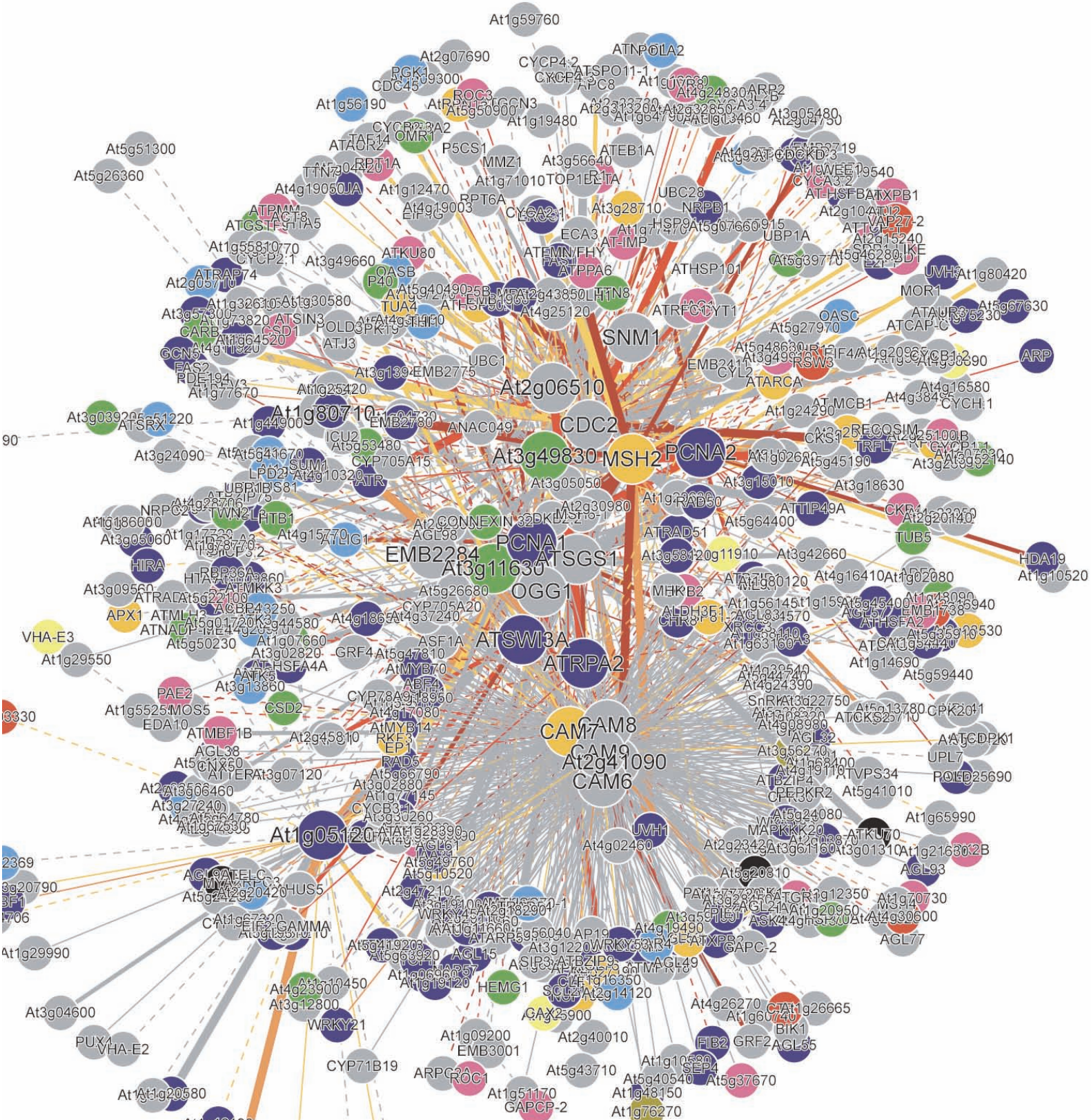


# GARNish

The official GARNet Newsletter



**BioGRID**  
**Reactome**

## Editorial

Previous issues of GARNish have set a high standard and we are heartened to know that readers find it a valuable source of information (2008 GARNet survey). We hope this 10<sup>th</sup> issue will be no exception. To keep you abreast of emerging developments, we present two articles describing new web-based datasets compiled and curated from the Arabidopsis literature. BioGRID documents protein-protein and genetic interactions for major eukaryotic model organisms including *Arabidopsis thaliana*. Given that the 2008 GARNet community survey identified a protein-protein interactome as the dataset you would find most useful for facilitating systems biology research, we are sure that you should find this article informative. Similarly useful is the article on the Arabidopsis Reactome, a curated knowledgebase of plant biological pathways currently being developed at the John Innes Centre. Also in this issue, our 'spotlight' series focuses on the breadth of plant science research being pursued at the universities of Lancaster, Leeds, Leicester and Liverpool. We also continue the initiative instigated by previous editor, Patrick Hussey, to highlight work that engages school-age children in the sciences, particularly the plant sciences. The Living Field at SCRI is one such initiative which incorporates a community garden and a study centre that are open to the public (and well-used by local schools) with a free CD-Rom downloadable from their web site.

Looking forward to 2009, work is already well-underway in preparation for the 20th International Conference in Arabidopsis Research (ICAR) which is to be hosted between 30<sup>th</sup> June and 4<sup>th</sup> July, in Edinburgh, by GARNet. ICAR is the essential annual platform allowing the international Arabidopsis community to keep up-to-date and exchange information, and the 20<sup>th</sup> meeting already has an impressive list of confirmed world-renowned speakers (including Jian-Kang Zhu, Mark Stitt, Ben Scheres, Andrew Millar, Alistair Hetherington, Nicholas Harberd, Jiri Firml, Joe Ecker, Caroline Dean and Enrico Coen). The Edinburgh meeting will be more geographically accessible to a wider proportion of UK researchers than recent previous meetings in Montreal and Beijing, or future meetings in Japan (2010) and USA (2011), so make sure to register early (at <http://arabidopsis2009.com/>) to secure your place!

Also being co-organised by GARNet (along with CPIB, The Centre for Plant Integrative Biology) is the 2nd Mathematics in Plant Sciences Study Group to be held on 5-8 January 2009 at University of Nottingham (see <http://cpib.info/study2008/index.shtml>). Over 30 mathematicians attended the first MPSSG and made significant progress in tackling five problems posed by plant scientists, initiating several new collaborations.

Finally, GARNet extends its very warmest congratulations to Prof. David Baulcombe who won this year's Lasker Award for Basic Medical Research – a very public demonstration of how fundamental plant biology research can make discoveries of such generality and importance that they have direct impacts even on medicine.

Wishing you all a very happy Christmas and a successful 2009.

Claire Halpin and Ruth Bastow

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Front cover image kindly supplied by Nick Provart. Many thanks to all who contributed to this issue, particularly Janet Higgins, Andrew Winter, Jie Song, Jane Taylor, Brendan Davies, Paul Jarvis, Anthony Hall, Debbie Harding and Claire Halpin.

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](mailto:ruth@arabidopsis.info).



## News and Views

### BBRSC Committee restructuring

BBRSC has recently announced changes to the way its peer review committees are organised. The changes follow extensive consultation with the BBRSC research community through a series of roadshows, and will ensure that BBRSC can deliver its mission of "Excellence with Impact".



The changes to Committee structure are in response to rapidly evolving changes in biological sciences such as genomics, systems biology, synthetic biology, nanotechnology etc., many of which are data rich and require extensive numerical data management and analysis and interdisciplinary approaches, as well as new tools and technologies to manage and exploit these data. It was felt that the current seven Committee structure with their fixed remits was increasingly unable to accommodate these scientific and technological changes, and that BBSRC needed to deliver more inter-disciplinary and strategically focussed science with greater demonstration of the impact of this science.

The changes will create four new research committees from the existing seven, comprising A: Animal Systems, Health & Wellbeing; B: Plants, Microbes, Food & Sustainability; C: Technological & Methodological Development, and D: Molecules, Cells & Industrial Biotechnology. These new committees will not have fixed remits, and will have a mixed membership of core members and a pool of reviewers to be co-opted for their specific expertise to allow much greater flexibility in assessing multi-disciplinary proposals. Other changes include: creation of a smaller number of policy and research priorities that will help researchers to consider the strategic relevance of their proposals when they make applications.

The new committees will still consider responsive mode, investigator-led proposals and the overall BBSRC remit will remain the same.

The first grants to be reviewed under the new system will be those submitted for the 14 January 2009 closing date. Applications submitted to the Winter grant round (15 October 2008 closing date) will continue to be reviewed using the old system.

Full details of the changes are available at: [www.bbsrc.ac.uk/funding/grants/roadshows.html](http://www.bbsrc.ac.uk/funding/grants/roadshows.html)

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### Of Models and a Man - David Baulcombe Wins the Lasker Award for Basic Medical Research

GARNet warmly congratulates Prof. David Baulcombe FRS on winning the 2008 Lasker Award for Basic Medical Research. Prof. Baulcombe received the award along with Victor Ambros (University of Massachusetts) and Gary Ruvkun (Massachusetts General Hospital) for ground-breaking work on small RNA molecules that regulate gene function in plants and animals. Prof. Baulcombe has recently become Professor of Botany at the University of Cambridge but conducted much of his pioneering research into small RNAs at the Sainsbury Laboratory, John Innes Centre.

In his commentary article published in *Nature Medicine* [1] 'Of maize and men, or peas and people: case histories to justify plants and other model systems', Prof. Baulcombe explains the evolution of his thinking and his discoveries in the small RNA field since the mid-1980s. The paper champions the use of plants as model systems with equal value to yeast, worms and other models, and cites several fundamental biological discoveries that were originally made in plants. These include Hooke's discovery of cells in cork in the seventeenth century, Mendel's pioneering genetic studies in peas, and McClintock's identification of mobile genetic elements in maize. In the case of small RNAs, it was early work on genetic modification that aimed to engineer virus resistance into tobacco via the introduction of viral genes (parasite-derived resistance), that set Baulcombe on the road to discovering the world of small regulatory RNAs. His subsequent work demonstrated the existence of small RNAs in plants, helping to bring attention to earlier work of Ambros and Ruvkun describing similar small RNAs in the worm. These discoveries along, with the work of Fire and Mello that demonstrated the involvement of double-stranded RNA in RNA-interference, laid the foundations for an explosion of research in the area. This ultimately led to the current understanding of the widespread roles of small RNAs and RNA silencing in regulating gene expression in plants and animals and in human health and disease.



1. Baulcombe D (2008) *Nature Medicine* 14: xx-xxiii. Also available at [http://www.laskerfoundation.org/awards/pdf/2008\\_b\\_baulcombe.pdf](http://www.laskerfoundation.org/awards/pdf/2008_b_baulcombe.pdf)

# Arabidopsis Reactome: A curated knowledgebase of plant biological pathways

<http://www.arabidopsisreactome.org>

Janet Higgins, Matthew Couchman, Michael Bevan and Sean Walsh. John Innes Centre, Norwich Research Park, Colney, Norwich, NR4 7UH, UK  
Authored and peer reviewed pathways by Alison Smith, John Doonan and Georg Seifert

## A Resource for the Arabidopsis Community

Arabidopsis Reactome [1] enables the computational analysis of biological knowledge through the capture of published information about biological pathways and processes. It provides the Arabidopsis research community with a platform to collate and analyse large amounts of data relating to molecular function. This leverages numerous applications in functional genomics, comparative genomics and in systems biology.

Pathway information is particularly challenging to compile and curate. Each pathway within the knowledgebase is derived from a mass of biological information distributed across multiple publications and other databases. This knowledge is mapped to an expressive and generic data model which is part of a software package developed to implement the human Reactome [2]. Other Reactomes are currently being developed for chicken, fruit fly, the nematode worm and Archaea.

In the Arabidopsis Reactome project we chose to import pathways from KEGG and AraCYC to make it a useful resource from the very beginning. We have manually curated a selection of pathways to demonstrate the potential of Reactome. Now we face the challenge of manually curating many more pathways with the help of expert scientists to increase the coverage from ~8% of the Arabidopsis proteome, making it more relevant to a wider range of plant research areas.

## Pathway Knowledge by Experts

Scientists who are already familiar with a given research field are best placed to make expert judgements on what constitutes good evidence for a reaction or pathway. These community-minded expert authors work together with the Reactome curator to create an electronic outline which defines the exact scope of the biological process to be curated, and to identify and order the reactions. This process is supported by a graphical Author Tool; the Systems Biology Graphical Notation (SBGN) version is shown in Figure 2. A PowerPoint presentation on authoring a pathway can be downloaded from the website. The completed pathway is peer-reviewed by another expert to ensure that the pathway reflects current understanding.

Curation of a pathway in Reactome is a useful addition to a review paper or research publication. It enhances impact, ensures free and open access to key reactions, and contributes to a unified network of metabolism, signalling and genetic control. Future objectives include working with journals to encourage the deposition of pathways into this resource.

We hope to extend the use of Reactome to the UK Arabidopsis research community. To start this process we will conduct a survey to identify research groups who would benefit through collaborative authoring and analysis of Reactome pathways and to prioritise these areas of biology for inclusion. To register an interest, please email [help@arabidopsisreactome.org](mailto:help@arabidopsisreactome.org).

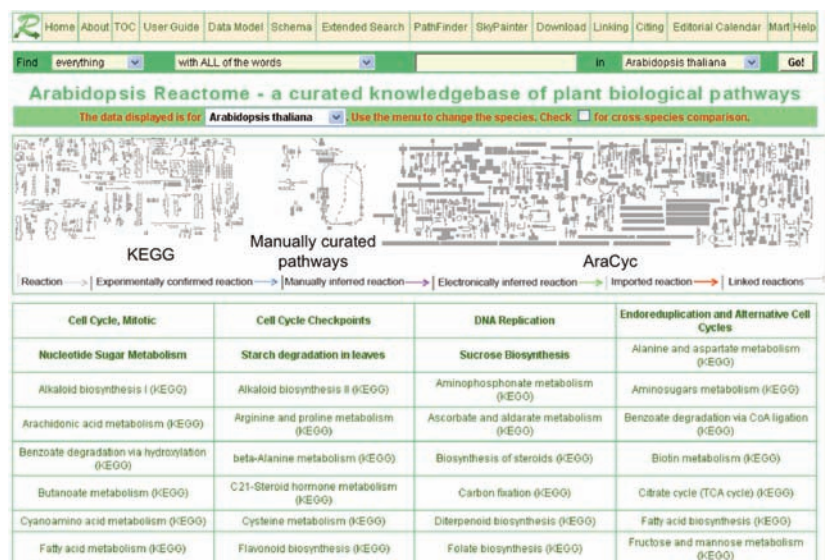


Figure 1. Overview of the Arabidopsis Reactome Home Page

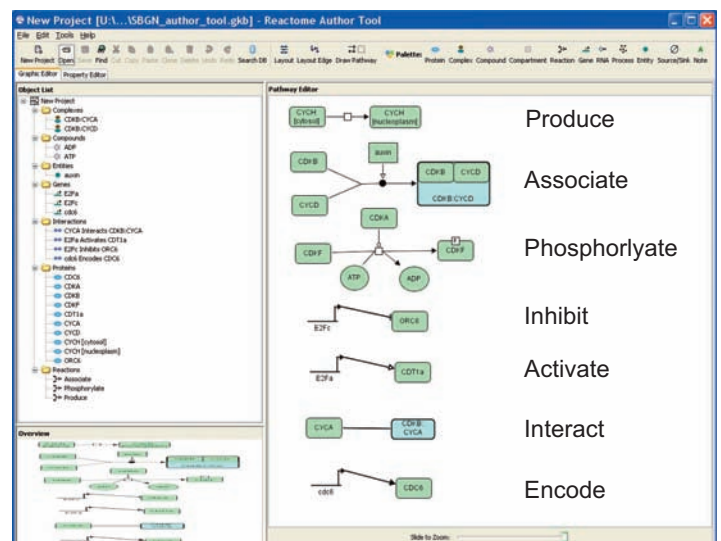


Figure 2. Author Tool for capture of pathway using SBGN glyphs

# Arabidopsis Reactome: A curated knowledgebase of plant biological pathways

## Using the Arabidopsis Reactome Resource

### SkyPainter – over representation analysis

This allows researchers to query the database with a list of genes from an experiment and find which pathways the genes are involved in. An example is shown in Figure 3 for a list of genes that have been up-regulated in response to the addition of glucose which co-ordinately induces a set of genes involved in cell division.

