

# GARNish

The official GARNet newsletter

December 2007. Edition 7



*Rosemary Wiese*

## Editorial

2007 has been a productive year for GARNet with rewarding collaborations at both the international and national level. It all began with an invite to attend a workshop at the Plant and Animal Genome Conference in January to consider the funding of plant genomics at an international level. As a result of this meeting several countries agreed to form an International Steering Committee for Plant Genomics (ISCPG) to promote collaborations between national programmes in plant genomics. ISCPG aims to launch a website next year to keep us up to date with a variety of international initiatives, so watch this space. Over the last 2 years GARNet has organised several meetings and workshops to encourage the uptake of systems biology, we are therefore pleased to announce that in the recent BBSRC Systems Approaches to Biological Research (SABR) initiative 3 out of 6 grants funded involved Arabidopsis research. [http://www.bbsrc.ac.uk/media/releases/2007/071127\\_systems\\_biology.html](http://www.bbsrc.ac.uk/media/releases/2007/071127_systems_biology.html) In addition, the community has also been the recipient of funding from the MATSYB initiative. The STEMN network, which aims to bring together biologists and theoreticians working on the spatio-temporal modelling of the growth and behaviour of Arabidopsis, was granted funds along with a cell signaling network (SIGNET).

In December GARNet will co host the inaugural mathematics in plant sciences study group with CPIB and next year we will link up with SEB to organise a 3 day plant symposium.

I hope you all have a happy Christmas and a successful new year. See you in 2008  
Ruth

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Front cover image of *Cardamine hirsuta*, kindly supplied by Miltos Tsiantis and Rosemary Wise.

Many thanks to all who contributed to this issue of GARNish, especially Malcolm Bennet, Christine Bunthof, Christine Foyer and Sophie Laurie.

If you have any comments about GARNish or would like to contribute an article to the next issue please contact Ruth Bastow, [ruth@arabidopsis.info](mailto:ruth@arabidopsis.info)

## GARNet 2007

The GARNet meeting this year provided an interesting mix of mathematical biology, hormones, pathogens, biomass biology, and informatics.

Session 1, Integrative Biology, brought together researchers trying to reconcile data and models for plant growth. Jan Traas focused on the apical meristem. It is known that leaves appear at sites of local maxima in auxin levels. However, to fully account for these observations, the notion that physical stress reorients microtubules needs to be included. The physics of foams provided Jan with mathematical methods to analyze cell shapes, and generate models which predicted, cells with less than 6 walls have convex walls and grow more slowly. If cell walls in such models are replaced by springs, stable patterns are generated that are consistent with observations of the apical meristem. Malcolm Bennett described the objectives of the new BBSRC/EPSCRC sponsored Centre for Plant Integrative Biology (CPIB) <http://www.cpiib.info/> at Nottingham which aims to create a multiscale model of hormone regulated Arabidopsis root growth and development. He described how CPIB researchers are integrating modelling and experimental approaches to determine how plant hormone signals control organ growth. Malcolm illustrated this point by describing how multiscale modelling of auxin transport in elongation zone tissues had led Nottingham researchers to experimentally demonstrate that auxin coordinates gravitropic root growth by targeting elongating epidermal cells. Pierre Hilson reported on a systematic effort of the Agronomics EU consortium (<http://www.agron-omics.eu/>) to understand leaf growth.

Sessions 2 and 3 strongly emphasized plant/pathogen interactions. Ralph Panstruga provided a beautiful account of investigations into the mechanism by which *mlo* mutations potentiate plant defence. Microarray analysis revealed many possible targets including WRKY38 and 53, as well as a nudix hydrolase and a flavin monooxygenase. Using double mutants of *mlo2* with various other genes, 3 methylamino indole made via *CYP79B2* and *B3* were shown to be important for resistance. Callose synthesis proved less important; in *mlo2 pmr4* double mutants, cell wall appositions were still made, and resistance was unaffected. Murray Grant introduced the subject of interactions between hormone signalling pathways and disease susceptibility. *Pseudomonas* DC3000 potentiates ABA signalling as part of its virulence strategy, and the effector AvrPtoB alone seems able to accomplish this. Complex interactions between JA, coronatine, ABA and SA signalling were revealed during a systematic analysis of the phenotypes and metabolomes of various mutants. Jim Beynon reported on effectors of *Hyaloperonospora parasitica*, that causes Arabidopsis downy mildew. He particularly focused on the effector ATR13, recognized by RPP13 in some race/host combinations. Surprisingly, *ATR13* alleles are not always recognized by RPP13, and *RPP13* alleles are not always involved in recognizing ATR13. In session 3, Jeff Ellis reported on the disease caused by rusts, both in cereals and in flax. Interestingly, rice is not susceptible to any rusts, but Ellis reported that this resistance is associated with active defence at sites of pathogen infection. In the flax/flax rust combination 4 different resistance loci have been cloned, all encoding resistance proteins of the TIR-NB-LRR class. Unlike other examples, there is direct interaction between the matching alleles of the rust AvrL567 protein and host R protein. I spoke next in this session and reported on investigations into why auxin promotes susceptibility to *Pseudomonas syringae*, and concluded that it could stimulate the JA signalling pathway, resulting in attenuation of SA-dependent defence. It appears that auxin can stimulate the JA signalling pathway, resulting in attenuation of SA-dependent defence. Intriguingly, DELLA proteins (previously regarded as primarily involved in gibberellin signalling) play a role in JA signalling. Jane Parker reported on the mechanisms by which the lipase homologs EDS1, PAD4 and SAG101 promote biotroph resistance, and data that implicate altered redox balance in their effectiveness. In session 4, Simon Turner provided new insights into the complexities of cell wall biosynthesis by analysis of Arabidopsis mutants, while Mike Bevan provided an update on the status of Brachypodium genomics and genetics to investigate cell wall synthesis in monocots. Kerrie Farr of IGER provided an interesting insight into the status and challenges of Miscanthus breeding. The final session focused on informatics. Chris Town talked about investigations into 4000 Arabidopsis genes of unknown function, and had verified the existence and expression patterns of many of them. Rodrigo Gutierrez reported on software platforms to represent and interpret systems biology data. Finally, Ewan Birney provided a tour-de-force presentation on the ENCODE consortiums analysis of the human genome, and included some surprising conclusions. For example, many factors at transcription start sites bind as often to sequences 3' to the start site as they do to classical promoter element sites 5' to the start. There are many more transcription start sites than previously realized, and many more transcripts. He suggested that a large proportion of transcription might occur to impose, change or sustain histone modification patterns, rather than vice versa. Comparisons between mammalian genomes suggest that there are many ancient conserved regions, and a significant proportion are associated with DNAase hypersensitive sites. Finally, he pointed out that the EBI now has responsibility for annotating all life, including plants, and hoped to engage with the Arabidopsis community to fulfil this part of its mission.



