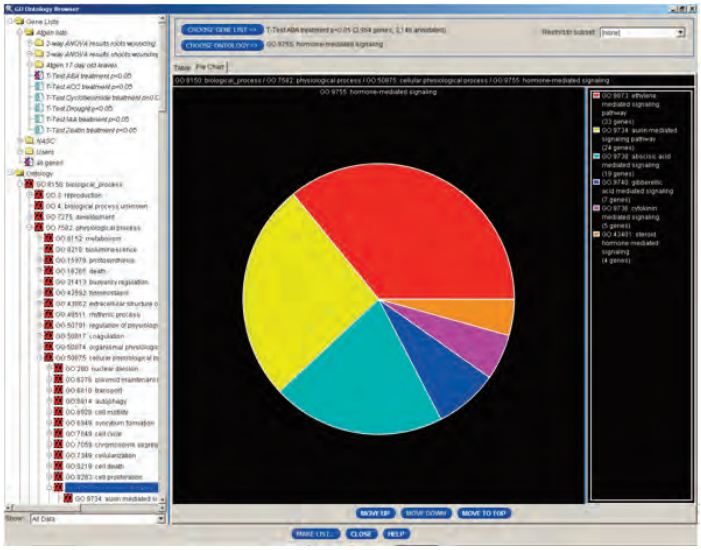


Figure 4 GO analysis of gene list

The raw data in the form of .CEL files can be downloaded in two ways. Selecting experiments > sample manager will display all the samples in the database (which can filtered on experiment, parameter attribute etc). Select the sample of interest and click inspect. This will display detailed information about that sample and clicking on “associated files” tab will allow you to download the .CEL file by highlighting it and clicking “extract file”.

Further information

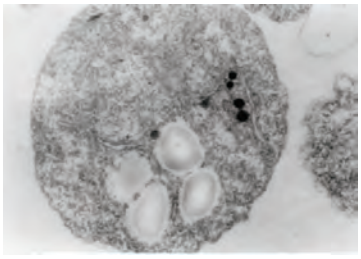
Further information and detailed instructions for using the web and Genespring viewer can be found at http://affy.arabidopsis.info/workgroup.html.

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, GARNet is focusing on geographical areas and institutions across the UK.
In this issue we continue our tour around the country highlighting the outstanding research being undertaken at the University of Manchester.

Spotlight on the University of Manchester

Researchers in Plant Sciences at Manchester aim to understand the endogenous and extrinsic factors which regulate plant growth, development, evolution and adaptation. Experimental approaches range from studies of individual molecules through to the whole plant in its natural environment. Well characterised model plants such as Arabidopsis as well as crops and natural species are used in interdisciplinary approaches which entail interactions between groups and across the Faculty of Life Sciences. Research projects are supported by a wide range of funding agencies, which includes the BBSRC, NERC, European Union, and industry.



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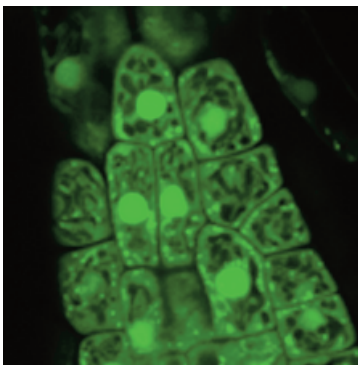
Research Area Plastid metabolism

Research Activities

Plants unlike animals have the ability to make their own food via photosynthesis. This produces carbohydrates, such as starch, and other important food products including amino acids, proteins and fats. The production of such products is highly integrated both within and between different subcellular compartments. The Bowsher lab has focused on the plastid as a unique location in plants for a range of assimilatory and biosynthetic processes including starch synthesis, nitrogen assimilation and amino acid synthesis. Investigating plastid metabolism at the level of transcription, translation and post-translationally has given a clearer insight into how plastid metabolism is integrated and coordinated. The group has also been able to identify spatial and temporal regulation of metabolic pathways and plastid types. Such an understanding provides scope for manipulating specific components of metabolic processes in a defined way. For example, the lab has characterized multiple isoforms of ferredoxin NADP+ oxidoreductase (FNR), an important enzyme not only in photosynthesis but a range of other metabolic processes, and discovered that variation in FNR forms and function helps plants to cope with different environmental conditions. By providing a greater understanding of how plants alter their metabolism to deal with environmental fluctuations the Bowsher group hope that their research will help to produce plants that can grow in previously inhospitable environments.