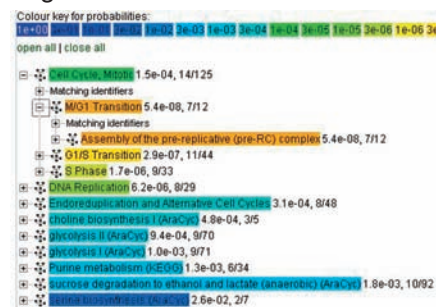


Figure 3. SkyPainter Overrepresentation Analysis of Glucose-Responsive Genes

### SkyPainter – movie

Changes in gene expression over a series of experimental samples can be visualised. Figure 4 shows the expression of cell cycle genes showing a peak in mitosis at the 12 hr timepoint in a synchronised cell suspension. The complete movie can be viewed at <http://www.plantcell.org/cgi/content/full/tpc.108.057976/DC1>

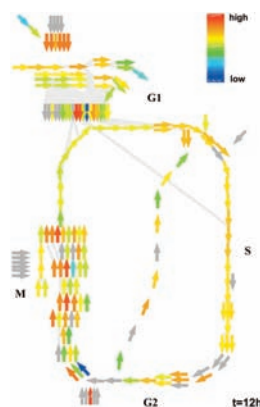


Figure 4 SkyPainter Analysis of a Cell Cycle Time-Course

### Merging with protein-protein interaction datasets

Pathways curated in Reactome can be merged with protein-protein interaction datasets. Pathways can be imported into Cytoscape in either BioPAX or SBML format and merged with protein-protein interaction datasets. Figure 5 shows the detection of clusters of interacting proteins highlighting additional proteins which interact with the cell cycle, that therefore are candidates for experimental investigation.

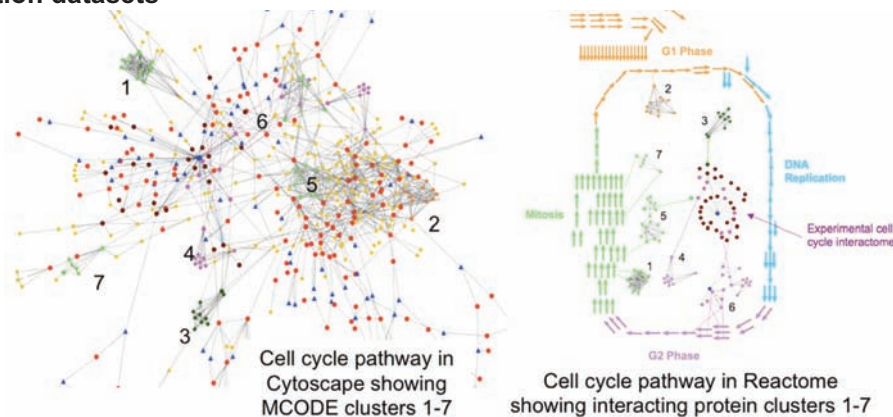
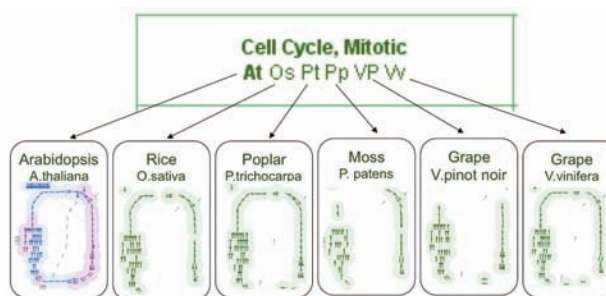


Figure 5 Pathway visualised in Cytoscape and Reactome

### Projecting pathways to other plant species

Arabidopsis Reactome pathways can be electronically projected to other plants with a complete genome sequence via putative orthologs. These inferred pathways are shown on the reaction map (Figure 6); they can be navigated and searched like the Arabidopsis pathways. The role of proteins in reactions and pathways can be used for annotation of newly sequenced genomes. In addition, protein-protein interaction datasets can be used to group proteins with similar function / in similar pathways.



| Experimentally confirmed reaction  
| Manually inferred reaction  
| Electronically inferred reaction

Figure 6 Electronically inferred pathways

1. Tsesmetzis *et al.* Arabidopsis Reactome: a foundation knowledgebase for plant systems biology. *Plant Cell*. 2008 Jun;20(6):1426-36.
  2. Vastrik *et al.* Reactome: a knowledge base of biologic pathways and processes. *Genome Biol*. 2007;8(3) R39.
- The Arabidopsis Reactome project is currently funded as part of the EU AGRON-OMICS. The project and was initiated through BBSRC BEP funding.

## The BioGRID database of protein and genetic interactions: A new focus on Arabidopsis

<http://www.thebiogrid.org> (Breitkreutz et al, NAR 2008, 36:D637-40)

Andrew G. Winter<sup>1</sup>, Julie Nixon<sup>1</sup>, Bobby-Joe Breitkreutz<sup>2</sup>, Chris Stark<sup>2</sup>, Lorrie Boucher<sup>2</sup> and Mike Tyers<sup>1,2</sup>

<sup>1</sup>School of Biological Sciences, The University of Edinburgh, Edinburgh, United Kingdom

<sup>2</sup>Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, Ontario, Canada

The BioGRID aims to systematically curate protein-protein and genetic interactions from the available literature for major eukaryotic model organisms. These literature-curated datasets serve as convenient look-up sources for biological interactions, as resources for network analysis, and as benchmarks for high-throughput interaction studies. Literature curation for the model yeasts *S. cerevisiae* and *S. pombe* has been completed (Reguly et al, J Biology 2006 5: 11-39) and is updated on a monthly basis; partial curation of interactions from *C. elegans*, *D. melanogaster* and *H. sapiens* is also ongoing. Here, we briefly describe the BioGRID web interface and the status of our recent efforts to curate interaction data for *Arabidopsis thaliana*.

### The BioGRID web interface:

BioGRID can be searched using gene names, and most gene, protein and sequence identifiers. Each page represents a gene, detailing names, links to other gene resources (including TAIR), and Gene Ontology terms. Interactor names are displayed as links to pages for those genes. Evidence codes supporting the interaction from a total of 16 physical and 9 genetic evidence types are presented, along with publications supporting the interaction (with links to PubMed). Downloads are available in a simple tabular format, or in the PSI-MI XML format and the Proteomics Standards Initiative data exchange format for molecular interactions. The entire BioGRID dataset can be downloaded in a single file, or in separate files for each organism or each evidence code.

### Arabidopsis curation at BioGRID:

Despite its importance as a eukaryotic model system, curation of Arabidopsis interactions has lagged behind that of other major model systems, with only a few hundred curated interactions recorded across different databases. As the extensive primary Arabidopsis literature reports protein and genetic interactions across virtually all areas of biology, Arabidopsis is a prime untapped organism for interaction curation, and imminent large-scale plant interaction datasets will be greatly leveraged by comparison to literature-derived interaction datasets.

We aim to systematically curate physical and genetic interactions from the entire Arabidopsis literature via a recently awarded Bioinformatics and Biological Resources grant from the BBSRC (UK). Our initial curation efforts have focused on circadian regulatory networks; we have curated all papers that cite one or more of the 50 known circadian clock-related genes (from an expert list kindly provided by Prof. Andrew Millar, University of Edinburgh). Curation of genetic interactions has proven difficult due to the complexity of phenotypes in *A. thaliana*, therefore our current literature-wide effort is focused primarily on protein interactions. We have systematically curated Arabidopsis publications from June 2008 onwards, as well as papers from Jan 2005 – June 2008 that were identified as 'most likely' to contain protein interactions as determined by the Textpresso text mining system (Muller et al, PLoS Biol 2004 2:e309). In addition, we are continuing to back-curate the literature as well as providing monthly updates for new papers. As of October 2008, we have examined over 2,500 publications (from a total of almost 26,000 in Pubmed that cite *A. thaliana*) and from these interactions have been curated for 237 papers. The resultant dataset comprises 966 redundant interactions (which include multiple sources and evidence codes) with 596 unique interacting pairs in a network of 459 proteins.

**BioGRID** BETA  
Search   
General Repository for Interaction Datasets  
home help / support contribute downloads mirrors about us

**At2g18790** *Arabidopsis thaliana*  
Aliases: MSF3\_17, PHYB, HY3, MSF3\_17, OOP1, OUT OF PHASE 1, PHYTOCHROME B, At2g18790  
Description: PHYB (PHYTOCHROME B), G-protein coupled photoreceptor/ signal transducer, protein coding  
Links: [Entrez-Gene] [TAIR]  
Gene Ontology: 14 total GO mappings for this record. [view list]  
Download interactions associated with At2g18790

Interaction Network Coming Soon...  
[JPG] [PNG] [SVG]

**At2g18790 was identified with 40 protein interactions and 15 genetic interactions**

Name	Aliases	Description	Evidence Code(s)	Role	Source(s)
At1g09530	• F14.9.T9 • F13 • F14.9.T9	PIF3 (PHYTOCHROME INTERACTING FACTOR 3), DNA binding / transcription factor/ transcription regulator, protein coding Gene Ontology: [View List]	Two-hybrid Reconstituted Complex	bait hit bait/hit	Reuss, E. (2006) Shen, Y. (2007) He, M. (1999) Martinez-Garcia, J. (2000) Shen, Y. (2000) Fackeldey, G. (2000) He, M. (1999) He, M. (1999) Shen, Y. (2004) Shen, Y. (2004) Shen, Y. (2002)
At3g59060	• PLE • PHYTOCHRO... • PHYTOCHRO...	PIF5 (PHYTOCHROME-INTERACTING FACTOR 5), DNA binding / transcription factor, protein coding Gene Ontology: [View List]	Biochemical Activity Reconstituted Complex Two-hybrid	hit bait hit hit	Shen, Y. (2007) Shen, Y. (2007) Shen, Y. (2004) Shen, Y. (2007)
At1g10470	• T10024.8 • ARR4 • ARR1	ARR4 (RESPONSE REGULATOR 4), transcription regulator/ two-component response regulator, protein coding Gene Ontology: [View List]	Two-hybrid Affinity Capture-Washout Reconstituted Complex	hit hit bait hit	Mira-Rodado, V. (2007) Svoboda, U. (2001) Mira-Rodado, V. (2007) Svoboda, U. (2001)
At2g25930	• F17W5.25 • ELF3 • EARLY FLO...	ELF3 (EARLY FLOWERING 3), protein coding Gene Ontology: [View List]	Two-hybrid Reconstituted Complex	bait hit	Liu, X. (2001) Liu, X. (2001)
At5g57360	• ZTL • ADO1 • PACT1-LIKE	ZTL (ZEITLUPE), ubiquitin-protein ligase, protein coding Gene Ontology: [View List]	Two-hybrid	bait bait	Reuss, E. (2006) Jenkins, J. S. (2001)

Figure 1. Screenshot of a typical BioGRID gene page

## The BioGRID database of protein and genetic interactions: A new focus on Arabidopsis

Analysis of the resultant data set (figure 2) illustrates that two-hybrid data constitutes almost half of the evidence for the curated Arabidopsis interactions, with *in vitro* reconstituted complex and *in vivo* affinity capture the next most prevalent evidence codes.

Currently, the largest component of the BioGRID Arabidopsis interaction network comprises about 50% of the network (shown below rendered in Cytoscape; Shannon *et al.*, Genome Res 2003 13: 2498-2504). The remainder of the nodes are less well connected with an average of 7 nodes per component. As curation progresses, we expect these components to become connected to the main body of the network. Alignment of these interaction networks with analogous networks from other species will enable prediction of new interactions and provide insight into conserved and divergent aspects of network architecture.