## News and Views

### Beyond Biofuels: Plant Products for Industry

The current interest in turning crops into gasoline and diesel marks the beginning of the end of our total dependence on fossil fuels and an awareness that in the future we will have to obtain far more of our industrial feed-stocks from renewable sources such as plants. Moving to such a bio-based economy poses major technical, commercial and social challenges and with terrestrial



**The science of chemurgy-biorefining**  
Basic plant based feed-stocks are acted on by fermentation or chemical processing to derive crude products which can be refined into a range of useful platform chemicals and specialty by-products.



**Primary Products**



**Value added products**



crops likely to be a major source of renewables, there are major opportunities for plant science to play an important future role in developing these new products for industry. The Bioscience for Business Knowledge Transfer Network (BfB-KTN) funded by the Technology Strategy Board, has a brief to encourage industry to move to bio-based production. In many cases the technologies required are totally undeveloped and realizing these ambitions will require a significant basic science input from plant, microbial and marine science. As part of its activities, the BfB-KTN is promoting the strategic importance of plant science and identifying routes by which it can deliver tomorrow's industrial products. The strategy which we have developed involves a three tiered approach. Initially we will utilize existing

plant materials and derive platform chemicals goals will be largely met through downstream

from them by biorefining technologies. These immediate chemical processing and biotransformation technologies.

In the second generation we will need to develop plants which are customized to produce specific products for non-food applications. These future plant products for industry (FPPIs) will require concerted breeding programmes for selecting novel traits and require the development of attendant basic science tools. The final longer term objective will be to re-engineer plants with completely new non-food traits to fully deliver products which in performance terms match those derived from oil-based chemical production. To date, the BfB-KTN has been engaged in discussions with industry, academics and government funding agencies in developing the first tier of projects, notably an initiative in Integrated Biorefining. Membership of the BfB-KTN network is open to all and we are actively working with GARNet and the National Non-Food Crop Centre to identify potential partnerships between academia and industry to develop new plant-based technologies in renewables. If you would like to learn more about the work of the network visit [www.biosciencektn.com](http://www.biosciencektn.com). Article written by Rob Edwards - Durham University

## The Future of Arabidopsis Research

You may be aware that the National Science Foundation (NSF) 2010 project to elucidate gene function in Arabidopsis is nearing its end. The US is carrying out a forward look meeting next year to generate ideas for Arabidopsis research in the next decade (2020).

The BBSRC along with others in Europe, particularly DFG, would like to garner European views on the future of Arabidopsis research after 2010 to input both to the NSF and other future transnational collaborative projects.

GARNet and the BBSRC would therefore like to ask for feedback from the UK community on the following areas.



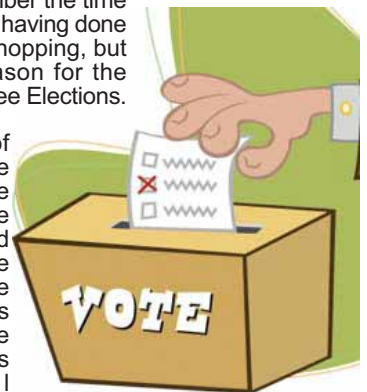
- What do you think are the strengths and weaknesses of plant functional genomics in the UK?
- What are the current technological strengths and weaknesses in the UK?
- Suggestions for a future scientific "vision" / research aims.  
(Please note we are looking for research aims which are specific for plants or which can not be easily solved in other model system (e.g. yeast, fly, worm, and mouse))
- Suggestions for new "hot" topics.

If you would like to provide us with your ideas on the future of Arabidopsis research then please e-mail your comments to Ruth Bastow ([ruth@arabidopsis.info](mailto:ruth@arabidopsis.info)) by 4<sup>th</sup> February 2008. Your comments will be used to formulate a UK perspective for a European discussion meeting next year.

## GARNet Elections

Not only is December the time to panic about not having done your Christmas shopping, but it is also the season for the GARNet Committee Elections.

This year three of our committee members are standing and we need to find suitable replacements. The community has nominated the following as potential candidates :-



Anna Amtmann - University of Glasgow  
Mary Byrne - John Innes Centre  
Alessandra Devoto - Royal Holloway, University of London  
Claire Halpin - University of Dundee  
Mark Hooks - Bangor University  
Patrick Hussey - University of Durham  
Julie Scholes - University of Sheffield

It is now up to you to decide who joins the committee. To cast your vote; e-mail ([ruth@arabidopsis.info](mailto:ruth@arabidopsis.info)) the names, in order of preference, of the 3 individuals who you would wish to appoint to the committee. Voting will close on Friday 21<sup>st</sup> December 2007.