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Research Area Seed germination and identifying molecular markers of seed quality

Research Activities

Seeds provide not only a concentrated and convenient dietary source of nutrients but also the major means by which genetic improvement of crops is delivered by plant breeders to agriculture and horticulture. Conservation of plant genetic resources is also reliant on seeds and their properties. Some degree of dormancy (failure of viable seeds to germinate under favourable conditions) in crop species is desirable to prevent precocious germination of grain in the ear and consequential loss of crop value and quality (up to £400M per year to UK wheat growers). But too much dormancy can be a significant problem e.g. dormant grains cannot be malted.
The Bray lab is particularly interested in understanding at the molecular level how seeds progress from a state of dormancy to germinative growth which represents the single most active phase of growth in the whole of the plant's life cycle. In particular the group are focused on:-

Spotlight on the University of Manchester

Cliff Bray Research Activities Contd.

- Establishing the biological relevance and importance of RNA silencing pathways in the genetic switch, which accompanies the transition from dormancy/quiescence to germination.
- Elucidating the role and importance of peptide transport activity in response to metabolite sens ing
- Defining the mechanism of signal transduction that links extracellular nutrient levels to peptide transport activity across the barley scutellum
- Establishing the role of DNA ligases and their interacting proteins in DNA damage pathways

Name Anil Day
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Research Area Chloroplast biology and biotechnology

Research Activities

Chloroplasts convert light into chemical energy fuelling life on earth. They contain their own expression apparatus and a small DNA genome with about 120 genes. Transplastomic technologies allow precise targeted integration of trait genes into chloroplasts without marker genes. Maternal inheritance of chloroplast genes prevents the pollen-mediated spread of transgenes providing a natural form of gene containment for the next generation of Biotech crops. Industrial and pharmaceutical proteins expressed in chloroplasts accumulate to extraordinarily high levels providing an attractive production platform for manufacture of high-value products for industry and health, which is both sustainable and carbon-neutral. Several Manchester projects focus on the high-yield-expression of potential vaccine epitopes and pharmaceutical proteins in chloroplasts. Biotechnological applications of this new and exciting area of science are underpinned by fundamental research on the genes present in chloroplasts. Despite the importance of chloroplast DNA to plant growth and development very little is known on the molecular mechanisms responsible for the maintenance of chloroplast genes. The Day group is studying the enzymatic machinery responsible for maintaining genes in chloroplasts. The study of gene maintenance mechanisms in chloroplasts is facilitated by the development, in Manchester, of functional assays to identify molecular components involved in targeted integration and excision of foreign genes transformed into chloroplasts. Exploitation of gene maintenance mechanisms in chloroplasts is expected to lead to improvements in transplastomic technologies and the design of transplastomic crops.

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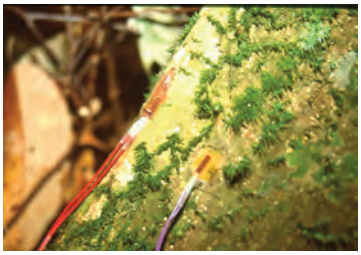
Research Area Origins and development of agriculture

Research Activities

Agriculture began in southwest Asia about 10,000 years ago. Initially it was thought that the transition from hunting-gathering was rapid but we now know that it took several thousand years with a number of intermediate stages before agriculture finally emerged. Researchers at Manchester are studying this process by genetic analysis of variable loci in einkorn wheat to establish the precise relationships between the wild and cultivated versions of this early crop. The Brown lab is also constructing *in silico* simulations of the domestication process in order to model the effects of different types of selection pressure on the rate of evolution of domesticated plants. After agriculture became established in southwest Asia it spread into Europe during the period 6000–4000 BC. The group is analysing genetic diversity in large numbers of wheat and barley landraces to understand the pattern of spread and to link this to archaeological interpretations of the factors underlying the development of early agriculture. The lab is also interested in genes for adaptive traits such as the response of flowering time to daylength and how the evolution of these genes may possibly explain the stop-start nature of the spread of cereal cultivation into northern Europe. Researchers are carrying out similar work in South America, including studying ancient DNA from archaeological maize specimens from Peru, Brazil and Argentina in order to understand the development of maize cultivation throughout the continent.