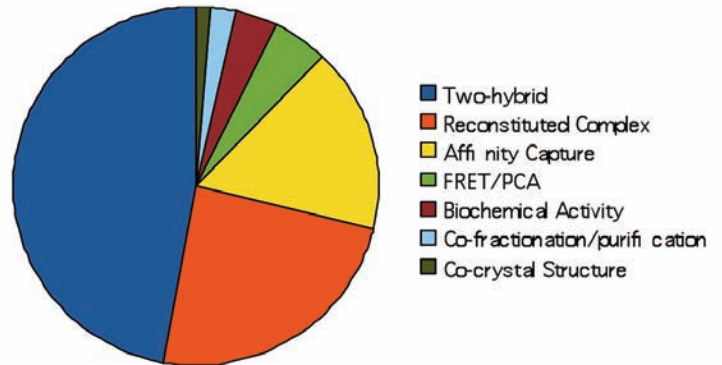


Figure 2. Analysis of Arabidopsis Interaction Dataset

### Future improvements:

In addition to continued curation, we will improve BioGRID associated functions including the ability to search on multiple fields, a web service to allow remote applications to link with BioGRID, graphical visualization tools to allow navigation through networks, and separate download options for high-throughput datasets. Sourcecode for BioGRID and the linked Osprey network visualization system are available without restriction from SourceForge. We welcome contributions of pre-publication and user-curated interaction datasets for deposition in the BioGRID. Please e-mail any questions, comments or corrections regarding the BioGRID to [biogridadmin@gmail.com](mailto:biogridadmin@gmail.com)

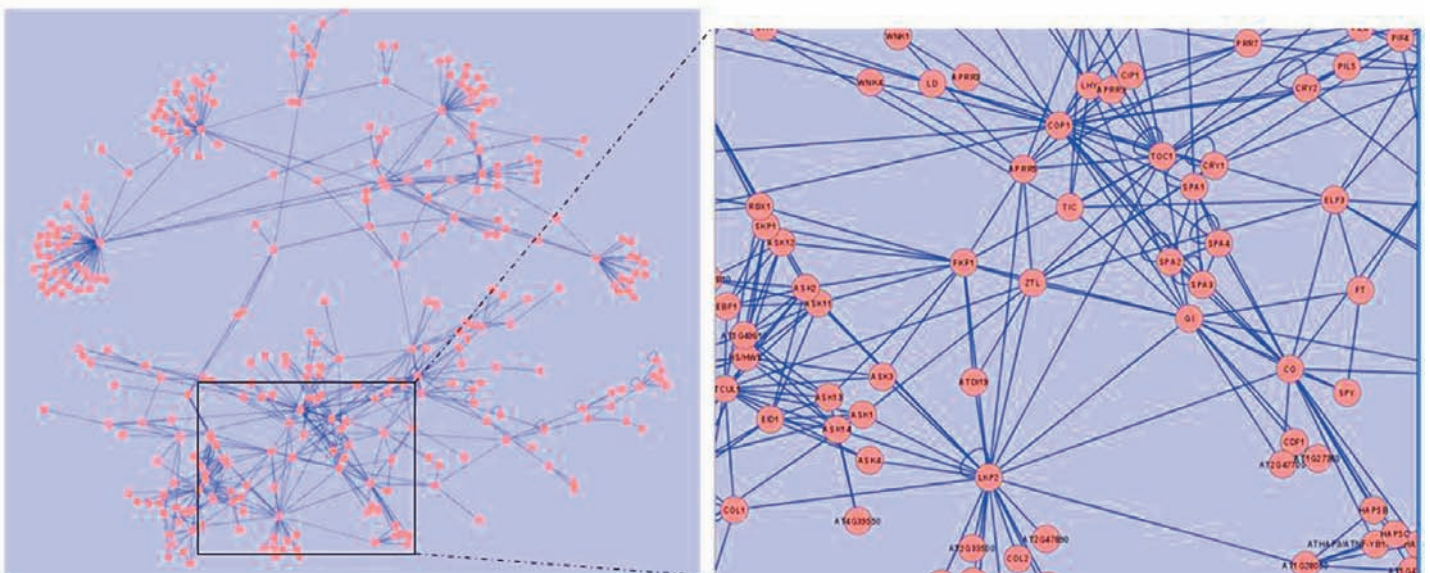


Figure 3. Biogrid Arabidopsis Interaction network

## GARNet - SEB Symposium 2008

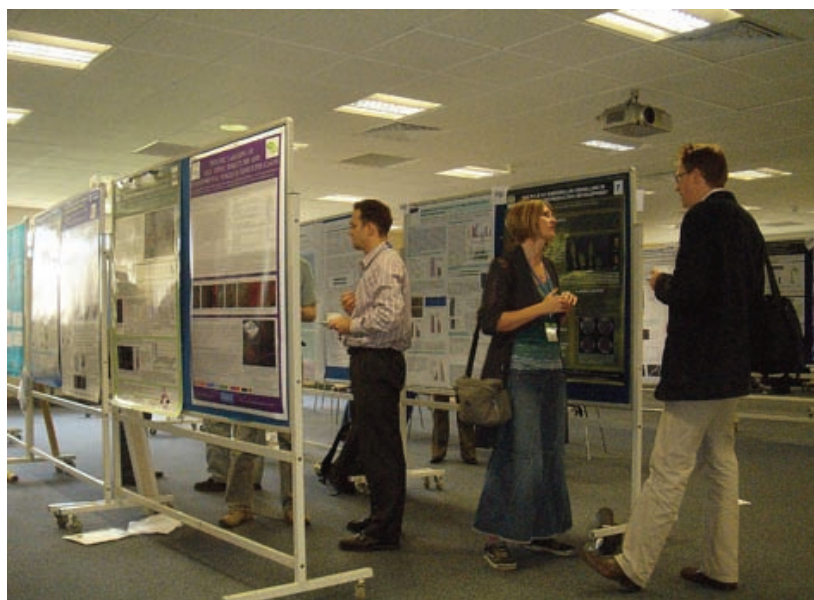
written by Jie Song, University of Nottingham, Plant Sciences Division, Sutton Bonington Campus.

This year's GARNet meeting was held jointly with the SEB Plant Symposium and provided an intensive three days of exciting talks and useful workshops, focusing on cell biology, plant growth and environment, reproductive biology, systems biology, existing and newly developed tools and resources. I enjoyed the meeting and so much loved the spirit and passion within the Arabidopsis community. Many thanks to the GARNet co-ordinators and the local organisers, for bringing us a brilliant meeting!

The first session was light and environment. Alistair Hetherington illuminated a complex intracellular signalling network controlling stomatal movements. Philip Mullineaux discussed how a water status signal transmitted into the chloroplast may control a retrograde signal to the nucleus. Kerry Franklin provided an insight into light and temperature crosstalk in plant environmental adaptation. Marc Knight discussed how plants adapt to low temperature by repressing the expression of *CBF/DREB1* through a novel protein SENSITIVE TO FREEZING6. Jeffery Leung described an innovative and powerful technique that combines biochemistry and mathematics to identify protein phosphorylation sites of the stress responsive OST1 kinase.



In the plant nutrient session, Peter Doerner talked about how phosphate availability influences root growth and development. To everyone's surprise, his data also suggested that the commonly used MS medium has an inhibitory affect on Arabidopsis root growth. For further information on the growth medium he used, please see Andrew Millar's letter in the Arabuk archives. Plant root systems develop into an amazingly complicated architecture, for optimal exploitation of diverse soil structure and nutrient conditions. Patrick Armengaud demonstrated how root architecture can be quantitatively analysed at real-time using their EZ-Rhizo software.



The second day focused on reproductive biology. Ueli Grossniklaus described the molecular basis of cell-cell communication during double fertilization and focused on a plant-specific receptor-like kinase *FERONIA*. David Twell presented their findings on the genetic control of male germ line development in Arabidopsis. Michael Holdsworth described how post-genomics approaches can be used in combination to investigate the control of germination. Zoe Wilson reported on the Arabidopsis *MALE STERILITY1* gene which plays a key role in tapetum degradation and pollen development. Her work also demonstrated how breakthroughs in Arabidopsis pollen biology can be applied to crop species of agricultural importance. Lars Ostergaard spoke about auxin dynamics throughout Arabidopsis fruit development and the valve margin identity factor *INDEHISCENT* involved in negative regulation of auxin polar trans-

port. Later, there were talks on a 'real' plant with eatable fruits, tomato. Maaïke de Jong reported on the *Solanum lycopersicum* auxin response factor 7 (*SIARF7*) which acts as a negative regulator of fruit set until pollination and fertilisation. Carol Wagstaff discussed senescence in Arabidopsis siliques in comparison to senescence in other tissues, leaf or petal, and its role in seed development and nutrition. The following session was on floral initiation/evolution. George Coupland reported on the study of vernalization response in both *Arabidopsis alpine* and Arabidopsis. Caroline Dean described how *FRIGIDA* causes plants to over-winter in the vegetative stage by up-regulating the flowering repressor *FLC*, and discussed how these pathways have changed in Arabidopsis variants adapted to different climates. Elaine Jensen talked about their study on flowering time in *Miscanthus* and the possibility of improving biomass yield and quality.



## GARNet - SEB Symposium 2008 continued

written by Jie Song, University of Nottingham, Plant Sciences Division, Sutton Bonington Campus.

Astrid Wingler discussed the correlation between leaf senescence and flowering time control and its genetic basis involving the interaction of functional *FRI* and *FLC* alleles. From the work on various plant species, including maize, orchids and tulips, Guenter Theissen reported that some classes of floral homeotic genes have been highly conserved throughout more than a hundred million years of evolution. Fabrizio Van Kerkhoven reported the analysis of a *CONSTANS* homolog in maize, *ZmCO*, which shared a similar expression pattern with *INDETERMINATE1*, a previously identified flowering time gene in maize.

On the third day, there were interesting talks on plant growth and development. Ottoline Leyser described how auxin, cytokinin, and a novel hormone control shoot branching. Their research suggested that this novel hormone functions by modulating auxin transport in the main stem, and thus may reveal an indirect mechanism for apical dominance. Nicholas Harberd focused on the GA growth regulatory network, and additional signalling pathways integrating environmental variables such as light, temperature and nutrient status. Daniela Dietrich reported the effects of ABA on root growth and architecture. Susana Ubeda-Tomas talked about investigations into GA signalling in root growth. Peter Etchells reported on the analysis of the regulation of vascular patterning, its key regulator PXY, and additional components of this signalling pathway. Filip Vandenbussche spoke about apical hook development and, involved in this process, auxin influx carriers, especially LAX3 and AUX1.

Later in the cell biology session, Natasha Raikhel described how chemical genetics served as a powerful tool in the study of protein trafficking. Again adopting a chemical genetic screen, Reka Toth reported their findings that an impaired actin network can result in altered circadian rhythmicity. Patrick Hussey discussed how cytoskeleton responds to signals and reorganise to support dynamic cell activities. John Runions provided evidence that alternation in the actin cytoskeleton might contribute to intramembrane protein dynamics in the ER and plasma membrane.

The final session was on systems biology. Currently, systems biology approaches and mathematical modelling are being developed and used to identify and analyze gene regulatory networks, including the control of root epidermal cell patterning and differentiation (John Schiefelbein), Arabidopsis leaf senescence (Vicky Buchanan-Wollaston), root growth and development (Malcolm Bennett). Tetsuro Toyoda described the Semantic Web, an information platform and a standard framework for arranging biological resources, and Andrew Millar provided updates on the modelling tool the 'Systems Biology Software Infrastructure'. There were also interesting workshops on various new tools, resources and developing technologies.

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## International Conference on Arabidopsis Research - ICAR 2009

GARNet is pleased to announce that the 20th International Conference on Arabidopsis Research will be held in the vibrant and historic city of Edinburgh, 30th June - 4th July 2009. <http://arabidopsis2009.com/> Registration for the meeting is now open <http://arabidopsis2009.com/registernow.html>.

To take advantage of the early bird discounts please make sure you register before March 27th 2009.

The preliminary programme of world-renowned speakers is now confirmed for ICAR 2009 and will include Enrico Coen, Caroline Dean, Joe Ecker, Jiri Firml, Nicholas Harberd, Alistair Hetherington, Andrew Millar, Ben Scheres, Mark Stitt and Jian-Kang Zhu. For a full meeting programme visit <http://arabidopsis2009.com/programme.html>

The program will include two plenary sessions each morning and four concurrent sessions each afternoon, which will include presentations chosen from submitted abstracts. As in the past, the conference will feature a number of community-led workshops that will provide opportunities for focused discussion, whilst three poster sessions will provide ample time for research discussion. Delegates will also have a free afternoon between the Friday morning sessions and evening poster session to engage in networking, scientific discussion and to explore Edinburgh and its surroundings.

### ICAR 2009 Deadlines

Abstract Submission Opens Jan 2009  
University Accommodation Available until 9th Jan 2009  
Early Registration Closes 27th March 2009  
Oral Abstract Submission Closes 1st April 2009  
Poster Abstract Submission Closes 1st May 2009  
Regular Registration Closes 15th June 2009



# New Phytologist Symposia 2009



22<sup>nd</sup> New Phytologist Symposium

## **Effectors in plant–microbe interactions**

Versailles, France 13–16 September 2009

Organisers: Marc-Henri Lebrun, Sophien Kamoun, Francis Martin, Nick Talbot.



23<sup>rd</sup> New Phytologist Symposium

## **Carbon cycling in tropical ecosystems**

Guangzhou, China 17–20 November 2009

Organisers: Yiqi Luo, Rich Norby, Juxiu Liu, Guoyi Zhou, Ian Alexander, Xuli Tang.

**For registration, information about grants, poster abstract submission and speakers visit**

[www.newphytologist.org](http://www.newphytologist.org)

# New Phytologist Tansley Medal

for excellence in plant science



The *New Phytologist* Tansley Medal will be awarded annually in recognition of an outstanding contribution to research in plant science by an individual in the early stages of their career.

Submissions are welcomed from both student and post-doctoral researchers with up to five years experience since gaining their PhD. The winner will receive a prize of £2000 and the successful article will be published in *New Phytologist*, which will be accompanied by a comment from the Editor-in-Chief.

### **Application process**

Submit an extended abstract (1000 words, with 1–2 figures) that describes (1) the research conducted, including the rationale, (2) methods, (3) key results and (4) the main conclusion, including key points of discussion. This abstract should be submitted along with your curriculum vitae, and a supporting statement from a scientist who has agreed to act as a referee for your application.

Successful applicants will be notified by Wednesday July 15<sup>th</sup> 2009 and asked to submit their work as a full research article no later than August 31<sup>st</sup> 2009. These articles will be reviewed by members of the *New Phytologist* Editorial board, and the winner announced by December 2009.

**Extended abstracts should be received by Monday 15<sup>th</sup> June 2009. To submit your application online or for further details please visit:**

<http://www.newphytologist.org/tansleymedal.htm>



New  
Phytologist

... promoting plant science

# THE SOCIETY FOR EXPERIMENTAL BIOLOGY ANNUAL MAIN MEETING GLASGOW 28<sup>TH</sup> JUNE - 1<sup>ST</sup> JULY 2009

## PLANT SESSIONS

SESSION TITLES

SPEAKERS INCLUDE

### Membrane Transport in Biotic and Abiotic Stress

Eduardo Blumwald (University of California at Berkeley)  
Julia Davies (University of Cambridge)  
Emanuel Epstein (University of California, Davis)  
Brian Forde (University of Lancaster)  
Frans Maathuis (University of York)  
Dale Sanders (University of York)  
Daniel Schachtman (Monsanto St. Louis)  
Mark Tester (ACPF, University of Adelaide)  
Gerhard Thiel (Technische Universität Darmstadt)  
Fangjie Zhao (Rothamsted Research)

### Flowering and Reproduction

Maria Albani (Max Planck Institute, Koln)  
Fuquan Liu (JIC, Norwich)  
Soraya Pelaz (CSIC, Barcelona)  
Salomé Prat (CNB, Madrid)  
Brian Thomas (WHRI, Warwick)

### Plant Responses to UVB

Carlos Ballaré (Institute for Agricultural Plant Physiology and Ecology, Argentina)  
Paula Casati (UNR, Argentina)  
Gareth Jenkins (University of Glasgow)  
Roman Ulm (University of Freiburg, Germany)  
Virginia Walbot (Stanford University School of Medicine)

### Photomorphogenesis

Giltsu Choi (KAIST, Korea)  
Chentao Lin (University of California, Los Angeles)  
Akira Nagatani (Kyoto University, Japan)  
Ida Ruberti (Università di Roma, Italy)  
Edgar Spalding (University of Wisconsin, Madison)

### Modelling Plant Systems: Molecules to Agro-ecosystems

Christian Fournier (INRA)  
Christophe Godin (INRIA)  
Graeme Hammer (University of Queensland)  
Steve Long (University of Illinois)  
Hendrik Poorter (University of Utrecht)  
Przemyslaw Prusinkiewicz (University of Calgary)  
Jean-François Soussana (INRA)  
Francois Tardieu (INRA, France)  
Fred van Eeuwijk (Wageningen University)  
Jan Vos (Wageningen University)  
Xinyou Yin (Wageningen University)

### Young Scientists in Plant Biology

We particularly encourage presentations by post-grads and post-docs and cash prizes will be awarded for the best talk and the best poster

## JOINT PLANT/CELL SESSION

### Leaf Form and Function

Jim Barber (Imperial College London)  
Gerrit Beemster (University of Ghent)  
Dominique Bergmann (Stanford University)  
Andrew Fleming (University of Sheffield)  
Christine Granier (University of Montpellier)  
Julian Hibberd (Cambridge University)  
Jim Murray (University of Cardiff)  
Neelimha Sinha (UC Davis)  
Miltos Tsiantis (Oxford University)

## CELL SESSIONS

### Protein Folding

Paul Workman (Institute of Cancer Research)  
Neil Bulleid (University of Manchester)  
Nigel Robinson (University of Newcastle)  
Simon Powis (University of St Andrews)  
Cheryl Woolhead (University of Glasgow)  
David Brockwell (University of Leeds)

### Evolution of Eukaryotic Cell

Tom Cavalier-Smith (University of Oxford)  
Christopher Cullis (Case Western Reserve University, Cleveland)  
Dennis Francis (University of Cardiff)  
John Raven (University of Dundee)  
Tom Richards (University of Exeter)  
Mark van der Giezen (University of Exeter)

### RMS Learning Zone

Part of the Royal Microscopical Society's remit to teach and improve microscopy, it offers scientists and technicians the opportunity to learn new techniques from their peers and the chance to discuss difficulties they may be having with specimen preparation.