# Arabidopsis Resources

## SUBA: The Arabidopsis Protein SubCellular Database

<http://www.suba.bcs.uwa.edu.au/>

written by Joshua L. Heazlewood, Julian Tonti-Filippini and A. Harvey Millar

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**Subcellular localisation** information can contribute towards our understanding of protein function, protein redundancy and of biological inter-relationships. While a variety of technologies are currently employed to determine the sub-cellular location of proteins much of this information is not available in an integrated manner. In an attempt to get a clearer picture of our experimental data and to more generally understand subcellular partitioning we have brought together various data sources to build SUBA, a **SUB**-cellular location database for **Arabidopsis** proteins. The database has a web accessible interface that allows advanced combinatorial queries to be undertaken on the contained data.

### Subcellular location data available in SUBA

Localisation information was obtained for Arabidopsis proteins from a variety of sources and referenced against the current annotation of the Arabidopsis genome (TAIR release 7) and include:

- proteins localised through chimeric fusions studies (comprising 1348 proteins from 922 publications)
- sets from sub-cellular proteomic studies (comprising 3140 proteins from 58 publications)
- localisation information derived from the gene descriptor fields (comprising 2701 proteins)
- UniProt annotated locations (comprising 1981 proteins)
- AmiGO (Gene Ontology) cellular component information derived from Direct Assay (comprising 877 proteins)
- predicted subcellular localisations of the entire Arabidopsis protein set using 10 distinct localisation programs

Combined these data provides 10 experimental sub-cellular location sets with localisation evidence for nearly 7300 proteins representing ~25% of the predicted protein coding capacity for Arabidopsis and significantly ~30% of all expressed genes. These include protein localisation information for mitochondria (1031), chloroplast (1679), ER (286), plasma membrane (1000), nucleus (2497) and vacuole (778).

### Using the SUBA resource

The SUBA interface has been designed as a navigatable application utilizing a series of tabs to query, view and manipulate search results without the use of the web browser's forward and back buttons.

SUBA is accessed through the URL: <http://www.suba.bcs.uwa.edu.au>

When initially arriving at the site the contents of the Search Tab are displayed (Figure 1). In the top window "Search for Arabidopsis proteins where..." is displayed and represents the beginning of the Boolean sentence that will form your query of the SUBA database. Each row of pull down menus work in combination to construct a query and each combination can be added to the main query pane by pushing the "Add" button at the end of the row.



Figure 2. Constructing a SUBA query examining proteins localised in the plastid through mass spectrometry.

constructed query in the top window. For example, to extend the initial query sentence above to include proteins localized to the plastid through GFP studies, the Boolean linker "AND" would be used. After selecting the linker the selection pull down menus



Figure 1. SUBA search interface which is used for the formulation of database queries.

### SUBA Query Construction

The first row of pull down menus provides access to the majority of experimental localisations data. Using the 3 pull down menus, a query can be built to investigate, for example, plastid localized proteins by mass spectrometry. To access such a set of proteins, the subject of the first pull down menu (Protein location) can be left as "is", while the second menu (inferred by) the option "MS/MS assay" is selected. The third pull down menu (to be in) contains the subcellular location tags and in this example "plastid" is selected. This query combination is then activated using the "Add" button at the end of the row. The built query sentence will appear in the top window under "Search for Arabidopsis proteins where..." with the statement "Protein location is inferred by MS/MS assay to be in plastid". The database can be queried now by pushing the "Submit" button in the command bar (below the top window) of the application (Figure 2).

However, more complex queries can be built from this initial statement by selecting the Boolean linker, "AND" or "OR" command buttons (or brackets for long complex queries). Any mistakes can be removed from the forming query sentence in the top window by using the "Undo" button (which removes the last entered query) while "Reset" will remove the entire

# Arabidopsis Resources

## SUBA: The Arabidopsis Protein SubCellular Database

become activated again allowing an extension to the initial query sentence to be added. To add plastid proteins identified through GFP analysis simply select "Protein location is", then "inferred by GFP assay" from the middle pull down menu on the top row and finally "to be in plastid" from the third pull down menu. The newly formed sentence (Protein location is inferred by GFP assay to be in plastid) is added to the above query in the top window by clicking the "Add" button at the end of the row. By selecting the "Submit" button, this more complex query will select the set confirmed to be in plastids by both GFP and mass spectrometry (Figure 3). If the Boolean linker "OR" was used between these two query sentences, a larger set would be retrieved where GFP, mass spectrometry or both GFP and mass spectrometry had located gene products in plastid.

Extremely complex queries can be constructed using the SUBA search tab interface. These can include an examination of subcellular claims by different research papers within the database using the "Protein location is/is not described in (any paper)" menu row. These queries can result in combinations of sets from specific papers (by using the "OR" linker) or for shared sets of proteins claimed by multiple papers (using the "AND" linker). While localisation information exists from experimental sources for around 7300 Arabidopsis gene products, SUBA contains pre-computed predictions of localisation for 10 prediction programs for all ~30,000 Arabidopsis proteins. Prediction information can be used to augment and refine experimental data queries, used in combinations to extract bioinformatic sets when little or no experimental information is available or as a means to corroborate contradictory experimental results. These data are accessed through the "Protein location is/is not predicted by (predictor) to be in (location)" menu row. Queries can also comprise text based searches of descriptor fields (e.g. protein kinase) through the "Protein information contains/does not contain keyword" menu row. A variety of physio-chemical parameters can also be queried including molecular weight, EST numbers and chromosomal locations. The SUBA database also provides a mechanism to extract all the above information on a user defined



Figure 3. Extending the initial SUBA query using the Boolean linker to examine proteins also localised to the plastid through GFP.