Spotlight on the University of Manchester



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Research Area Plant Biomechanics

Research Activities

Using a range of techniques, work in the Ennos lab investigates the engineering of structures in plants and their interactions with animals. The anchorage systems of a wide range of plants have been studied and it has been shown that the buttress roots of tropical trees have a mechanical function, preventing failure at the junction between the roots and trunk. These highly stressed regions are packed with mechanical fibres at the expense of reduced investment into vessels, with concomitant reduction in hydraulic permeability. Another field of study (in collaboration with Prof. Sue Hartley, University of Sussex) is the role of silica bodies in grasses in providing mechanical defence against herbivory. It has been shown that the silica reduces the palatability and digestibility of grasses, largely due to mechanical effects; the silica bodies wear down the teeth of herbivores and prevent the teeth from crushing protein-rich chlorenchyma cells. Finally, the compliance of tree branches is being examined in a project which seeks to determine whether human bipedality could have evolved as a method of walking efficiently in the trees, like a person on a trampoline.

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Research Area Programmed Cell Death

Research Activities

Programmed Cell Death (PCD) is a process that is critical to all organisms for development and defence against pathogens.

PCD is well characterized in animals but few plant homologues of animal PCD genes have been reported to date, indicating that the process of PCD in plants is unlikely to mirror what has been described in animal apoptosis. In particular, major animal regulators such as the Bax / Bcl2 family and the caspase family are absent from plants genomes. Plant PCD is therefore predicted to be a novel, alternative pathway that has yet to be discovered.

Research in the Gallois lab is focussed on discovering core components of PCD in plants using the power of Arabidopsis molecular genetics. The lab has shown that a UV-C stress induces apoptotic-like changes in Arabidopsis seedlings and protoplasts. These changes include fragmentation of the genomic DNA resulting in the detection of a DNA ladder, changes in nucleus morphology (crescent shape) and nucleus fragmentation. But what is causing these responses? In animals, caspases are key components of apoptosis and caspase activities can be detected in both animal and plant cells. However there are no orthologous caspase sequences in plant genomes. The Gallois lab has shown (and published) that the pan caspase inhibitor, p35 suppressed PCD is induced by high doses of UV and similar results have also been reported for caspase-3 inhibitors (DEVD). These results would indicate that caspases-like activity is involved in PCD. Sequence and structural analysis have shown that a diverse range of caspase- like proteases exist across the phyla, with metacaspases being found in plants. Plant metacaspases however do not have caspase-like activity although metacaspase-8 was shown by the group to be involved in PCD. A major challenge therefore remains to identify the plant proteases that are responsible for caspases activities in plants and how these relate to animal caspases. This work will help to unravel the molecular mechanism of plant PCD and will have implications for the understanding of PCD evolution in eukaryotes and for biotech applications in plants.

Other work in the lab deals with PCD during development with a focus on the root cap and the embryo suspensor. A mutant analysis project has lead to the identification of a gene that may function in a manner analogous to the pro-apoptotic Bax gene.

Spotlight on the University of Manchester

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Research Area Regulation of photosynthesis in response to environmental stress

Research Activities

The process of photosynthesis is uniquely sensitive to fluctuations in a plant's environment. Imbalances between the amount of light absorbed by chlorophyll and the rate at which the captured energy is assimilated can give rise to reactive oxygen species, including singlet excited oxygen, superoxide, hydrogen peroxide and hydroxyl radicals. Plants are however largely unable to control their environment and light, temperature and water availability all vary significantly across the year. The Johnson group is interested in understanding how plants cope with such variations and how they minimise reactive oxygen production. Recent work has focussed on two aspects of this, operating on very different timescales. Over rapid timescales (sec-mins), the group are interested in the regulation of electron flow, with down regulation of the electron transport chain occurring to limit the production of superoxide. Recent work has identified a novel feedback loop, mediated by the redox poise of the NADP/NADPH pool. Over longer timescales, they are investigating how plants are able to adjust the composition of the photosynthetic apparatus to suit the prevailing conditions and in particular are interested in the pathways by which the status of the chloroplast might be signalled to the cytosol to control the synthesis of photosynthetic proteins. A key component in this pathway has been identified as being a glucose-6-phosphate/phosphate translocator, GPT2, a protein that was previously written off as having no specific function.