### General Molecular Cell Biology

We particularly encourage presentations by post-grads and post-docs for these sessions

### General Thermal Biology

Submit a paper now - [www.sebiology.org](http://www.sebiology.org)

## 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 universities of Lancaster, Leeds, Leicester and Liverpool.

### Spotlight on Lancaster University



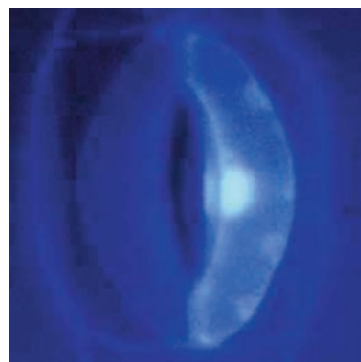
Plant Science research in Lancaster is situated in the Lancaster Environment Centre (LEC) which is a joint investment by NERC/CEH and Lancaster University. The plant scientists are part of the research theme 'Organisms and the Environment', one of four interdisciplinary research themes within LEC. The theme's primary research interests are in the physiological, ecological and evolutionary responses to the environment of individual organisms, communities and ecosystems. Research in the plant science group covers a range of topics and scales. At the cellular and molecular level, scientists study intra- and inter-cellular chemical signalling and water and ionic relations. At the crop and landscape scale, researchers investigate the mechanistic basis of responses to biotic and abiotic stresses, with a view to exploitation of this understanding in agriculture.



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**Research Area** Soil-plant interactions and nutrient cycling

#### Research Activities

The study of soil biological communities and their influence on ecosystem properties is a relatively new field of ecology. Although it has been known throughout history that soil organisms are integral to soil fertility, it is only during the last few decades that ecologists have begun to explore soil communities and their functional significance for plant communities and ecosystem processes. The Soil and Ecosystem Ecology Laboratory at Lancaster is interested in exploring the various roles that soil organisms and biotic interactions in soil play in terrestrial ecosystems, with special focus on their contribution to nutrient cycling and the productivity and diversity of plant communities. The group's work is mainly focused on grasslands, but researchers also carry out research in a wide range of ecosystems, including temperate and tropical forests, and arctic and alpine tundra. Recent projects focus mainly on aspects of nitrogen and carbon cycling, and include studies on: (a) how changes in vegetation diversity and composition influence the sequestration of carbon in soil as a result of altering C inputs to soil and their processing by the microbial community; and (b) the significance of organic N use by plants, and understanding how plants compete with microbes for different chemical forms of N, and how preferential use of N forms might provide a mechanism to partition the N pool and hence contribute to species coexistence. A number of other studies are considering how herbivores influence plant-soil interactions and the significance of this for ecosystem nutrient cycling and carbon storage.



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**Research Area** Drought stress biology and sustainable use of water in agriculture

#### Research Activities

The Davies lab works to understand the factors controlling the growth and functioning of plants under drought stress. The group have helped elucidate a role for long distance chemical signalling in droughted plants and shown that plants have the capacity to 'measure' the water available to them in the soil and communicate this information to the shoot. Analysis suggests that stomata can process root signalling information along with other climatic impacts, and the combined effect is a regulation of stomatal behaviour such that the processes in the leaf that are most sensitive to environmental stress are effectively protected. Even well watered plants contain sufficient ABA to modify stomatal behaviour if the pH relations of the leaf are appropriate. Current work in collaboration with CEH Bangor shows how even modest increases in tropospheric ozone concentration (a component of climate change) can disrupt the plant's capacity to control water balance through chemical regulation of stomata.

## Spotlight on Lancaster University



**Bill Davies Continued**

### Drought stress biology and sustainable use of water in agriculture

#### Research Activities

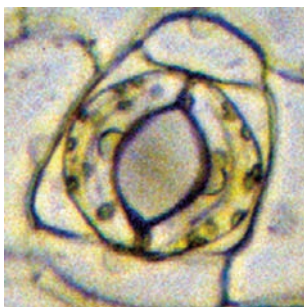
Against a background of increasingly limited water resources, there is a need to develop efficient crop production systems in which water and nutrients are utilised effectively in line with principles of sustainable development. In recent years, a novel irrigation technique (Partial Rootzone Drying, PRD) has been developed to exploit new understanding of plant long distance signalling. This technique has delivered substantial increases in water (and nutrient) use efficiency into agriculture on several continents. Current work addresses the possibility that naturally occurring rhizobacteria can impact on chemical signalling via the production or the metabolism of plant growth regulators. Field testing suggests that introduction of such low cost soil additives into agriculture can result in 'more crop per drop' when irrigation water is not available or in short supply.



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**Research Area** Plant-nutrient interactions

#### Research Activities

Of the many functions performed by plant roots, the most important is the extraction of water and nutrients from the soil. To achieve this efficiently in the face of competition from other organisms, roots have acquired a sophisticated suite of adaptations. Understanding the molecular basis of these adaptations will be important for improving crucial agronomic traits such as nutrient-use efficiency. The Forde lab is particularly interested in the molecular processes that underlie patterns of 'foraging' behaviour in plant roots. The efficiency with which roots explore the soil is greatly enhanced by their ability to preferentially colonise nutrient-rich soil patches. Using *Arabidopsis* as a model, Brian's group has previously identified a MADS-box gene (*ANR1*) which is a key component of a signalling pathway that enables root growth to respond positively to the external presence of nitrate. By engineering transgenic lines in which *ANR1* over-expression is dexamethasone-inducible, the group have shown that up-regulation of *ANR1* in one part of the root system is sufficient to initiate a 'foraging' response, even in the absence of nitrate. Recent progress, in collaboration with Alain Gojon's group at INRA-Montpellier, suggests that the identity of the long sought-after 'nitrate sensor' that lies upstream of *ANR1* may now be known. Current evidence suggests it takes the form of a protein previously known for its role as a dual-affinity nitrate transporter, *NRT1.1*. Other work is looking at the ability of root tips to respond to external signals from the amino acid L-glutamate (L-Glu). It now appears that the external presence of L-Glu (but not other amino acids) is able to induce major changes in *Arabidopsis* root architecture that are quite distinct from those elicited by nitrate. Using a combination of approaches, including QTL mapping and forward and reverse genetics, Brian's group is aiming to determine the molecular basis of the root's ability to sense external L-Glu.



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**Research Area** Plant stress signalling

#### Research Activities

Environmental stresses such as drought, increased atmospheric levels of carbon dioxide and pollutants, are major limiting factors to plant growth that have the potential to affect both biodiversity and agricultural productivity. These stresses therefore have significant ecological and economic consequences and can deleteriously affect food availability. Furthermore, predicted changes to the global climate and continued population growth will put increasing pressures on agriculture. The McAinsh lab is interested in the response of plants to environmental stresses at the community, whole plant, cellular/molecular levels. Research in the lab focuses on the role of calcium ions as signalling molecules and the regulation of apoplastic calcium in the response of wild and crop plants to climate change-related stresses. The work aims to address outstanding questions relating to signal specificity and crosstalk between the signalling pathways by which these plants respond to environmental stresses. These studies are extending our understanding of the molecular basis of stress tolerance, and the impacts of climate change on crops, vulnerable plant communities and the maintenance of biodiversity, and in doing so, are providing exciting insights into potential targets for mitigating these effects.

## Spotlight on Lancaster University



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**Research Area** Whole plant responses to biotic and abiotic stresses

### Research Activities

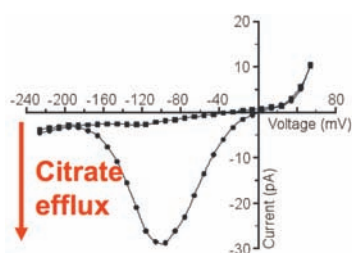
Nigel is a whole-plant biologist who looks to link ecophysiological responses to the larger scale of organisation of natural or agro-ecosystems. His research falls into two broad areas with the shared priority of building links between fundamental plant science and its application in sustainable agriculture and horticulture. His interest in interactions between plants and their natural enemies, invertebrate herbivores or pathogenic microbes, is founded on understanding the ecology of such interactions in non-crop systems (e.g. *Senecio vulgaris* or *Rumex* spp. and their associated pathogens and herbivores). His interest in the ecology and physiology of these systems has expanded to build links between ecological studies of defence (especially defence against multiple enemies) and molecular research into similar topics (in collaboration with Mike Roberts and Jane Taylor at Lancaster). These cross-disciplinary studies have formed the foundation of more applied research into new approaches to pest and disease control in sustainable agriculture. His other focus is the effect of solar UV radiation, which was originally stimulated by concerns over increases in the intensity of UV-B radiation reaching the biosphere as a result of stratospheric ozone depletion. However, much of his current research into UV radiation now has a strong applied thrust, seeking to exploit biological responses to UV (of crops and their pests and pathogens) in sustainable horticulture.



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**Research Area** Regulation of plant responses to stress

### Research Activities

Even under intensive farming practices, crop yield is limited by environmental stress. Abiotic stresses such as variations in light, temperature and water availability, and biotic stress, such as attack by pests and pathogens, both have negative impacts on plant growth. Plants have a range of tolerance and resistance mechanisms to help them cope with such stresses, and understanding how these defences interact and are regulated is important in maximising yield. Research in the Roberts lab currently focuses on understanding the regulation of plant stress responses at the molecular level, and in particular, how different stresses interact. The group use mechanical wounding, insect herbivory and plant pathogen interactions as models in both *Arabidopsis* and tomato. On the applied side, the group are helping to increase our knowledge of plant pest and disease resistance systems to develop 'natural' techniques to enhance endogenous defence mechanisms in crop plants. These approaches take advantage of the potential of 'priming' which occurs when prior exposure to a particular stimulus sensitises a plant to express a more efficient defence response to future stress. The lab have shown that treatment of seeds with jasmonic acid can increase pest resistance in plants grown from those seed, even many weeks after germination. Alongside work towards its commercial exploitation, the group are investigating the mechanistic basis for this phenomenon. Other recent work includes the identification of rhizobacterial strains that activate systemic resistance against rice blast and sheath blight diseases in rice, and a genomic-level study of the effect of the light environment on the *Arabidopsis* wound response.

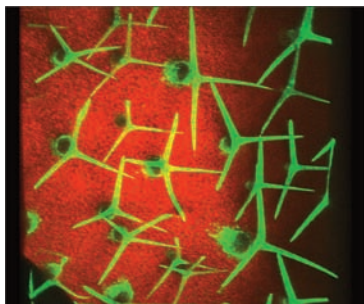


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**Research Area** Membrane transport

### Research Activities

Primary research interests centre on the regulation of ion transport across the membranes of plant and fungal cells. The group is currently focussed on elucidating the pathways responsible for organic anion secretion from higher plant roots and filamentous fungi. Secretion of organic anions plays important roles in nutrient acquisition, metal ion detoxification and pathogenicity. Surprisingly, the pathways by which organic anions cross the plasma membrane of plant and fungal cells are not well characterised and little is known of the molecular mechanisms that regulate the exudation of organic acids from these organisms. Theoretical considerations and the bulk of the experimental evidence (some of which is published by the Roberts lab) suggest a rate-limiting role for anion channels in organic anion secretion. For example, the Roberts lab have identified a novel citrate efflux channel activity in the plasma membrane of *Arabidopsis* epidermal root cells which is regulated by soil phosphate availability, consistent with a key role in phosphate acquisition.

## Spotlight on Lancaster University



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**Research Area** Responses to biotic stress and science policy

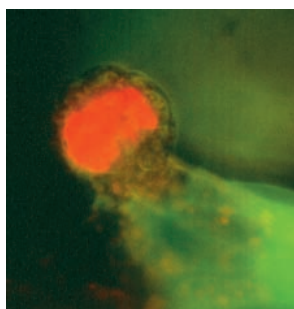
### Research Activities

In the natural environment plants have to deal with dynamic changes in their immediate environment. These include responses to many forms of biotic attack, both as individual events and in response to the simultaneous attack by multiple enemies. Jane's major focus is to examine the basis of plant responses to herbivore and pathogen attack via a multidisciplinary approach through the use of molecular, biochemical and physiological studies. In collaboration with Nick Hewitt and Nigel Paul at Lancaster the lab is also investigating the role of plant volatiles in defence responses to a range of herbivorous pests. This work is enabling the development of technology that may be used in applications both in horticulture and in agriculture. In addition Jane is associated with CESAGEN (ESRC centre for Economic and Social Aspects of Genomics) at Lancaster, exploring issues surrounding the knowledge based bio-economy. The work with CESAGEN examines forms of governance, new forms of knowledge exchange, epistemic dimensions of bio-knowledge, and the impact of commercialization on knowledge production.

## Spotlight on the University of Leeds



The Centre for Plant Sciences (CPS) ([www.plants.leeds.ac.uk](http://www.plants.leeds.ac.uk)) spans the full range of plant research from basic molecular mechanisms through to field trials and environmental assessments. The centre has an extensive range of plant growth facilities, from on-site controlled growth chambers and glasshouses up to a nearby farm, and occupies contiguous laboratories in the heart of the Faculty of Biological Sciences. The CPS runs the annual Gatsby Plants scheme ([www.gatsbyplants.leeds.ac.uk/](http://www.gatsbyplants.leeds.ac.uk/)) to engage the brightest UK science undergraduates with plant science, and is a central participant in a new interdisciplinary initiative in Human Health and Food Security in Sub-Saharan Africa. CPS welcomes enquiries at any level, especially from prospective independent fellows.