Figure 4. Extending the initial SUBA query using the Boolean linker to examine proteins also localised to the plastid through GFP.

organised using mouse drag and drop functionality and new columns can be added to the Results through the function menu. Only 50 rows of data are displayed with further rows available using the "Next Page" button at the bottom left of the Result tab window. All results can be downloaded as a tab delimited file by using the button at the top left of the Result tab window. Each AGI on the displayed Results matrix provides a link to a Summary page for the entry which contains a detailed breakdown of experimental localisation information, sub-cellular prediction information, physio-chemical characteristics, a hydropathy plot, an Interpro domain summary and links to the same entry at other Arabidopsis databases (Figure 5).

### Final Remarks

The SUBA resource provides a powerful tool to investigate subcellular localisation in Arabidopsis through the unification of disparate datasets and through the provision of a web accessible interface for the construction of powerful user based queries resulting in a one-stop-shop for protein localisation in this model plant.

set of Arabidopsis proteins using a list of AGI identifiers through the "Arabidopsis Gene Identifier is in list/is not in list" menu row. All these extra query options can be added to an existing query sentence or can be used as a standalone queries using the same procedures outlined above i.e. define the query (each row contains related parameters) then use the corresponding "Add" button, and if required the Boolean linkers to expand the query.

### SUBA Results

Once a query sentence has been finalized the "Submit" button (found on the command bar) will interrogate the SUBA database with the query string. The contents of the Result tab will automatically display any information resulting from the query sentence (Figure 4). The results are presented in tabular form, with information for each AGI code presented on a row. By default 8 columns will be displayed. The AGI, the TAIR descriptor, location summaries of predictors, location by Mass Spec (proteomics), location by GFP, location by annotation (TAIR), location by AmiGO and location by UniProt. The codes or unique identifiers (uid) beside each location in the Result tab are links to the primary data source for each entry at PubMed or ISI. Results can be sorted by field using the function menu activated by selecting the arrow in the column header. Columns can be added to the Results through the function menu.



Figure 5. SUBA AGI summary page containing detailed localisation information and hyperlinks to other databases. Screenshot is a truncation of the summary page.

## An invitation to join EPSO, the European Plant Science Organisation

Article provided by Isabelle Caugant EPSO

**EPSO** is an independent academic organisation representing 57 institutional members bringing together more than 140 research institutes, departments and universities from 25 European countries. EPSO has seven institutional members in the UK:

- The Plants and Environment Research Group, Lancaster University
- Rothamsted Research, Harpenden
- The Sainsbury Laboratory, Norwich
- John Innes Centre, Norwich
- The Scottish Crop Research Institute, SCRI, Dundee
- Warwick HRI, the University of Warwick
- The Centre for Plant Sciences (CPS), Faculty of Biological Sciences, University of Leeds



The association was founded in 2000 to represent the needs and interests of the European plant science community. Since then, it has focused its work on two areas: science policy and support to plant scientists.

EPSO's mission is to improve the impact and visibility of plant science in Europe. Its top priorities are to facilitate a greater understanding of the importance of plant science to policy makers, to boost funding for basic research and to coordinate research activities on the national and European levels – and beyond.

EPSO has two European industrial organisations and individual companies as observers. It is a member of the Initiative for Science in Europe (ISE) and of the European Life Sciences Forum (ELSF), and has links to specialised organisations in the area of plant and life sciences in Europe and worldwide.

### Science policy

EPSO provides recommendations on European science policy to the European Commission, members of the European Parliament and national politicians. EPSO made key contributions that ensured funding is available for plant research in the Sixth and Seventh Framework Programme for Research (FP6 and FP7) and fostered the establishment of the ERA-NET on Plant Genomics, an EU-supported network which supports international research efforts in the field. EPSO, through membership of ISE and ELSF, helped define and establish the European Research Council (ERC).

In 2004, EPSO and EuropaBio started one of the first Commission-backed European Technology Platform, 'Plants for the Future', that recently launched with great success its final Strategic Research Agenda (SRA) at the European Parliament in Brussels. The SRA presents how a previously published vision paper for the next 20 years can be realised to address key socio-economic challenges facing Europe. Work towards the implementation of the SRA is currently under way and activities at national level can start in 2008.

EPSO regularly publishes position papers to make the voice of plant scientists heard and to outline the opportunities they offer to address current societal challenges. Released in September 2007, EPSO's position paper on bioenergy and renewable materials presents insights into plant research activities that can contribute to energy security and alleviating global climate change.

### Supporting scientists

EPSO has built a strong reputation among scientists in Europe and has become the preferred European contact for scientists and companies worldwide interested in plant-related issues.

EPSO organises a biannual conference that attracts top level scientists and speakers. This major gathering brings together plant scientists from Europe and other continents to present and discuss cutting-edge science and, uniquely, plant science policy and societal relevance. Together with scientists in other disciplines, they build an interface to new areas. The next conference will take place in France, from 22 to 26 June 2008, and registration is now open.

Like its conferences, EPSO workshops have established a reputation for being visionary and high-quality think tanks in emerging areas of plant science. These workshops bring together disparate disciplines so as to overcome barriers and facilitate collaboration. After two days of thorough discussion, workshop participants compile a white paper defining prioritised objectives that are then communicated to the European Commission and national policy-makers. The next workshop, on biofuels, will take place in May/June 2008 in Umeå, Sweden.