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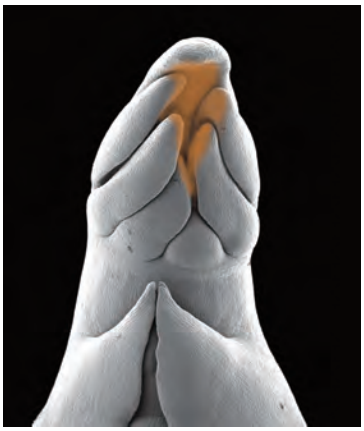
Research Area Plant-microbe interactions – nutrient cycling and stress

Research Activities

The root systems of plants nurture a complex ecosystem of many different organisms, including bacteria, fungi, protozoa, and invertebrate species. Many of these species play important roles in protecting plants from pathogen attack and stimulating nutrient uptake. Most of the current research in the Kertesz lab concerns how these interactions between bacteria and plants are managed, concentrating on sulfur and phosphorus mobilization from the soil for plant utilization and on community interactions in model systems. The Kertesz group has recently shown that the ability of certain pseudomonads to desulfurize sulfonates under sulfate-limiting conditions is connected with plant-growth-promoting activity, and that particular bacterial rhizosphere genera (e.g. *Variovorax*) appear to be intimately involved in mobilization of bound sulfur. Bacteria also respond to phosphate-limiting conditions in the rhizosphere, and the group is focusing efforts on understanding how plants direct the bacterial phosphate-starvation response at the transcriptomic level (changes in exudate composition and flux, specific signals, etc), with the aim of improving P-mobilization for plant nutrition.

Other investigations in the lab are focused on a relatively new area; genetic interactions between members of larger communities. A collaborative effort with Richard Preziosi at Manchester has yielded some very interesting results which show that that bacteria in the rhizosphere can significantly affect growth rates of above-ground insect herbivores and their predators. In addition researchers are looking at model phytoremediation systems to explore how plants may recruit bacteria into the rhizosphere to help degrade harmful contaminants, hence building functional rhizosphere communities.

Spotlight on the University of Manchester



Name Minsung Kim
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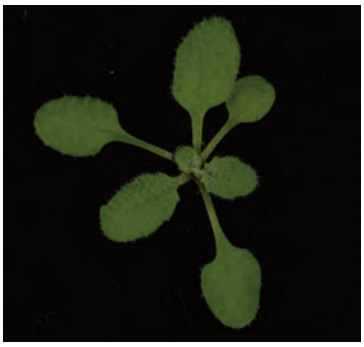
Research Area Evolution of leaf and floral form

Research Activities

Throughout the evolutionary history of plants, novel traits have emerged and disappeared, creating the incredible diversity of plant forms. To understand this diversity, it is essential to trace and test histories of underlying developmental mechanisms which generate certain traits or structures and identify how these genetic mechanisms were involved in the evolution of plant forms. Genetic changes responsible for morphological evolution could have been invented anew or recruited from the common toolkit of mechanisms that already existed. It is interesting to test if the same (parallelism) or different (convergence) genetic mechanism(s) were utilized to generate a novel trait or structure. It is also important to address why certain traits (or genetic mechanisms) are common in some groups but not others, and what selection pressures constrain a trait in a certain niche. Minsung is particularly interested in the evolution of genetic mechanisms controlling diverse flower shapes and leaf forms. Flowers and leaves are highly adapted structures and the key elements of plant evolution. Recent advances in understanding how model organisms develop, and enriched genome data from other related species, are providing a great opportunity to understand the evolution of developmental mechanisms controlling leaf and flower forms. The group are currently studying genetic components of leaf shape variation in Potentillas and Arabidopsis, and flower head development in *Senecio vulgaris*, an aster family.