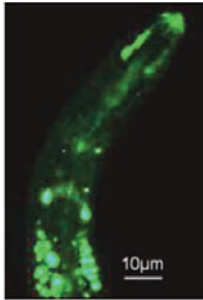


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**Research Area** Cyanobacteria: gliding motility, plant symbiosis and bloom formation

### Research Activities

Cyanobacteria are the largest group of nitrogen-fixing bacteria on earth and are the ancestors of the chloroplast. Many are filamentous and develop specialized cells such as the nitrogen-fixing heterocyst, and motile filaments known as hormogonia, which are the infective agents in cyanobacteria-plant symbioses. As models for their studies on cyanobacteria-plant symbiosis, the Adams lab uses two host plants, the liverwort *Blasia* and the flowering plant *Gunnera*. The group are currently studying the importance of hormogonia motility, adhesion and chemotaxis on plant infection, by constructing mutants inactivated in genes involved in the formation and function of pili, which are external protein fibres thought to be involved in all three processes. Understanding plant infection is the first step in the possible development of artificial nitrogen-fixing symbioses between cyanobacteria and crop plants. The mechanism of cyanobacterial gliding motility is unknown. However, the group has identified a parallel array of protein fibrils in the cyanobacterial cell wall, which they believe acts as a novel molecular motor, generating thrust for gliding. Researchers hope to visualise motor function using Atomic Force Microscopy of live, immobilised cyanobacteria. Planktonic cyanobacteria form large populations, known as blooms, in water bodies, and frequently release potent neurotoxins and hepatotoxins. As temperatures increase due to global warming, such cyanobacteria are likely to become an increasing problem in the UK. The group is currently using molecular genetic techniques to identify toxigenic cyanobacteria in local water bodies, and are examining the use of rotting barley straw to control bloom formation.

## Spotlight on the University of Leeds



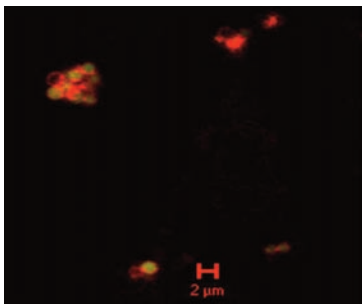
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**Research Area** Plant parasitic nematodes

### Research Activities

Howard's research focuses on molecular plant nematology, plant/nematode interactions, plant biotechnology, biosafe transgenic crops and issues surrounding their future deployment in developed and developing world agriculture. Arabidopsis has been used as a model host to develop fundamental understanding of plant interactions with both cyst and root-knot nematodes. The entry in this article by Peter Urwin gives more information on the joint efforts in this area, funded primarily by BBSRC. Howard's role in this collaboration centers on the developing world aspects of the research and this has led to involvement in capacity building and translational research activities in Sub-Saharan Africa, India and S. America. Prof. Atkinson has recently begun to engage with the UK media and general public on the contribution that transgenic crops could make to assure future food security. For example, the need to develop public global goods such as the generation of nematode resistance for cooking bananas and plantains via transformation by scientists in Africa (funding from BBSRC/DFID SARID initiative and USAID ABSP11). Researchers have also been developing a joint molecular nematology programme with the Indian Agricultural Research Institute, New Delhi, India.

Howard is currently leading a major University of Leeds interdisciplinary initiative in Human Health and Food Security in Sub-Saharan Africa. Three appointments will be made in early 2009: a new Chair in Plant Sciences with research interests relevant to African needs, a nutritionalist (in the Faculty of Medicine & Health) working at the interface between plants and human nutrition, and an ecologist active in ecoservices or a related area.

In addition to this work, Prof. Atkinson also holds a visiting Chair tied to the CPS joint laboratory with The Chinese Academy of Sciences in Beijing.



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**Research Area** Peroxisome biogenesis and function

### Research Activities

Peroxisomes are highly dynamic organelles that impact many aspects of plant biology; reserve mobilisation, photorespiration, hormone synthesis, defence responses and development. Proteins are delivered to the peroxisome from the cytosol using a unique targeting and translocation mechanism that can accommodate the import of folded, even oligomeric, proteins. The Baker group are interested in the transport of molecules across peroxisome membranes. The mechanism of protein import is being studied using a range of biochemical, molecular genetic and chemical genetic approaches. Using an *in vitro* approach researchers are analysing the interaction between a translocation intermediate and the import machinery to try to understand the sequence of events within the import pathway. RNAi and regulated expression of dominant negative mutants is yielding insights into the *in vivo* function of essential peroxisome biogenesis genes. As defects in peroxisome formation have profound effects on plant development, in collaboration with Dr Stuart Warriner (School of Chemistry), the group are using small molecules to interrogate import pathways. Small molecules provide tools that are potentially titratable and reversible, and which can help to overcome issues of redundancy and lethality inherent in genetic approaches. A second area of interest is transport of substrates into peroxisomes for metabolism via  $\beta$ -oxidation. In collaboration with Profs. Ian Graham (York), Michael Holdsworth (Nottingham), and Dr Freddie Theodoulou (Rothamsted Research), the Baker Lab have characterised the peroxisomal ABC transporter COMATOSE (CTS) which acts as a broad specificity transporter for  $\beta$ -oxidation substrates. Current work in collaboration with Prof Steve Baldwin and Dr Theodoulou addresses the structure-function relationship of this important protein.



## Spotlight on the University of Leeds



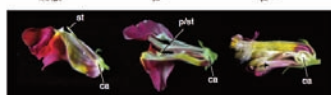
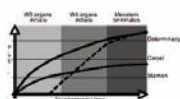
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**Research Area** Physcomitrella for comparative genomics

### Research Activities

“Evo-Devo” studies require taxonomically-divergent and experimentally-amenable model organisms. The moss *Physcomitrella patens* provides a comparative model system that complements *Arabidopsis thaliana* for the study of plant cell biology and development. As a bryophyte, it represents the earliest group of plants to diverge from the land plant lineage, and thereby provides insights into the evolution of plant developmental mechanisms. Its anatomical simplicity facilitates *in vivo* cell imaging. The recent sequencing of the *Physcomitrella* genome, coupled with its capacity for high-efficiency gene targeting for sophisticated genetic manipulation and ‘reverse genetic’ analysis, enhances its utility as a model system. The recent construction of a genetic linkage map additionally enables the ‘forward genetic’ isolation of genes identified in mutagenic screens.

Vegetative dehydration tolerance is a trait that is widespread among bryophytes, but has been lost in most vascular plants where tolerance is restricted to specific stages of the life cycle (in seed and, sometimes, in pollen development). *Physcomitrella* retains an ABA-mediated dehydration tolerance response throughout its life-cycle, and this is being studied through the characterization of ABA-non-responsive mutants, and by functional analyses of the multiple genes encoding the *ABI3* transcription factor. In the vascular plants, a single *ABI3* gene mediates ABA-induced desiccation tolerance, specifically in seeds. Evolutionary loss of *ABI3* gene family members may have resulted in the developmental sequestration of this stress-response.

Gene targeting in *Physcomitrella* reflects the organism’s preferential use of the homologous recombination-mediated DNA repair pathway. Understanding how this mechanism operates in moss will support efforts to develop gene targeting technology in flowering plants.



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**Research Area** Plant development and nonsense-mediated mRNA decay

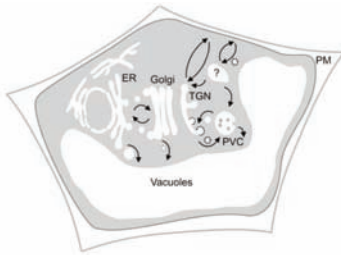
### Research Activities

Research in the Plant Development laboratory is mainly focused on trying to understand the mechanisms behind development in plants and investigating a little-understood posttranscriptional gene regulatory mechanism known as nonsense-mediated mRNA decay (NMD). The group has a long-standing interest in flower development and, although the group primarily use *Arabidopsis* as a model system, they also use comparisons with *Antirrhinum* to highlight differences and similarities and to obtain an insight into the evolution of regulatory mechanisms.

**Plant Development:** Studying the establishment of floral organ identity in two different species led the group to investigate how differences in protein-protein interaction potential can be translated into the activation of specific downstream target genes. The Davies lab are involved in several collaborative, systems-based approaches to address this question. This line of investigation led to an interest in MADS-box transcription factors and their role in plant development. The group has also showed that the meristem maintenance factor, *WUS*, interacts with members of a small family of transcriptional co-repressors (TOPLESS-related, TPR, originally called WSIP) and researchers are continuing to work in this area.

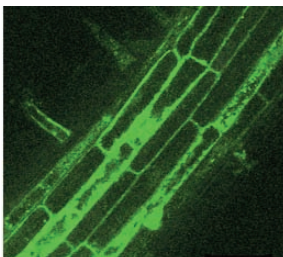
**NMD:** This is a mechanism that is used by eukaryotes to prevent translation of potentially harmful mRNA and/or to regulate the expression of a large set of genes by modulating transcript stability. The group has identified a series of NMD mutants in *Arabidopsis*, all of which share common developmental abnormalities, and are using them to investigate how certain mRNAs are targeted for NMD in plants. Microarray studies suggest that NMD might play a role in the plant’s response to changing environmental conditions.

## Spotlight on the University of Leeds



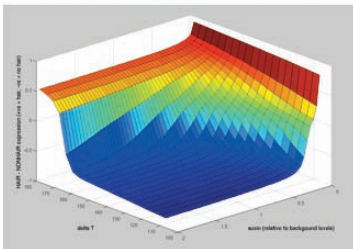
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**Research Area** The secretory pathway  
**Research Activities**

The secretory pathway synthesizes and delivers proteins, lipids and carbohydrates to various locations in the cell. Due to its tremendous importance in the production of edible protein for humankind, and its potential for the production of vaccines and high value proteins, a good understanding of this fundamental pathway is timely and important. Research focuses on the mechanisms controlling protein synthesis by the endoplasmic reticulum and the transport of proteins to the vacuoles or the extracellular matrix. In order to dissect individual steps in these pathways, the group uses a broad range of methods including genetic engineering, protein chemistry, live bio-imaging using confocal laser scanning microscopy and quantitative biochemical transport assays. Although most of the work is fundamental and curiosity driven, the lab has started to establish innovative bio-fermentation and cell perfusion reactors, based on their expertise in this area. Products include high value pharmaceutical proteins as well as hydrolases for the sustainable plant-based bio-fuel production.



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**Research Area** Auxin-regulated plant development  
**Research Activities**

A key question in plant biology is how the hormone auxin controls such a diversity of developmental events. Research in Stefan's lab is focused on understanding how the specificity, which can account for this control, arises in the auxin signalling system. Although the current qualitative model of this complex system provides a conceptual framework for understanding how auxin can turn genes on and off, it is unclear how and where specific information is carried in the system and thus how auxin pulses of differing length and amplitude can be translated into quantitatively different genomic outputs both within and between various developmental contexts. To address these questions, Stefan's group is obtaining quantitative and cell-type-specific genomic and biochemical data to parameterize comparative mathematical models of auxin response in juxtaposed developmental contexts, beginning with cells/zones of the root epidermis and shoot apical meristem, to understand how auxin operates throughout development. Because of the desire to model, as far as possible, at the level of the single cell and with realistic binding preferences among protein components, the group is heavily involved in single-cell-type sampling techniques and *in vitro* and *in vivo* quantification of protein interactions and abundance. Stefan's group works closely with modellers at CPIB in Nottingham and the Computational Biology Group at Leeds to integrate the experimental and theoretical aspects of the work.



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**Research Area** *Physcomitrella patens*. Research-led teaching  
**Research Activities**

The moss *Physcomitrella patens* complements other model plants. Its attributes are that, as a bryophyte, it is a member of the group of organisms that overcame the challenges of colonising land, evolving mechanisms to deal with water and other environmental stresses. It is also haploid for most of its life-cycle and has the ability to recombine homologous sequences in somatic cells at high frequency enabling gene targeting in this plant. With many years experience working on gravitropism and transformation, as well as general aspects of *Physcomitrella* biology, Knight is now editing the first research book on *Physcomitrella* with colleagues David Cove and Pierre-Francois Perroud (in press, Wiley-Blackwell - June 2009).

Knight has focussed recently on the critical lack of interest in plant sciences shown by undergraduates and within schools. With the help of the Gatsby Charitable Foundation, she established Gatsby Plants and leads her team to ensure that the annual summer school for UK first year undergraduates, and lecturers' web-based teaching resource, support the educational objectives of the plant science research community.

## Spotlight on the University of Leeds

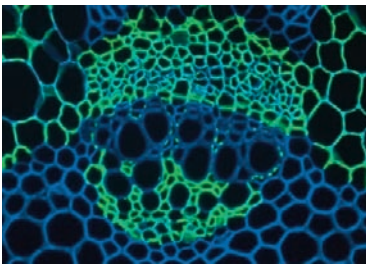


### Celia Knight Continued

#### *Physcomitrella patens*. Research-led teaching

##### Research Activities

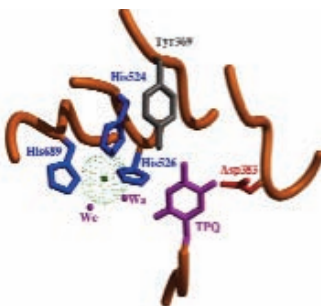
Knight leads another initiative focussing on the research abilities of final year undergraduates. Bio-science Horizons is a new journal, created by a UK universities consortium and published by Oxford University Press. It publishes research from the best final year undergraduate research projects and was awarded a certificate for publishing innovation by the Association of Learned and Professional Society Publishers (ALPSP).



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**Research Area** Plant cell walls

##### Research Activities

Professor Knox is interested in understanding the structures and functions of plant cell walls. Cell walls are compacted composites of diverse polysaccharides making them difficult to study. He is developing sets of molecular probes (monoclonal antibodies and carbohydrate-binding modules) that can be used in conjunction with microscopies to detect cell wall polysaccharides *in situ* thus enabling the imaging and study of cell wall architectures. These cell wall probes can be used in various ways to extend the cell biological understanding of cell walls. For example, they can be used to determine the polysaccharide configurations that underpin cell wall properties and the cell walls of distinct cell types. These studies indicate that polymers are present in cell walls in spatially-ordered architectures and that polymer structures are also highly dynamic within organs and in relation to processes such as cell elongation and cell adhesion. Current projects are exploring polymer links within cell walls and polymer dynamics in relation to growth and mechanical impacts. The sets of cell wall probes are also extremely useful tools for the high throughput microarray and chromatographic approaches to understand cell wall polymer populations. In addition to being central to many plant processes cell walls are also important cell components that determine the properties of plant materials. Prof Knox is using the insights and tools developed for the study of cell wall biology for the analysis of cell walls in applied contexts such as their use as sources of industrial fibres and feedstocks for bioenergy production.



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**Research Area** Protein engineering, molecular farming and structural proteomics

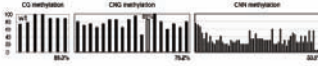
##### Research Activities

**Protein engineering:** Many enzymes generate novel cofactors from active site amino acids. Work in Mike's group focuses on structural and functional analysis of a number of enzymes to elucidate cofactor formation, catalytic mechanism, oxygen activation and to engineer improved variants. The lab also work on protease inhibitors for anti-nematode defence and are using a consensus version and other small binding proteins as the basis for engineering libraries of novel binding proteins as co-crystallisation domains and for developing protein chips.