*EPSO News*, the organisation's bimonthly e-newsletter, presents the latest developments in plant research and provides EPSO members with information on the various international, European and national funding programmes. The online newsletter is only accessible to EPSO members.

### Two types of membership: institutional and personal

Institutional membership is open to universities, research institutions and departments thereof conducting research in the field of plant science worldwide. Institutional members decide on and actively participate in EPSO's science policy work. They are key actors in advising on the future European plant research policy.

Several departments from different universities (up to five) can jointly form a 'University Cluster'. The number of units in a cluster depends on the size of the plant sector in each of them.

Research institutes and universities from new Member States or candidate countries to the EU have the opportunity to form a 'New Member State Cluster'. It is possible for one country to form several clusters, each one regrouping units from up to five universities or institutes.

The annual institutional membership fee depends on the number of people working on plant science in the institute or university. It is €2,500 for small research units (below 50 people) and new Member State Clusters. For medium and large entities and university Clusters, the fee is €7,500. For very large entities (beyond 600 people), the fee is a multiple of these figures.

Personal membership is targeted at individuals interested in plant science, regardless of their nationality, profession, seniority or age. This opportunity is free for individuals working in an EPSO member institute or university. For others, the annual fee depends on their career stage: students (€40), post-docs (€60) and professionals (€100).

EPSO personal members have access to information gathered by EPSO, such as information on funding opportunities in European countries and the FP7 online broker. They can also use the FP7 partner finding tool, browse the database of plant scientists and the EPSO online portal; and read the bimonthly newsletter. Moreover, personal members can apply for an EPSO Conference support grant.

EPSO is looking forward to welcoming you as a member.

For more information: [www.epsoweb.org](http://www.epsoweb.org)

Membership information available at: [www.epsoweb.org/about/membership.htm](http://www.epsoweb.org/about/membership.htm)

Contact: [epsos@epsomail.org](mailto:epsos@epsomail.org)

Fourth

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# Plants for Life

Toulon (Côte d'Azur), France

22 - 26 June 2008



## Plant Science in Europe - Science Policy

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*The challenges for tomorrow's agriculture*

### Understanding, preserving and using plant diversity

*Genome structure and evolution;*

*Plant adaptation, domestication and conservation;*

*Climate change and challenges for the next decades*

### Preserving our future by reducing the inputs in agriculture

*Reducing water input; Reducing fertilizers;*

*Reducing pesticides*

### Improving plant product quantity and quality

*Developmental biology; Improving yield; Food and feed*

### New products

*Plant based biofuels: how to improve them?;*

*Biomaterials, biopharmaceuticals and other new products*

### Confirmed Speakers:

Anne-Françoise Adam-Blondon, Birgitte K. Ahring, Claus Andersen, Ian Bancroft, Michael Bevan, Dirk Bosch, Inge Broer, Enrico Coen, Catherine Feuillet, Chris Field, Richard B. Flavell, Andrew D. Friend, Yuri Gleba, Wilhelm Gruissem, Marion Guillou, Timothy Hall, Luis Herrera Estrella, Stephen Hopper, Jonathan Jones, Sophien Kamoun, Jay D. Keasling, Peter Langridge, Ottoline Leyser, H el ene Lucas, Joachim Messing, Karin Metzloff, Franco Miglietta, Graham Moore, Javier Paz-Ares, Kaisa Poutanen, Matin Qaim, Rudy Rabbinge, Roberto Ranieri, Babis Savakis, Mark Stitt, Bj orn Sundberg, Frank Takken, Fran ois Tardieu, Wim Van Camp, Nicolaus von Wir en, Robert Watson, Lothar Willmitzer, Jian-Kang Zhu

Coordinators: Karin Metzloff, EPSO and H el ene Lucas, INRA, France  
Information and registration at [www.epsoweb.org](http://www.epsoweb.org)

# Beyond Arabidopsis: New crucifer systems for comparative genetics

written by Angela Hay, Emily Abrash and Miltos Tsiantis.

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What does crucifer leaf shape have in common with dipteran insect wing pattern? Not a lot from a functional point of view. But from an evolutionary perspective, natural variation in both characters presents us with one of biology's most intriguing and fundamental questions. Namely, how have developmental processes diversified over time to generate the breathtaking variety of forms observed in nature? Thanks to the past thirty years of developmental genetics and the burgeoning field of evo-devo, we are now poised to start providing concrete answers to such questions. The study of model species has provided key insights into the fundamental mechanisms that pattern an organism by delineating the genetic hierarchies that direct its development. Thus, a conceptual framework now exists that can support efforts to understand the mechanistic basis of the vast morphological and biochemical diversity exhibited in different lineages of the tree of life. Here we will discuss how comparative studies of *Arabidopsis thaliana* and its relatives can empower such efforts, and we point out recent advances and future opportunities in the field.

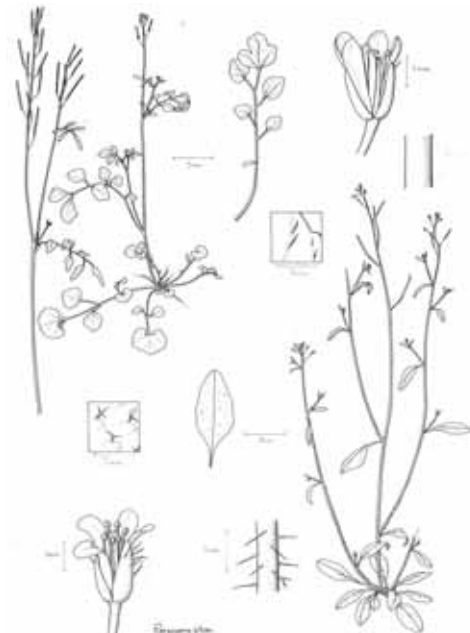
An obvious question to ask is what can be gained from comparing closely related species as opposed to more divergent model organisms such as maize and *Arabidopsis*. The answer is that lineages that diverged relatively recently show strong similarity in both DNA sequence and overall regulatory organization. This reduces the "noise" of changes unrelated to the trait of interest, and facilitates the identification of specific differences that are likely to be responsible for morphological divergence. This approach is not only powerful from a basic research perspective, but can also greatly inform efforts to modify traits for agricultural or biomedical purposes. For example, it is likely that comparative research on *Arabidopsis* relatives will substantially enrich efforts for the improvement of Brassica crops.