Name Paula Kover
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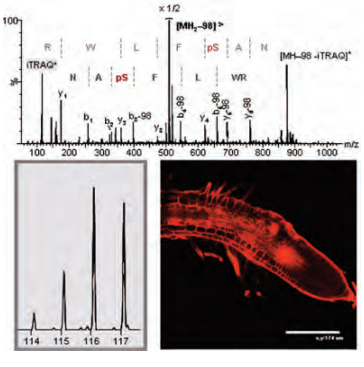
Research Area Natural variation in quantitative traits

Research Activities

Most traits of agronomical and economical interest (seed dormancy, flowering time, fruit production and disease resistance) vary quantitatively and are likely to have complex genetic inheritance. Their phenotypic expression is determined by the combination of many genetic and environmental factors. Much of the genetic basis of natural variation in plant growth and development remains unresolved. The goal of the Kover lab is to understand how genetics interacts with an organism's ecology to determine the evolution of traits under natural selection. To reach this goal the group aim to dissect the genetic basis of complex traits such as flowering time, branching and disease resistance, and study the evolutionary significance of this allelic variation under different environmental conditions. To achieve these objectives the lab is developing a new set of recombinant inbred lines derived from a heterogeneous stock, formed by the intermating of 19 Arabidopsis thaliana accessions; recombinant inbred lines from a heterogeneous stock (RIHS). This new resource significantly improves the ability to fine map QTLs in Arabidopsis, the data will also be supported by the resequencing of the 19 parental accessions. The intermated population is also being used to unveil the genetic basis of adaptation through artificial selection in the laboratory, and natural selection in the field.



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Research Area Cell wall feedback signaling

Research Activities

During plant growth, the rearrangement and *de novo* production of cell wall polysaccharides must be coordinated with the increase in cell size and surface area. How is information about the dynamics, composition and structural integrity of the wall fed back into the cell? Remodeling of cell walls also occurs during plant interactions with both symbiotic and pathogenic fungi and bacteria as well as with nematodes and parasitic plants. To what extent does the detection of cell wall damage contribute to plant resistance against invading microbes? Unlike in other eukaryotes, cell-matrix interactions are poorly understood in plants. Fungal cell walls also withstand osmotic pressure and require controlled rearrangement to allow growth. Here, a dedicated

Spotlight on the University of Manchester

Thomas Nühse Research Activities Contd.

integrity signaling pathway monitors cell wall status during growth, differentiation and stress. Identifying the analogous pathway in plants is the central effort in the lab. Quantitative phosphoproteomics is used to study the acute response to cell wall damage, such as inhibition of cellulose biosynthesis with the herbicide isoxaben. Focusing on plasma membrane-associated proteins, individual phosphorylation sites are quantified on the level of peptides with mass spectrometry. The long-term goal is to understand the role of cell wall integrity signaling in development and its connection with other stress and immune signaling pathways.

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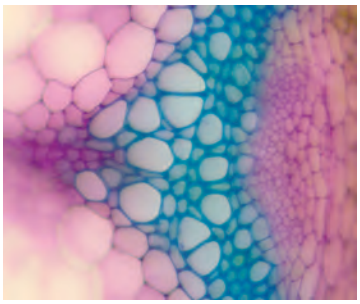
Research Area	Genetics of species interactions, conservation and evolutionary ecology

Research Activities

All species are influenced by the environment in which they exist. Much of the environment a species experiences is comprised of the expressed genomes of other species. Work in the Preziosi lab focuses on the genetic basis of species interactions (community genetics) using both quantitative genetic and genomic approaches. Current research is being carried out using model plant–herbivore (Barley-aphid, Bean-aphid), plant–parasite (Barley-rhinanthus) systems and in complex natural ecosystems (Phorophyte-epiphyte associations in tropical forests).

Recent results from The Preziosi lab have demonstrated the importance of interactions between different genotypes of plants and aphids in response to different environments. For example the response of both plant and aphid to the presence of rhizosphere bacteria depends on the interaction between plant and aphid genotypes as well as the presence or absence of bacteria. If parasitoid wasps are added to the system, response in the parasitoid is mediated by the interaction between plant, aphid and bacteria. These results suggest that community structure and interactions between associated species are dependent on the specific combinations of genotypes present as well as species combinations.

This work has wide ranging implications for community dynamics, one of which is the role of genetic diversity in conservation. Other work by Richard's group looks at the genetics of biodiversity conservation, both in natural communities (tropical forests, UK grasslands) and in ex situ collections.