**Molecular farming of self-assembling and bioactive peptides:** Designed peptides that self-assemble in a responsive manner are being produced by recombinant systems. These peptides have a number of applications including tissue engineering matrices. Researchers are using both microbial and plant systems for the production of such peptides, and are also generating modified variants that contain additional bioactive domains including those with cell adhesion and signalling functions.

**Structural proteomics of membrane proteins:** The group have established high-throughput systems for the cloning, expression, functional analysis, purification and crystallization of membrane proteins. The primary focus has been on bacterial proteins, and there is scope for exploring plant membrane proteins.

## Spotlight on the University of Leeds

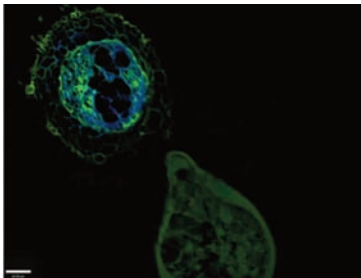


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**Research Area** Epigenetics

### Research Activities

Epigenetic mechanisms play an important role in genome organisation, developmental programming and environmental response, and they control the activity of transgenes and mobile elements. Research in the Meyer lab focuses on signal sequences and endogenous targets of epigenetic systems. One aspect is the examination of natural antisense transcripts (NATs) as regulators of sense gene expression in petunia and Arabidopsis. This work investigates whether the joint transcription of overlapping gene pairs arranged in opposite orientation, interferes with transcript elongation or processing, or if it generates double stranded RNAs, which are processed into small RNAs. Another topic is the characterization of the RPS element, a DNA region that attracts *de novo* methylation. RPS is an unusual epigenetic target as neither initiation nor maintenance of RPS methylation requires RPS transcription or the RNA-dependent DNA methylation pathway. Instead, methylation appears to be attracted by a characteristic secondary structure. The RPS element therefore serves as a model for transcription-independent initiation and spreading of DNA methylation and histone modification patterns.

Peter collaborates with other members of the epigenetic community as a participant of the EU funded Epigenome NoE. He is responsible for the Epigenome website, which serves as a platform for discussion and technology exchange among the European epigenetics research community.



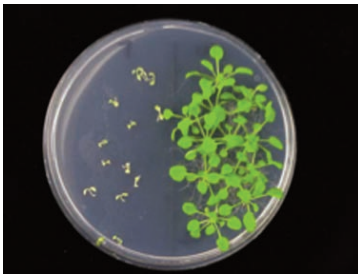
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**Research Area** Plant parasitic nematodes

### Research Activities

*Arabidopsis thaliana* is an excellent model for crop science and has particular importance in pathology, specifically nematology. Peter's laboratory has gained many vital insights into the plant/nematode interaction using *A. thaliana* at the molecular and cellular level. This translational work then informs work on crop plants, which in the UK context focuses on potato but expands to banana and rice for the work in Africa and India respectively. The group conduct a wealth of strategic science aimed at delivering biotechnological resistance to plant parasitic nematodes and have conducted several field trials with transgenic potatoes at their university farm, each delivering a major advance in nematode resistance. This resistance work is presently being continued by combining different technologies to deliver a robust additive defence. Researchers are also exploring the possibility of using green manures or intercropping as a means of nematode control. For details of strategic overseas work see the entry of Prof. Howard Atkinson. The laboratory is also interested in defining the relative efficacy of RNAi in plant parasitic nematodes and the efficacy of RNAi-based technology as an *in planta* defence. The Urwin group also utilise *Arabidopsis* to study combinatorial stresses in plants, by investigating the interactions that result from biotic and abiotic stress. A collaboration with the Wellcome Trust Sanger Institute, Rothamsted Research and Scottish Crop Research Institute will sequence the genome of the plant parasitic cyst nematode, *Globodera pallida* – the major nematode pest in the UK. There is also interest in sequencing the major cyst nematode pathogen on crops in India, *Heterodera avenae*.

Additionally the laboratory also works on the close relative of *A. thaliana*, *Arabidopsis lyrata petraea*. This species has defined range margins, is not a human commensal, and does not naturally out-cross. This makes it the perfect focus for looking at species distribution and adaptation at the molecular ecological level.

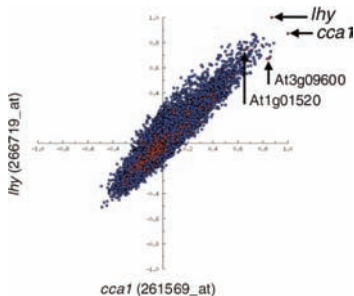
## Spotlight on the University of Leeds



**Name** Chris West  
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**Research Area** DNA repair and recombination in plants  
**Research Activities**

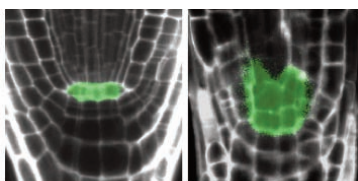
Work in Chris West's lab uses the model plant *Arabidopsis thaliana* to investigate DNA repair and recombination pathways using reverse genetics, protein expression, interaction and biochemical analysis, and cell biology approaches. Initial studies characterised components of the illegitimate recombination pathway, termed non-homologous end joining (NHEJ). Mutations in NHEJ genes resulted in hypersensitivity to reagents that cause double strand breaks, indicating the importance of this repair pathway in the response of *Arabidopsis* to genotoxic stresses. However, NHEJ mutants still displayed high levels of illegitimate recombination, and mechanism(s) of these NHEJ-independent end joining pathways are the focus of current research.

Recombination pathways are important in generating genetic diversity during meiosis and therefore underpin breeding strategies for crop improvement. These DNA repair pathways also safeguard the genome against DNA damage inflicted by environmental stresses, ensuring both growth and development and the faithful transmission of genetic material to the next generation. Of significant interest to both researchers and biotechnologists is the role of recombination in DNA insertion into the host genome during the process of generating transgenic plants. A greater understanding of these mechanisms will help us develop novel approaches to promote gene targeting to allow the precise and directed manipulation of the genome. High levels of illegitimate recombination mean that targeted insertion of transgenes occurs very rarely in higher plants. Current approaches use insertional mutant lines to determine the effects of manipulating the relative activities of the recombination pathways in *Arabidopsis* on the frequency of gene targeting.



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**Research Area** Bioinformatics  
**Research Activities**

The Westhead group is interested in prediction methods for biological problems based on machine learning and statistical methods. Recently projects have included predicting protein structure, protein-protein interaction sites and the functional effects of single nucleotide polymorphisms. Another major interest is functional genomics and systems biology, the group are also interested in predicting molecular networks (particularly metabolism in parasites for drug target applications) using genome sequence data, and the use of large genomic data sets (DNA microarrays, proteomics etc) in gene function and gene network prediction.



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**Research Area** Post-embryonic root development in higher plants  
**Research Activities**

Post-embryonic root development plays a predominate role in the construction of the root system of higher plants. The main focus of Hanma's research is to understand how this developmental process is regulated. His current research activities include the following three areas:

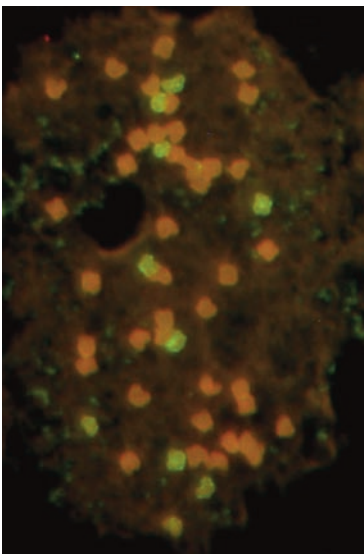
- 1) Nutritional regulation on root architecture. This interest stems from his early work on the effects of nitrate on lateral root development in *Arabidopsis*. This work led to the finding that nitrate regulated lateral root development via two regulatory pathways (a localised stimulatory pathway and a systemic inhibitory pathway) and to the identification of a key signalling component of the stimulatory pathway, ANR1. Hanma's current efforts in this area focus on the identification of genes that act in the systemic inhibitory pathway.
- 2) Regulatory role of abscisic acid (ABA) in lateral root meristems. This line of research is based on the group's findings that ABA suppresses the activation of newly formed lateral root meristems in *Arabidopsis*. A genetic approach was used to dissect the signalling mechanism of this novel ABA function, which led to the isolation of several *labi* (lateral root ABA insensitivity) mutants and cloning of three *LABI* genes.
- 3) Role of ABA in root meristem maintenance. This is a relatively new research area in Hanma's laboratory and is based on some preliminary physiological and genetic evidence that ABA may play an important role in root meristem maintenance in *Arabidopsis*. He is currently working to gather further supporting evidence for this novel ABA function and is trying to identify genes involved in this function.

## Spotlight on the University of Leicester



Plant science research at Leicester is located within the Department of Biology. This is one of four non-clinical departments that constitute the School of Biological Sciences, which is itself part of the broader College of Medicine and Biological Sciences. The department has a strong international reputation for its research, and this is reflected in the score of 5 from the UK Research Assessment Exercise, RAE2001, and by the editorial board duties of staff members for several international journals. Researchers in the department are exploring fundamental and applied aspects of plant growth, development and evolution. This work encompasses molecular, genetic and epigenetic mechanisms involved in environmental signalling and reproductive development, the biochemistry and cell biology of organelles, genome organization, biodiversity and systematics. Intensively studied model plants such as *Arabidopsis* are used, as well as important crops and other species. Research projects are strongly supported by a number of different funding agencies, including BBSRC, NERC, the Royal Society, the European Union, international organizations, and industry.

The Department of Biology is situated on the main campus in the Adrian Building (see picture), along with the Department of Genetics, and has excellent facilities for research with all of the laboratories having recently undergone complete refurbishment. Growth facilities for plants are extensive, and include a range of controlled environment chambers, custom-built growth rooms off the laboratories, glasshouses on the Adrian Building roof, and additional glasshouses (equipped with a quarantine facility) and outdoor growing space at the university's 16-acre botanic garden off-campus, probably the most diverse garden in the region. Other resources include advanced facilities for confocal and electron microscopy, photobiology, and radioisotope usage. The department also houses an extensive herbarium, containing over 125,000 vascular plant specimens, and which hosts the taxonomic database of the Botanical Society of the British Isles.



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**Research Area** Plant cyto-taxonomy and alien invasive plants

### Research Activities

The reproductive biology of the invasive alien *Fallopia japonica* (Japanese Knotweed) has been the main focus of John's research for many years, producing some 30 publications. This has involved many overseas partners and several visits to Japan for plant collecting. A very large live collection of plants is maintained at Leicester, some in the quarantine house. Examination of clones from Eastern Europe and America are ongoing. Molecular approaches have demonstrated the clonal nature of Japanese Knotweed, and since it is all male sterile there has been extensive hybridization with it all around the world. Work continues on some exciting putative hybrids from the Southern Hemisphere (see GISH picture). The areas in Japan where our European clones originated have been identified using chloroplast haplotype comparisons. This informed the Biological Control group at CABI Biosciences where to collect potential control agents. In collaboration with Trude Schwarzacher and Pat Heslop-Harrison, GISH and FISH studies are ongoing on an ever-changing range of taxa including *Petunia*, *Brassica* and *Crocus*. The role of plant cytologist of 'last resort' has produced a number of overseas collaborations with groups working on invasive plants with small numerous chromosomes, i.e. *Spartina Salsola* and *Crassula helmsii*, additionally the following non invasives have been studied *Sorbus*, *Potamogeton* and *Butomus*. Many visitors have been to the lab to learn the art of plant cytology.



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**Research Area** The evolution and development of flower and fruit development

### Research Activities

Fruits and seeds come in many shapes and sizes and are the source of nutritious oils, starches or important alkaloids. Fruit types are as widely disparate as the fleshy fruits of tomato, siliques of *Arabidopsis* (both core eudicots), capsules of poppy (a basal eudicot) and caryopses of wheat and other monocots. Research in the Drea lab investigates how the genetic mechanisms that influence fruit and seed development are conserved or have diversified in species with different fruit types. The differences or similarities could be caused by diversification or conservation in master regulators of development; in their gene number, gene expression patterns, sequence profiles and protein functions. There are two main systems of interest in the lab that represent important crops: the capsular fruit of the opium poppy and the grain or caryopsis of the temperate cereals (e.g., wheat and barley). In the latter case *Brachypodium distachyon* is being used as a model system and both forward and reverse genetic approaches are being exploited to investigate caryopsis development. Poppy is a basal eudicot and *Brachypodium* is a monocot and so the research will provide insights into the evolution of development throughout the angiosperms.

## Spotlight on the University of Leicester



**Name** Kerry Franklin  
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**Research Area** Light and temperature-regulation of plant development  
**Research Activities**

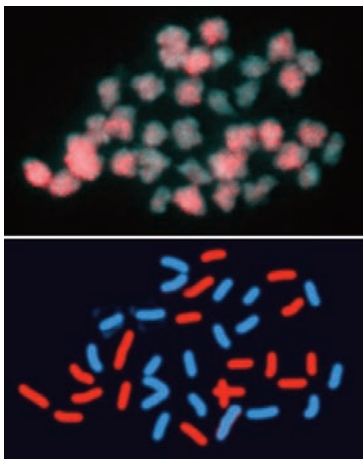
Light and temperature are two of the most important environmental stimuli regulating plant development. Plants perceive light using specialised information transducing photoreceptors which include the red and far-red light-absorbing phytochrome family. The Franklin lab focuses on investigating the interactions between light and temperature signalling in *Arabidopsis*. The group have established that plants display multiple temperature-dependent light foraging strategies in response to the threat of vegetational shade. The lab has additionally shown that light signals can enhance plant freezing tolerance in an ambient temperature-dependent manner and identified shared molecular components in light and temperature signalling pathways. Current work is focussed towards elucidating the molecular mechanisms regulating temperature-dependent light foraging strategies, dissecting high temperature signal transduction pathways and investigating the role of chromatin remodelling in plant environmental adaptation.



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**Research Area** Plant taxonomy and evolution  
**Research Activities**

As part of the global effort to complete an inventory of the world's plants, recent work has involved a floristic account of saxifrages for the Flora of China (216 species), and this is now being extended in to similar work on the Flora of Nepal. Also in production is an account of saxifrage genera for the Flora of North America. In addition to floristic work, phylogenetic analyses of the various groups are also underway using both morphological and molecular data. Alongside taxonomic studies is work on the population genetics of aquatic plants. Previous work has investigated the extent to which bird-mediated dispersal affects the genetic structure of populations and has demonstrated quantitatively the distances over which bird traffic has an impact on genepool structure.

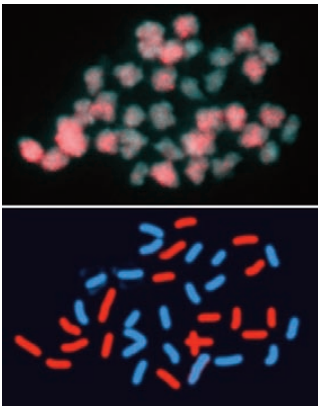
Backing up the floristic studies is a herbarium containing ca. 125,000 specimens, chiefly from Europe and the Mediterranean basin. The herbarium is the focus of a nationwide census, conducted in partnership with the Botanical Society of the British Isles (BSBI), of British and Irish herbaria, many smaller ones of which are under threat of disposal. There is an innovative programme to digitise specimens and have the images freely available on-line through the Herbaria at Home project (<http://herbariaunited.org/atHome/>). Collection details are transcribed by site visitors into a database which then contributes the data to the National Biodiversity Network – an important source of records when tracking and modelling the potential effects of climate change. This is all part of BSBI database work, which is currently hosted and supervised (in part) by the Leicester herbarium. Also underpinning biodiversity research is the Botanic Garden, a 16-acre facility some three miles from the main campus. In addition to educational displays and activities for schools (8000 children per year) it also houses important research greenhouses.