Any effort to understand the molecular basis of biodiversity is greatly enhanced by whole genome sequencing, which is becoming increasingly cheaper with the advent of next-generation sequencing technologies. However, functional tests are required to elucidate how genetic hierarchies diversified to create novel properties in different species. Sequence information provides a powerful springboard to develop such functional tests. For example, it firstly provides the complete set of genes and known biochemical activities present in a given organism, secondly it expedites the identification of genes from mutant or trait analysis, thirdly it facilitates global evaluation of gene expression, fourthly it allows detailed analysis of natural variation within a species and hence an understanding of the dynamics of microevolutionary change. Finally, comparative genomics permits analysis of the role of genome evolution events, such as chromosomal rearrangements or changes in ploidy, in the diversification of organisms. Thus, genome sequencing efforts, led by Detlef Weigel, for two *A. thaliana* relatives, *A. lyrata* and *Capsella rubella*, will be an invaluable community resource (*A. lyrata* traces available at <http://www.ncbi.nlm.nih.gov/blast/mmtrace.shtml>) (1). The diversity in morphological and physiological traits within Crucifers makes them exciting subjects for comparative study (2,3). Comparisons between self-compatible *A. thaliana* and self-incompatible *A. lyrata* have determined how molecular evolution of a signalling system for self/non-self discrimination, resulted in the loss of self-incompatibility in *A. thaliana* (4). The ability to interbreed self-compatible *C. rubella* with its outcrossing relative *C. grandiflora* provides an exciting opportunity to test whether similar molecular routes were taken during repeated evolution of this same trait (5). The monosymmetry of *Iberis amara* flowers is another trait that contrasts markedly with the polysymmetry of *A. thaliana* flowers, and recent comparative approaches have revealed that differential expression of TCP growth regulating proteins underpins the evolution of this morphology (6). Similarly, comparison of flowering time control in annual *A. thaliana* and perennial *Arabis alpina* species should provide key insights into the mechanisms underlying perenniality, as will comparison of the inflorescence-flowering *A. thaliana* with rosette-flowering crucifers provide insight into the regulation of flowering habit (7).



The monosymmetric flowers of *Iberis amara* may facilitate insect-mediated pollination. Image courtesy of S. Zachgo.

Comparative analysis of *A. thaliana* with parthenocarpic *Boechea* species also presents an exciting opportunity to determine how sexual reproduction can be by-passed in certain plant lineages – a trait with considerable applied value for the asexual reproduction of elite crops. Crucifers with diverse physiological traits also promise to provide a valuable functional framework for understanding adaptations of seed plants to adverse environmental conditions and herbivory (8). Such species include salt-tolerant *Thellungiella halophila*, for which genome sequencing is in progress (9), and heavy metal-tolerant *Thlaspi caerulescens* and *Arabidopsis halleri*. (10).



*Cardamine hirsuta* and *Arabidopsis thaliana*. Botanical drawing: R. Wise

The common garden weed *Cardamine hirsuta* has recently been developed, with BBSRC funding, into an excellent comparative system in which to study morphological evolution. Placed side-by-side, *C. hirsuta* and *A. thaliana* differ most strikingly in leaf form; unlike its famous cousin, *C. hirsuta* produces compound leaves, each consisting of a rachis bearing leaflets. Other differences between the two species include floral organ number, shoot architecture, trichome branching and density, and response to gibberellin. Despite these differences, *C. hirsuta* shares many of the characteristics that make *A. thaliana* a tractable model organism. As a diploid species with small genome (1.2x *A. thaliana*), *C. hirsuta* is amenable to forward genetics, and mutants have been successfully isolated from EMS screens. Similarly, plants can be transformed by *Agrobacterium*-mediated floral dip, allowing reverse genetic manipulations. *C. hirsuta* also resembles *A. thaliana* in its wide, bihemispheric distribution, permitting analysis of intraspecific variation. Such parallel studies of microevolution in *C. hirsuta* and *A. thaliana* may reveal the extent to which related morphological adaptations arise via similar evolutionary mechanisms.

Researchers working with *C. hirsuta* have a variety of resources for mapping, mutant identification, and analysis of natural variation at their disposal. For instance, a BAC library with 5,000 ends sequenced and cDNA libraries are currently available, while a linkage map and a database of ecotype-specific polymorphisms are under construction. Moreover, sequence-based resources from *A. thaliana* can often be carried over directly to *C. hirsuta*, thanks to a high degree of nucleotide conservation. Collectively, these resources make *C. hirsuta* a tractable comparative system, one that will become increasingly powerful as its associated resources expand. Currently,



## Beyond Arabidopsis: New crucifer systems for comparative genetics

*C. hirsuta* is a fully functional system for evo-devo research, as demonstrated by a recent study implicating *cis*-regulatory evolution in the diversification of leaf form (11).