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Research Area	Cell wall biosynthesis and vascular development

Research Activities

Plant cell walls play a critical role in a whole range of industrially important processes, from food processing to paper production. Recently they have received considerable attention as a potential sustainable source of CO_2 neutral biofuels. However, there are several problems that need to be overcome before we can efficiently use cell walls. Research in the Turner lab is focused on the woody, secondary cell wall since this constitutes the majority of plant biomass. The secondary cell wall is composed predominantly of three polymers: cellulose, xylan and lignin. While it is possible to identify a number of targets that could improve cell wall quality, such as less cross-linking of carbohydrates to phenolics and greater cellulose content our lack of basic understanding, of how cell wall polymers are made, what controls cell wall quantity and composition and what physical properties different polymers confer upon the wall, limits our ability to make beneficial changes. In order to overcome the problems associated with a conventional biochemical approach the group has taken a genetic approach to identify *irregular xylem (irx*) mutants of Arabidopsis, which are deficient in several different cell wall polymers. More recently, the lab have used microarray-based expression data and reverse genetics to identify a large number of genes involved in secondary cell wall function. The current challenge is to understand the function of these genes, determine what they contribute to cell wall formation and how they function together as a system.

Science, Art and Writing (SAW)- the answer to outreach

Written by Anne Osbourn, John Innes Centre, Norwich Research Park, Colney Lane, Norwich. NR4 7UH

The Science, Art and Writing (SAW) initiative breaks down traditional barriers between the arts and sciences. SAW uses images from science as a starting point for scientific experimentation, art and creative writing and in doing so stimulates creativity and scientific curiosity. School children realise that science and the arts are interconnected – and they discover new and exciting ways of looking at the world. SAW projects stimulate exploration, enquiry and creativity. And they are fun!

How do you get involved in a SAW project? You may already have links with a school, perhaps as a parent or as a visiting scientist. Schools are always pleased to have scientists volunteer to go in and work with the children. The first step in setting up a SAW project is to talk with a teacher and define a scientific theme that you would both like to explore. This may be a science curriculum topic (e.g. photosynthesis or magnetism) or another relevant theme (e.g. the local environment) (you can see highlights of some examples of the SAW projects that have been run so far on the SAW Trust website [www.sawtrust.org]). Alternatively it could be your own scientific research area. Don't be frightened by this idea – you can manage to make your research area accessible to children!

Next, find high quality images that illustrate the science behind your chosen theme. These may be images generated by you/your colleagues or they may be images that you find on the internet. A very good source of keyword-searchable images can be found on the Science Photo Library website (www.sciencephoto.com). Assemble a collection of 6-8 carefully selected images illustrating the different facets of your scientific theme, making sure that these images are intriguing rather than obvious. The theme and images that you have will now form the starting point for adventures. You can go ahead and plan the science that you would like to do with the children based on this starting point. Define a lesson with some fun practical work. Work closely with the teacher on making sure that your plans are realistic, on identifying equipment needs and on risk assessment well in advance of the lesson. Examples of images selected by Sam Mugford and Melissa Dokkary (two young scientists in the Osbourn group) for a BBSRC-funded SAW project on plant-derived natural products are shown in figure 1. Sam and Melissa worked with teacher Heather Delf and children aged 7-9 at Martham Primary School, Norfolk (figure 2). In selecting the theme and images and planning your science lesson you should never underestimate what children can take onboard and enjoy. Don't talk down to them. They are little philosophers – just like you, but smaller (although you will, of course, need to avoid jargon and use accessible language). Maybe they can even solve some of your research problems!