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**Research Area** Molecular cytogenetics, genome organization and evolution  
**Research Activities**

The plant molecular cytogenetics project is investigating biodiversity, changes during domestication of wild species, and aspects of genome and sequence evolution in Brassicas, forage grasses, oil palm, linseed, cowpea, banana and other species. The group have shown amplification of transposable element domains that are specific to the C genome in *Brassica napus* (see picture; Alix *et al.*, Plant J., Dec 2008). By analysing the amplification of different genomic components in the three genomes involved in the major crops, researchers can understand how the genomes evolve and interact. Current work aims to characterize sites where elements have inserted or been deleted during recent evolutionary history using informatic and PCR approaches. In the wheat progenitor species *Triticum tauschii*, application of retroelement-based markers has both shown the diversity within the species and allowed the lab to suggest its geographical dispersion and sites where unexploited useful diversity might be found. In this and other species, the group are investigating the

## Spotlight on the University of Leicester

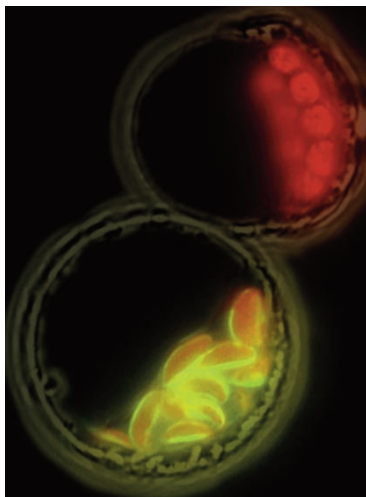


**J.S. (Pat) Heslop-Harrison Continued**

**Molecular cytogenetics, genome organization and evolution**

**Research Activities**

nature, diversity and expression of key genes that are involved in resistances to biotic and abiotic stress. The systems biology programme in the lab ([www.sblab.org](http://www.sblab.org)) aims to develop and exploit tools from systems and control engineering to biological systems. Currently, this has focused on the robustness and effects of time-varying interactions, noise and spatial heterogeneity on biochemical networks. The models are also investigating switching and coupling processes, including the evolutionary signatures of different selective pressures. Advances in this work will complement QTL projects in grasses and the ultimate aim is to use marker data to model dynamic behaviour and crop responses to the environment. The group are also developing novel fluorescence detection technology for quantitative analysis of colour of single photons. Further details of research projects, other activities in training, editing and management committees, as well as abstracts and publications, are available from the website [www.molcyt.com](http://www.molcyt.com).



**Name** Paul Jarvis

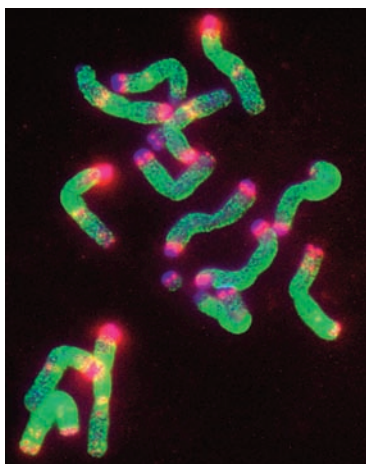
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**Research Area** The protein import machinery of Arabidopsis chloroplasts

**Research Activities**

Although chloroplasts retain a fully-functional genetic system, the plastid genome encodes less than 10% of the proteins required to build a fully-functional organelle. The majority of plastidic proteins are encoded in the nucleus and synthesized on free cytosolic ribosomes. They are made in precursor form, each one bearing an amino-terminal targeting signal, or transit peptide. The transit peptide directs the protein through a post-translational targeting pathway, and is cleaved upon arrival inside the plastid. This targeting or import process is mediated by the coordinate action of two proteinaceous import machines, one in each of the envelope membranes. The import machinery of the outer envelope membrane is called TOC (Translocon at the Outer envelope membrane of Chloroplasts), and that in the inner membrane is called TIC. In the last two decades, several components of the TOC and TIC complexes have been identified using biochemical approaches and isolated pea chloroplasts. Paul's group has sought to complement the biochemical data generated in pea by conducting molecular-genetic studies on homologous translocon components in Arabidopsis. One particularly interesting avenue of research relates to the fact that several translocon components (notably receptors of the TOC complex) are encoded by small gene families in Arabidopsis. Paul's group has used genetics to dissect the functional significance of these gene families, and the results indicate that the different receptor isoforms operate in different import pathways with distinct precursor recognition specificities; i.e., different import pathways exist for different precursor protein classes. The existence of such substrate-specific import pathways might play a role in the differentiation of different plastid types, and/or act to prevent deleterious competition effects between abundant and non-abundant precursors.



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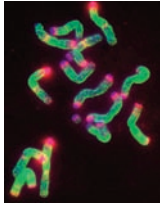
**Research Area** Repetitive DNA sequences, genome organization and epigenetic mechanisms in polyploid plant species

**Research Activities**

Most estimates suggest that 50% of plant species are recognisable and evolutionarily recent polyploids. Trude's lab is studying the interaction of genomes, chromosomes and DNA sequences in polyploids and hybrids in cereals, petunia and banana. Her work concentrates on repetitive DNA sequences, both tandemly repeated satellite sequences and dispersed transposable elements, their diversity and evolution, as well as their epigenetics as evidenced by chromatin organisation and methylation. Her studies indicate methylation repatterning involving *de novo* methylation and demethylation mechanisms when genomes are combined in polyploid and hybrid cereals and current work is investigating the epigenetic changes when alien chromosomal segments are transferred to wheat in breeding programmes. Trude's lab and European collaborators have studied genomic integration of pararetroviruses, a recently discovered repetitive sequence class in plants that in petunia and tomato form a significant part of the genome, although often degenerate and rearranged. Trude's lab has recent evidence for pararetrovirus elements in sugar beet and other angiosperms and is in the process of sequencing full elements. Activation of integrated, but dorm



## Spotlight on the University of Leicester

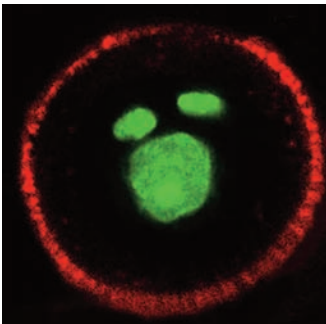


**Trude Schwarzacher** Continued

**Repetitive DNA sequences, genome organization and epigenetic mechanisms in polyploid plant species**

### Research Activities

-ant pararetroviruses can be caused by wide hybridization and can lead to disease outbreaks through tissue culture or environmental stresses, but is possibly suppressed by epigenetic silencing mechanisms and DNA methylation. Pararetroviruses are closely related to pseudoviridae retroelements and are often found in their physical proximity. Comprehensive analysis of repetitive DNA elements in banana have also found close chromosomal proximity and insertion within each other of LTR-retrotransposons, tandem repeats and 5S rRNA genes, postulating a possible link in their evolution and to gene expression.



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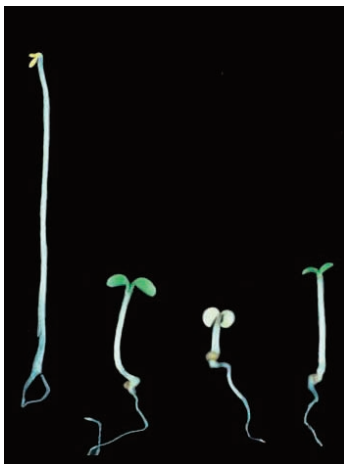
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**Research Area** Regulatory processes in plant sexual reproduction

### Research Activities

Flowering plants possess a unique mode of sexual reproduction that involves production of twin male and female gametes and their union at 'double fertilisation'. This remarkable process has a vital role in crop breeding and seed production, yet our knowledge of the molecular mechanisms involved in gamete development and fertilization is limited. Research in the Twell Lab focuses on regulatory processes in male reproductive (pollen) development and the molecular mechanisms that govern plant germline development. Previous work has generated many *Arabidopsis* mutants defective in key stages of male gametophyte development and genes regulating cytokinesis and microtubule reorganization during asymmetric division are being studied. The lab has also established a global perspective through transcriptome analysis of male gametogenesis. Recently, the lab has discovered two key regulators in the cellular networks that control germline cell proliferation, an E3 ubiquitin ligase complex (SCF<sup>FBL17</sup>) and the germline-specific transcription factor DUO1, that also specifies germ cell fate. The Twell lab is also exploring the role of epigenetic mechanisms and small RNA pathways in pollen development. Current work is focussed on developing a robust regulatory framework for male germline development that links cell cycle control and gamete specification. Collectively, this information will advance knowledge of regulatory mechanisms in gamete development and fertility in flowering plants, and will inform strategies for the manipulation of gametogenesis, gene flow and male sterility in plant breeding.



**Name** Garry Whitelam

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**Research Area** Phytochromes and photomorphogenesis

### Research Activities

A major focus of research in the Whitelam laboratory over recent years has been to determine the roles of individual phytochromes and their co-actions and interactions. Towards this aim, a combination of physiological, genetic and molecular biological approaches have been employed. The selection/creation and analysis of mutants of *Arabidopsis thaliana*, which have altered complements of phytochrome (PHY) gene products, has been the central theme of this research. Related lines of research include the identification of mutants that define genes encoding components of the signal transduction pathway downstream of the phytochromes, particularly in relation to the perception of red:far-red ratio signals, as well as studying how photoreceptor signalling interacts with other signalling systems. The Whitelam laboratory was the first to describe confirmed null mutations at PHYA, PHYC and PHYE, the loci encoding the apoproteins of phytochromes A, C and E, as well as mutations at loci that define genes specifically involved in phytochrome A signalling. More recent research has identified a role for the circadian clock in regulating plant responses to light quality signals and the molecular dissection of early shade avoidance signalling pathways.

## Spotlight on the University of Liverpool



The University of Liverpool is one of the UK's principal research universities. The Department of Botany was home to the first stages of the Flora Europaea project, pioneering work in evolutionary biology and its applications to land restoration under the late Tony Bradshaw. Plant Science research is now based in the School of Biological Sciences (RAE5) and the Institute for Sustainable Water, Integrated Management & Ecosystem Research (SWIMMER). A key theme is to develop a comprehensive understanding of how different physiological systems are coordinated within the context of the whole organism using model and agricultural plants and fungi (*Arabidopsis*, barley, rice, *Kalanchoe fedtschenkoi*, garlic, onion, *Artemisia spp.*, *Aspergillus nidulans*). Research projects emphasise the understanding of sensing and the response to the environment, with projects extending from fundamental molecular modelling in plants and fungi to applications in food security. In addition, fundamental and applied projects work with natural, semi-natural and agricultural ecosystems in the UK and abroad, and across a range of communities from sub-tundra to tropical rain forests.

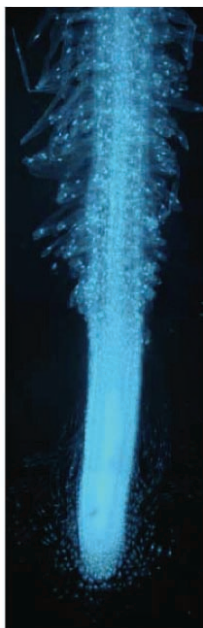
The School of Biological Sciences occupies the new £25 million Biosciences Building, with all the facilities of a major biosciences research centre including transgenic plant glasshouses and temperature and photoperiod controlled growth rooms, as well as core facilities in cell imaging, genomics/transcriptomics, functional proteomics and bioinformatics.



**Name** Richard Bradshaw  
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**Research Area** Ancient DNA

### Research Activities

Richard works with Gina Hannon and Lee Bradley on the long-term history of beech (*Fagus sylvatica*) in Europe through the study of sub-fossil pollen, macrofossils and ancient DNA. Molecular genetic research is carried out in cooperation with James Hartwell and several European laboratories within the EVOLTREE network of excellence (<http://www.evoltree.org/>). The group are investigating where beech populations survived the last ice-age and how beech colonised Europe during the present inter-glacial. Genetic markers are helping researchers to trace the movement and development of specific populations. Richard's group was among the first to have successfully isolated DNA fragments from sub-fossil plant material. Beech DNA sequences of up to 70 base-pairs in length have been extracted from leaves, nuts and bud-bracts preserved in sediments from up to 8000 years ago. The group works with time-series samples from Italy and Denmark and is beginning to understand how the present-day genetic structure of European beech populations has developed.



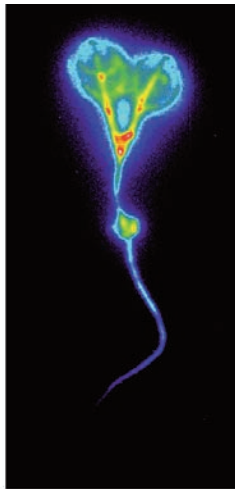
**Name** Mark Caddick  
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**Website** [www.liverpool.ac.uk/bio](http://www.liverpool.ac.uk/bio)  
**Research Area** Gene expression and regulation

### Research Activities

Mark's research centres on eukaryotic gene expression and its regulation. This primarily involves work with the fungus *Aspergillus nidulans* as a model system. His work explores the mechanisms underlying coordinated gene expression and regulated RNA stability and he has recently begun to exploit comparative genomics to investigate regulatory signals in the *A. nidulans* genome. An extension of this fungal work resulted in the transfer of an *A. nidulans* regulatory system into plants with the aim of developing regulated gene switches for the expression of transgenes. A simple two-component system has been developed, which includes a single transcription factor (AlcR), which activates expression at the alcA promoter in the presence of various alcohols and ketones. This has proved effective in directing gene expression in plants including tobacco, tomato, potato, maize, oil-seed rape and *Arabidopsis*. In the absence of inducers there is negligible basal activity, but the application of ethanol, at concentrations that are not detrimental to plants, leads to gene expression throughout the plant within a few hours. Induction can be reversed or maintained for significant lengths of time, and varied by manipulating the concentration or form of the inducer. Tissue specific promoters have also been utilised to facilitate temporal and spatial regulation.

The alc switch is available for academic use (contact [liang.shi@syngenta.com](mailto:liang.shi@syngenta.com)) and has been utilised in a large number of laboratories world-wide. Mark's group have used the inducible gene switch to investigate the function of specific cell cycle genes in collaboration with John Doonan (JIC).