In conclusion, the ability to study many traits in parallel in several crucifer species, allows us not only to isolate specific genes underlying biodiversity, but to understand more broadly the developmental logic that underpins the diversification of form in multicellular eukaryotes. Understanding which molecular avenues were followed during evolution to result in morphological or biochemical diversification is not only a major challenge to resolve in biology, but also holds considerable applied research potential. For example, an understanding of which nodes in developmental networks are modified during evolution to produce morphological change, versus which nodes cannot tolerate change, will inform efforts towards crop improvement. Future plant research will therefore benefit from an emphasis on developing tools that allow the functional dissection of natural variation.

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## European Research Area Network in Plant Genomics (ERA-PG) 1<sup>st</sup> Call - The Facts and Figures

### Summary

ERA-PG is a collaborative network now consisting of eighteen funding organisations and was initiated under the ERA-NET instrument of the sixth Framework Programme of the European Commission. The goal of the network is to contribute to the development of the European Research Area and to build a strong knowledge-base in Europe to strengthen the competitiveness in plant genomics. Aiming towards collaboration, scientific excellence, synergy and cohesion, ERA-PG developed its first joint call for research '**Structuring Plant Genomic Research in Europe**'. The call, launched on February 1<sup>st</sup>, 2006, was addressed to plant genomic researchers in Belgium (Flanders), Denmark, Finland, France, Germany, Italy, The Netherlands, Norway, Portugal, Spain and United Kingdom. With a budget of over 35 million euros this is one of the largest coordinated multinational research programmes in the ERA-NET scheme.

Developing an ERA-PG call with minimal bureaucracy and maximum transparency with the participation of twelve different funding agencies and ministries was a challenge. Implementing the first call was a valuable experience and the success of the process provides a strong basis for continued collaboration. A second call is now planned to strengthen the programme, transcending national and where appropriate European boundaries, as efficiently as possible.

### Setting up the call

In 2006 the ERA-PG network consisted of seventeen funding organisations, of which twelve participated in the 1<sup>st</sup> call (Table 1). These twelve funding organisations (of eleven countries) earmarked a budget in the order of 30 million Euros to support the call. Each national funding organisation only awarded grants to the project participants from its own country.

The call was divided into two Sub Calls:

- Sub Call A: Broad Call for Publicly Funded Research in Plant Genomics;
- Sub Call B: Trilateral Partnership and beyond; the Future for European Public-Private Partnerships in Plant Genomics.

Sub Call (A) was open to applications from researchers from nine countries; Belgium, Denmark, Finland, Italy, Netherlands, Norway, Portugal, UK and Germany. Additional research partners from other countries, including industrial partners, were welcome provided that they could bring their own funds and demonstrate true added value to the partnership. The public-private Sub Call (B) built upon positive experiences of the partners of the trilateral initiative between France, Germany and Spain and funds of BMBF, MEC and ANR are exclusively devoted to Sub Call B. Three other partners, BBSRC, FCT and AKA, were keen to support research teams from their country participating in Sub Call B projects. Thus, researchers from six countries (France, Germany, Spain, UK, Portugal and Finland) could apply for grants within Sub Call B. This Sub Call was also open to additional research partners

Country	Organisation	Sub Call A	Sub Call B
Belgium (BE):	Flemish Government, Dept of Economy, Science and Innovation (EWI)	X	
Denmark (DK):	Danish Agency for Science, Technology and Innovation (DASTI)	X	
Finland (FI):	Academy of Finland (AKA)	X	X
France (FR):	National Research Agency (ANR)		X
Germany (DE):	Federal Ministry of Education and Research (BMBF)		X
Germany (DE):	German Research Foundation (DFG)	X	
Italy (IT):	Ministry of University and Research (MUR)	X	
The Netherlands (NL):	Netherlands Genomics Initiative, Netherlands Organisation for Scientific Research (NGI/NOW)	X	
Norway (NO):	The Research Council of Norway (RCN)	X	
Portugal (PT):	Foundation for Science and Technology (FCT)	X	X
Spain (ES):	Ministry of Education and Science (MEC)		X
United Kingdom (UK):	Biotechnology and Biological Sciences Research Council (BBSRC)	X	X
Austria (AT)	Federal Ministry of Education, Science and Culture (BMBWK)		
Israel (IL)	Ministry of Agriculture and Rural Development (MORAD)		
Sweden (SE)	Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning (FORMAS)		
Switzerland (CH)	Swiss National Science Foundation (SNF)		

These ERA-PG partners did not participate to the first call for proposals

Table 1: ERA-PG members and their participation to the first call

## European Research Area Network in Plant Genomics (ERA-PG) 1<sup>st</sup> Call - The Facts and Figures

bringing their own funds and demonstrating true added value to the partnership.

The first call aimed to be as broad and inclusive as possible in terms of research themes. The call stated that: 'Scientific approaches had to be genomic and/or post-genomic in nature and not primarily address the elucidation of function of single genes. A combination of various genomics and quantitative genetics tools should be employed.' Within this framework the opportunity was given to emphasise specific activities as outlined below for the two Sub Calls.