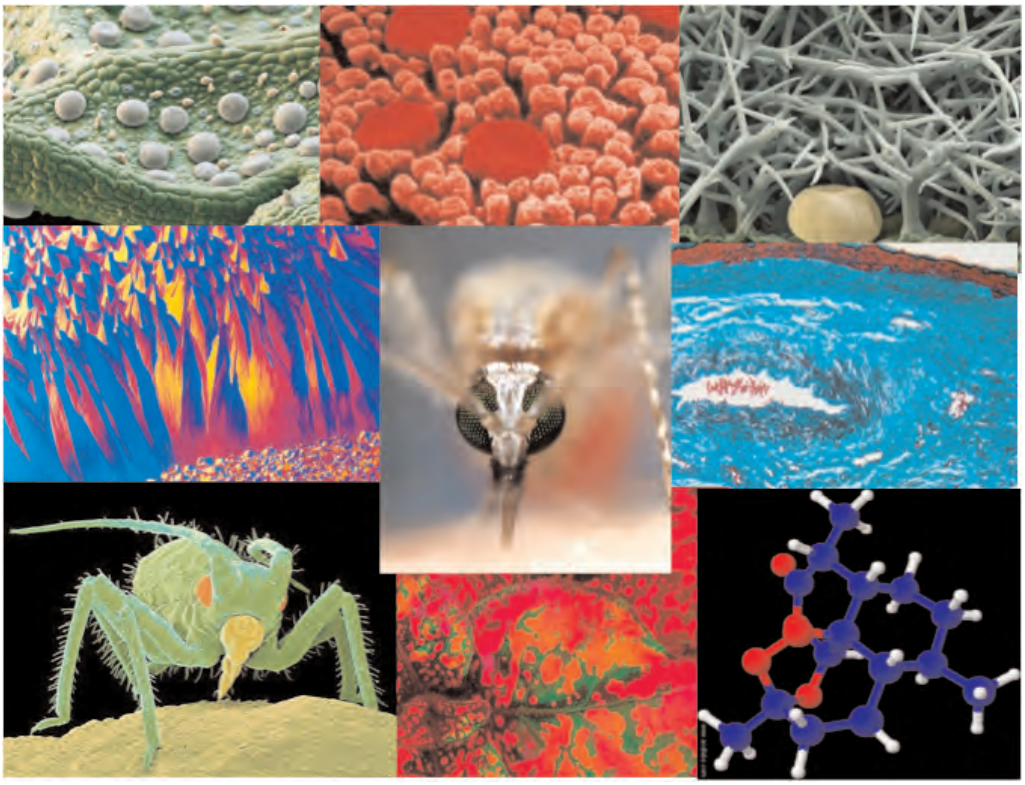

Figure 1 Scientific images chosen by Sam Mugford and Melissa Dokkary, two young scientists in the Osbourn group, for a SAW project on plant-derived natural products. Full descriptions of indivdual images listed at end of article.

Figure 2 Melissa Dokkary (left) and Sam Mugford (right) showing 7-9 year olds at Martham Primary School, Norfolk, how to extract and analyse pigments from plants.

The theme that you introduce in your science session can then be explored in subsequent lessons through visual art, poetry and perhaps other approaches too (with the teacher and perhaps also with visiting artists, poets, etc). This will provide an intense learning experience for the children – total immersion in the theme. The images provide a crucial anchor in this process as the children move from science to the other disciplines. In the Martham Primary School project the children did some three dimensional "molecular modelling" inspired by the structure of the malaria drug artmesinin with artist Chris Hann (figure 3). They also wrote some beautiful poetry with poets Mike O'Driscoll and Joe Mugford (see opposite).

Science, Art and Writing (SAW) - the answer to outreach

So – have a go with SAW. Experiment with it. Have fun. You can find out more about SAW by reading See Saw, an anthology of children's poetry and artwork on scientific themes from the first SAW project (SAW Press, 2005; ISBN 0-9550180-0-5), by visiting the SAW Trust website (www.sawtrust.org) and/or by contacting Professor Anne Osbourn (anne.osbourn@bbsrc.ac.uk). Perhaps its time for a new version of the Arabidopsis manual – written by 7-9 year olds?

The SAW Trust (registered charity no. 1113386) depends on grants and donations to support its activities. Donations are gratefully received and should be sent to Anne Osbourn, John Innes Centre, Norwich NR4 7UH, made payable to the SAW Trust. Anne Osbourn would like to thank Society in Science and the BBSRC for funding for her outreach activities.

Figure 3 "Modelling" the structure of the malaria drug artemisinin.

Reference

Osbourn A, Pirrie J, Nicholson J, Holbeck K and Hogden S (eds). (2005) See Saw. An anthology of Poetry and Artwork around Science by children from Rockland St. Mary County Primary School and Framingham Earl High School, Working with Matthew Sweeney and Jill Pirrie. The SAW Press, Norwich, UK. ISBN 0-9550180-0-5.