## Spotlight on the University of Liverpool



**Name** Anthony Hall  
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**Website** www.liverpool.ac.uk/bio  
**Research Area** Circadian biology and temperature adaptation  
**Research Activities**

Anthony's research centres on the circadian clock mechanism and how the clock adapts to temperature change in the model plant *Arabidopsis*. Current work in the Hall group focuses on understanding the molecular mechanism of temperature compensation in the clock and the role of GI, TOC1, LHY and CCA1 in this mechanism. The group use transcriptomic, genetics, circadian leaf movement assays, luciferase imaging and time lapse confocal imaging to address these questions.

Research in the laboratory is now extending to understand other buffered signalling pathways within a large BBSRC-funded systems biology project (RoBuST, in collaboration with York, Edinburgh and Warwick Universities). Anthony is also interested in clock function at stress temperatures and is investigating both the molecular mechanisms and the role of the clock at these extreme temperatures. To exploit the group's research, they are developing barley as a model circadian system (in collaboration with Cambridge, NIAB and the JIC).

In addition to his interest in clocks and temperature Anthony is also developing high-throughput sequencing technology for studying genomes and gene expression in *Arabidopsis* and wheat in collaboration with Neil Hall.



**Name** Neil Hall  
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**Research Area** Genomics and bioinformatics  
**Research Activities**

Neil leads the Advanced Genomics Facility at the School of Biological Sciences which is using high throughput pyrosequencing technology to study genomes and transcriptomes. The facility utilises a Roche 454 GS-FLEX Titanium and a short read Applied Biosystems SOLiD 3 system. These machines, accompanied by the latest computational tools and a team of trained staff, are able to deliver bioinformatic services for data handling and analysis.

Neil's primary area of study is parasite evolution and genomics. His research has included whole genome sequencing of the causative agents of human diseases such as *Plasmodium falciparum* (malaria) and trypanosomes (sleeping sickness, leishmaniasis and Chagas' disease) to identify the genes involved in host interaction.

Since his appointment to the University of Liverpool, Neil has built a number of collaborations that apply the methods and technology of next generation sequencing to plant science. He also has interests in sequencing "non-model" plant species and plant pathogens.



**Name** James Hartwell  
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**Website** www.liverpool.ac.uk/bio  
**Research Area** Crassulacean acid metabolism (CAM), primary metabolic pathways, metabolism and the circadian clock, high throughput sequencing for gene discovery and transcriptomics of non-model species.  
**Research Activities**

Metabolic adaptations of photosynthesis such as CAM and C4 provide significant improvements in water-use efficiency, photosynthetic efficiency at high temperature and yield. Importantly, both CAM (*Agave sp.* and *Opuntia sp.*) and C4 (*Miscanthus x giganteus*) species are some of the most promising candidates for second generation biofuel crops suited to marginal land.

The Hartwell group focuses on developing a detailed understanding of the molecular-genetic basis for CAM and C4. The core project in the lab is a BBSRC-funded large scale transcriptome sequencing project aimed at developing *Kalanchoe fedtschenkoi* as an amenable model system for the study of CAM. In collaboration with Neil Hall, this uses the next-generation ultra high-throughput sequencers housed in Liverpool's state-of-the-art Advanced Genomics Facility (www.liv.ac.uk/agf/) for in-depth transcriptome sequencing of C3 and CAM leaves. The group plan to move from the transcriptome to the proteome and metabolome in order to understand the systems biology of CAM with the long-term goal of the project to engineer further improvements in water-use efficiency and yield in CAM species to enhance their value as biofuel crops for semi-arid environments.

## Spotlight on the University of Liverpool



**James Hartwell Contd.**

**Molecular cytogenetics, genome organization and evolution**

### Research Activities

The Hartwell lab is also involved in other high-throughput sequencing projects including one to identify the genes required for C4 photosynthesis in the C3 and C4 subspecies of the grass *Aloteropsis semialata* in collaboration with Colin Osborne (University of Sheffield). A further link with Sheffield (Richard Leegood and Julie Gray) uses high-throughput sequencing to identify the genes involved in C4 metabolism in the marine diatom, *Thalassiosira weissflogii*.

Finally, their group's newest project is the whole genome sequencing of *Genlisea aurea*, a fascinating carnivorous member of the Lentibulariaceae from Brazil. *G. aurea* has the smallest genome yet recorded in the Angiosperms (63 Mbp cf. *Arabidopsis* at 157 Mbp). This genome sequence will reveal the basis for its loss of roots and development of modified trap leaves, which capture and digest protozoa.



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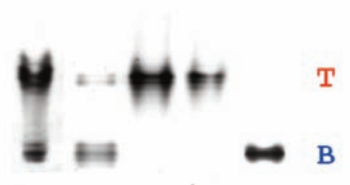
**Research Area**

Directed evolution of biocatalytic enzymes and biosynthesis of metabolites in *Artemisia* spp.

### Research Activities

Lesley's group have a growing interest in the use of bioinformatic and molecular techniques for the identification and directed evolution of novel biocatalytic enzymes from plants and fungi, working with collaborators in the Department of Chemistry at Liverpool. Her current projects centre on isolating and characterising potential haloperoxidases from the fungus *Stropharia aeruginosa*. Interest in biocatalysts is growing due to increased environmental concerns and demands for greener production methods by the pharmaceutical industry. In addition there is a need to develop new methods for generating the increasing number of complex chiral pharmaceuticals that are difficult or impossible to manufacture using traditional chemistries.

Additional work in the laboratory centres on the secondary metabolites of *Artemisia* sp. through collaboration with Rupi Vij (University of Central Lancashire). Historical work on the use of *A. annua* in traditional medicine indicates at least two distinct kinds of plants are involved (*A. annua* L., *A. caruifolia* Buch.-Ham.), with *A. annua* used predominantly in the West. To explore *A. caruifolia* and its relationship with *A. annua*, the group are using cytotoxic and analytical methods to assess both species



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**Research Area**

Stress physiology and molecular biology

### Research Activities

Meriel's research centres on responses to environmental stress and she is co-ordinator of the EU Marie Curie FP6 EST Host Fellowships project Sensible (Sensing and the biological response to the environment in plants). Flooding is an agronomically important abiotic stress and, in collaboration with Martin Mortimer, they are testing how rice cultivars differ in response to flooding stress at germination. This work combines morphometric analysis with mathematical modelling and molecular biology. Nitrogen availability is a different stress and a collaboration with Mark Caddick has used *Aspergillus nidulans* for many years to study gene regulation using molecular biological, proteomic and transcriptomic approaches. This has now moved on to examining the cell machinery for controlled mRNA degradation. One consequence of climate change will be to alter plant distributions, and, in further collaborative work at Liverpool, Meriel's group are developing microsatellite markers in the bee orchid (*Ophrys apifera*) suitable for determining variation in the species' mating system and concomitant population structure as it approaches its range margin.

Her group also work with the secondary metabolites that are the source of flavour in onions and garlic. These alk(en)yl cysteine sulphoxides are cleaved by the enzyme alliinase to yield the characteristic flavour and odours and are of importance to the food and pharmaceutical industries as well as to cookery. Her research focuses on the biosynthetic pathways that lead to the flavour precursors, using molecular biology approaches to identify relevant genes combined with analytical methods to detect the precursors.

## Spotlight on the University of Liverpool



**Name** Ed Maltby  
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**Website** www.liverpool.ac.uk/swimmer  
**Research Area** Peat, wetland soil and ecosystem processes, functions and values, and changes due to management and human activities.

### Research Activities

Ed's interests are in the impacts of agriculture and other human activities on soil and peat management, development and nutrient dynamics. As Director of the Institute for Sustainable Water, Integrated Management & Ecosystem Research (SWIMMER) he is involved in implementation of the 'Ecosystem Approach' and long-term sustainable solutions to river basin management. Collaborative work underway at SWIMMER relates to world conservation strategy, management and implementation, with special reference to wetlands. These projects focus on water use aspects along with ecosystem and catchment management, and the design of supportive, fundamental and applied scientific research.



**Name** Rob Marrs  
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**Website** www.appliedvegetationdynamics.co.uk  
**Research Area** Applied vegetation science

### Research Activities

Rob's main passion is to develop solutions to land management problems that are based on sound ecological science. These approaches are combined in structured surveys of populations linked to a wide range of potential explanatory environmental variables. Recent examples have included woodland in Great Britain, plant community composition in wet meadows, and species change in response of upland moor burning.

Rob's group also undertakes long-term experimental studies where management treatments are tested to restore plant communities for conservation policy reasons. This work has concentrated mainly on the control and subsequent restoration of habitats affected by invasive weed species (recently bracken and purple moor grass), but also has ongoing heather burning experiments.

Modelling studies involve complex multivariate analysis to tease out the important driving variables controlling vegetation composition. Rob has carried out these types of studies in a range of situations and he is currently fitting niche models to derived environmental gradients.



**Name** Martin Mortimer  
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**Website** www.liverpool.ac.uk/bio  
**Research Area** Agroecology of rice-based cropping systems and adaptations to climate change

### Research Activities

Martin's current research focuses on the impact of climate change on food security and, particularly, the application of agro-ecology to the sustainability of rice-based cropping systems that underpin food security for millions in south and south-east Asia. In these systems, variation in water supply is the major factor governing the underpinning ecosystem services. Shortage of water for agriculture has already caused unprecedented changes in the ecology of agricultural and rice landscapes which will be further accentuated by the increasing variance in seasonal water availability due to climate change. Martin is pursuing three research themes (via international donor funding) to try and help overcome these problems. The first is agro-ecosystem functioning in response to climate change and the development of sustainable cropping systems in irrigated direct seeded rice (DSR) in India. Long-term experimentation is assessing the impact of changes in cropping practices and in natural resource management, particularly water supply, on variability in crop yields (DSR, wheat, pulses) and the long-term dynamics of pests, particularly weeds, in the Indo-Gangetic plains. A second theme is ecosystem services and decision support frameworks in agro-ecosystems. Agro-ecosystems both provide, and depend on, ecosystem services in contributing to food security in productive and resource poor environments. Under a UKIERI programme on the 'Impact of climate change on the water cycle and ecosystem functioning at the river basin scale' Martin is collaboratively working on adaptations to climate change and the socio-economic implications of policies of water management in the Manjira basin in Andhra Pradesh. Finally, Martin also works on the impact of transgene outcrossing to wild and 'weedy' rice.

## Spotlight on the University of Liverpool



**Name** Hugh McAllister  
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**Website** www.liverpool.ac.uk/bio  
**Research Area** Phylogeographic and cytotoxic monographic studies on temperate N. hemisphere plant genera, particularly *Hedera*, *Sorbus*, *Betula*.

### Research Activities

Hugh's work has led to the discovery of apomixis in rowans (pinnate-leaved species of *Sorbus*) and the publication of a Kew monograph. This work has completely revised the classification of the genus and suggested evolutionary relationships which are now being investigated in collaborative molecular work with Yale. A parallel project is underway on ivies (*Hedera*) with colleagues in Spain, and it is hoped the imminent publication of a monograph on birch (*Betula*) will stimulate similar work on this familiar but previously taxonomically-confused genus. The mature wild-sourced trees of these and other woody tree genera at the University of Liverpool's botanic gardens at Ness, are an almost unique resource for such studies.

A usable taxonomy, and correct identification, documentation and vouchering of material, are all essential prerequisites for meaningful molecular phylogenetic work. Lack of these has led to a considerable amount of published work being of little value, and recorded sequences being miss-assigned through misplaced trust in the correct identification of trees from unknown sources in botanic gardens. Co-operation between traditional taxonomists, horticulturalists and molecular phylogeneticists is required to advance knowledge of the evolution and dispersal of living organisms, especially over the last 60 or so million years as modern Angiosperms have come to dominate the flora of the Earth.



**Name** Mike Wood  
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**Website** www.liverpool.ac.uk/swimmer  
**Research Area** Contaminant uptake and the implications for trophic transfer

### Research Activities

Mike's research focus is environmental pollution and he has worked on the interception and uptake of chemical and radioactive pollutants. Recent work has included the UK Soil and Herbage Survey (UKSHS), which established a UK baseline for organic, inorganic and radioactive pollutants in soil and vegetation.

His studies on heavy metals and radionuclides includes work on the mercury concentration in plants and crops around crematoria and assessment of the risks to human health, while an investigation into the interception and uptake of radionuclides discharged into the marine environment from Sellafield included analysis of their subsequent deposition onto the West Cumbrian coastline via the sea-to-land transfer mechanism. Mike has also been scientific advisor to a project investigating the use of plants as bioindicators of multi-contaminant (chemical and radionuclide) exposure at the Semipalatinsk Test Site, a former Soviet nuclear weapons test site in Kazakhstan.

He has developed strong collaborative links with a number of national and international research centres, especially the Centre for Ecology and Hydrology and the Russian Institute of Agricultural Radiology and Agroecology (RIARAE).

## The Living Field

Sharon Neilson, SCRI, Invergowrie, Dundee, DD2 5DA, Scotland, UK

The Living Field is a series of projects and activities through which the science of farmed habitats is shared with schools and the public. The projects explore the biology of plants, invertebrates and the environment through resources accessible to all ages, including a CD-Rom, The Living Field Community Garden and the Living field Study Centre.

The Living Field CD-Rom is a free educational resource containing more than 300 pages of high quality images, sound, games and activity sheets linked to science and the environment in a stimulating, interactive and challenging manner. It was developed by the Scottish Crop Research Institute (SCRI) with the support and assistance of the Scottish Government Education Department and LTScotland. The CD-Rom reinforces the Scottish 5 - 14 National Guidelines for Environmental Studies: Science and was distributed to every primary and secondary school in Scotland. It is also relevant to UK-wide environmental science and is available for download, free of charge, from the Living Field Website <http://livingfield.scri.ac.uk>

The Living Field Community Garden was opened at SCRI in 2005 and is part of the SCRI Science Stroll. The garden is freely open to the public and links with our network of public pathways. The garden contains crop and habitat demonstration areas which contain information about arable wildflowers, the environment, habitats, plant care and farming information. The crop demonstration area is used by schools to carry out experiments such as the effect of fertilisers on different cultivars.

The garden highlights the science of the seedbank-based food web, explaining that, whilst some seedbank species are a burden, as weeds or reservoirs of crop pests, other species benefit farmland wildlife, support natural predators, stabilise the soil and reduce loss of nutrients. We grow these plants to provide living material for training and to gain an understanding of their biology.



The Living Field Study Centre opened in 2007 and is a base from which visitors can study the flora and fauna of arable land in Scotland. The centre has strong working links with volunteer groups and NGOs and its' focus is on raising awareness of the diversity of plants and animals in the local region, their contribution to the functioning of ecosystems and their importance in sustaining productive farmland. The Centre provides facilities that are freely accessible to people of all ages and abilities with an interest in biodiversity. It is open throughout the year and visits can be organised for visitors, including schools, conservation volunteers, wildlife watch groups and other interested parties who wish to develop their understanding and appreciation of diversity in plants, seeds, flowers and insects using digital and interactive technologies, including whiteboards, microscopes and computers.





# **20<sup>th</sup> International Conference on Arabidopsis Research**

**Edinburgh**  
Scotland, UK

**30th June - 4th July 2009**

<http://www.arabidopsis2009.com/>

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**Environmental Responses**

**Natural Variation**

**Plant Defence**

**Cell Biology**

**Genome Organisation**

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