Figure 1 Legend - From top left to bottom right:
1. The surface of a mint leaf showing the trichomes (specialised cells that store the chemicals that give mint its smell and taste). Image: Eye of Science/Science Photo Library
2. A human tongue. Image: Omikron/Science Photo Library
3. The surface of a lavender leaf. The round structure is a gland that stores lavender oil. Image: Eye of Science/Science Photo Library
4. Polarised light micrograph of crystals of taxol. Taxol is an important anti-cancer drug found in the bark of yew trees. Image: Michael W Davidson/Science Photo Library
5. A mosquito sucking up blood. Mosquitoes carry the parasite that causes malaria. Image: Sinclair Stammers/Science Photo Library
6. The skin inside a nose. Image: Astrid Kage/Science Photo Library
7. An aphid feeding on a leaf. Many plants make chemicals that provide protection against attack by aphids. Image: Volker Steger/Science Photo Library
8. Coloured leaves. Image: Steve Taylor/Science Photo Library
9. Molecular model of artemisinin, a drug produced by wormwood (*Artemesia annua*). This compound is a very important drug for treatment of malaria. Image: Sam Mugford

Selected Poems

Scaly, Green Sea Monster

Scaly green sea monster in the dark, gloomy ocean.
Frightening other creatures and devouring them.
Taste buds appear like white chocolate buttons.
Spots stick to his crinkly back and cover his massive spongy tail.
He has prickly horns, vicious jaws and a thousand eyes.
His skin is as green as a Christmas tree.
With his quick reflexes, no one dare go past.
One sudden movement from his fearless jaws
And a fish disappears in seconds.
The scaly sea monster rules the ocean,
Nobody goes near.

Alex Sawyer Year 3

Plant Science

Leaves with millions of molecules
Fighting plant-eating bugs.
Multi-coloured petals wave
At the tips of long, thin stems.
Bright yellow pollen is collected
By busy, buzzing bees.
Spotted red ladybugs
Drift through the air.
Bright petals spring forth
Like a Jack in a box.
Lovely purple lavender
fills the air with a colourful scent.

Xena Dyball Year 4

Science Nose

As I crush the molecules with my fingers
Cells explode like a bomb.
Chemicals zoom upwards into my nostrils.
Strange smells make my brain dance.

Lloyd Sayer Year 4

Crushing Leaves

Crushing up the delicate plant leaves
Creating a dark green spinach-like paste.
I pour it slowly into the plastic test tube
It reminds me of chlorophyll glue.

Sian Tibble Year 4

A crowd of people looking up to the sky

A crowd of people in a restaurant,
Waiting for their food.
Strawberries, tomatoes, spaghetti bolognaise.
Red icicles, like fruit sweets,
Squidgy and gooey like marshmallows and peas.
Bright pink coral under the sea.
People with their tongues hanging out,
Tasty, microscopic molecules
Drowning in a whirlpool of flavours.

Darcie Lines Year 4

Spreading Colours

Colourful flames, the light looks alive,
Spreading slowly across the paper.
Multi-coloured molecules
Chemicals mixing together,
Sparkling in the light,
Dancing in the alcohol.

Olivia Hesseltine Year 3

SEB Plant Symposium / GARNet2008

University of Nottingham
September 8 - 10, 2008

Meeting Themes

Light and Environment
Nutrients
Floral Initiation / Evolution
Reproductive Biology
Hormones and Signalling
Cell Biology and Imaging
Systems Biology

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Speakers to Include

Mark Aarts (Wageningen)
Malcolm Bennett (Nottingham)
Vicky Buchanan-Wollaston (Warwick)
Tzyy-Jen Chiou (Academia Sinica, Taipei, Taiwan)
George Coupland (MPI Cologne)
Caroline Dean (JIC)
Peter Doerner (Edinburgh)
Ueli Gronsilakus (Zurich)
Nick Harberd (Oxford)
Alistair Hetherington (Bristol)
Patrick Hussey (Durham)
Marc Knight (Durham)
Jeff Leung (Gif-sur-Yvette)
Ottoline Leyser (York)
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Natasha Reikel (UC Riverside)
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