Research Themes for Sub Call A

- Genomic approaches to adaptation and acclimation to abiotic stresses
- Genomic approaches to adaptation and acclimation to biotic stresses
- Yield stability of plants
- Intrinsic genetic potential of plants including natural variation and biodiversity
- Crop breeding
- Development of crop and forage plants for low input systems including protein crops for Europe and crops for animal feed
- Quality traits including traits associated with food storage and processability, quality modification for foods and feeds, specialised uses of crops
- Genomic research into non-food uses for crops including; trees for fuel and fibre production; other plant sources of fuel, fibre and biodegradable packaging materials; bioproduction of therapeutics and other nutraceuticals
- Joint development of genomic tools (technologies and resources), where this addresses and supports the overall scientific objectives of ERA-PG

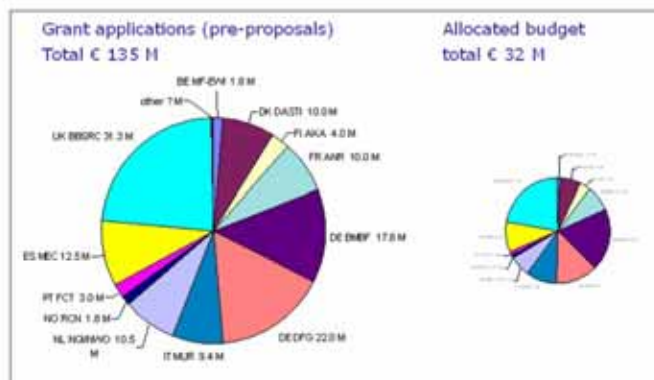


Figure 1. Oversubscription of allocated budget

Abbreviation	Project title	Main applicant	Size	Granted budget (€)
ACT	Genome wide analysis of auxin-cytokinin cross-talk	Prof. Y. Helariutta	3	976,494
ARelatives	Leveraging the genome sequences of two <i>Arabidopsis</i> relatives for evolutionary and ecological genomics	Prof. D. Weigel	8	2,263,398
BARCODE	Genomics-assisted dissection of barley morphology and development	Dr. R. Waugh	3	1,532,940
CISCODE	Conservation and diversity in transcriptional regulation of developmental processes in crop and model plant species	Prof. G.C. Angenent	7	2,210,517
Effectormics	Understanding host plant susceptibility and resistance by indexing and deploying obligate pathogen effectors.	Prof. J.L. Beynon	4	1,295,221
EXBARDIV	Genomics-assisted analysis and exploitation of barley diversity	Prof. A.J. Flavell	7	2,020,953
MultiStress	Multiple stress responses and adaptations	Prof. J. Mundy	7	1,788,397
PLANT STEM CELL NETWORK (PSCN)	Integrated analysis of stem cell function in plant growth and development	Prof. J.A.M. Murray	5	1,950,060
PRECIAR	Proteomics analysis of endosomal compartments in <i>Arabidopsis</i>	Prof. G. Jürgens	6	939,059
RLPRLKs	RLP- and RLK-mediated innate immune responses in <i>Arabidopsis</i> and tomato triggered by pathogen-associated molecular patterns (PAMPs) and avirulence factors (AVRs)	Prof. P.J.G.M de Wit	8	1,919,664
Seeds for growth	Seeds for growth - Identification of transcriptional programs controlling seed growth and development from <i>Arabidopsis</i> to rice	Dr. A. Schnittger	3	717,450
STRESSNET	Regulation of the plant metabolic network during stress	Dr. A.R. Fernie	3	1,444,045
STRESSsRNA	Genome-wide analysis of short RNAs as modulators in dehydration stress tolerance using tolerant and genetic model systems	Prof. D. Bartels	3	895,638
TRANSLEG	Using translational genomics to underpin germplasm improvement for complex traits in crop legumes	Dr. L. Sköt	4	975,970
TRITOP	Thrips resistance in tomato plants	Prof. P.G.L. Klinkhamer	3	639,396

Table 2: List of granted projects in Sub Call A

### Research Themes for Sub Call B

- Improved quality in food and feed
- Sustainable agriculture with improved productivity and yield stability under low input production systems and under biotic and abiotic stress
- Plants for innovative uses such as energy crops or plants as factories
- Plants to improve and stabilize our environments

For effectiveness and efficiency a two stage application and selection procedure was adopted. The main applicant of each consortium submitted a pre-proposal which was assessed by a scientific panel (programme board). A subset of pre-proposals was then invited to submit a full proposal. The full proposals were evaluated by external reviewers (3-5) coming from within as well as outside Europe. The programme board performed the final assessment based on the evaluation reports of the external reviewers, taking into account the rebuttals from applicants where appropriate, and individual expertise of each board member. The recommendations of the Programme Board were presented to the Sub Call Moderating Panels, who developed the final list taking into account budgetary considerations (for Sub Call A), and budgetary and strategic considerations (for Sub Call B). The funding recommendations reached by the Panels were then communicated to the national funding bodies.

### Outcomes of the call

The plant genomics scientific community responded well to the call with a total of 107 pre-proposal applications, one of which was not eligible, leaving 106 applications to be considered. This resulted in a large over subscription of the allocated budget; overall the 106 applications requested five times as much budget as preliminary allocated (Figure 1).

### Sub Call A

The academic sub call attracted 343 applicants from 20 countries, applying within 70 collaborative projects. The largest populations of applicants in the academic Sub Call A come from the UK and Germany, then from The Netherlands, Italy and Denmark, followed

## European Research Area Network in Plant Genomics (ERA-PG) 1<sup>st</sup> Call - The Facts and Figures

by the other countries of funding bodies contributing to this call. Of these 70 pre-proposals 44 were selected to submit full proposals to the Programme Board. The ERA-PG consortium granted the 15 highest ranked proposals with a total budget of nearly 21 million euros. Five of the granted projects are headed by a German coordinator, also five by a UK coordinator, three by a Dutch coordinator, one by a Danish coordinator and one by a coordinator from Finland. The 15 selected projects are listed with abbreviation, title, main applicant, consortium size and total granted budget in Table 2 (opposite page).

The total project budgets in Sub Call A range from 0.6 million euros for project TRITOP to 2.3 million euros for ARelatives. The average total granted budget for a Sub Call A project is 1.47 million euros. Relative to the total budget BBSRC contributes almost 40 %, DFG over 20 %, DASTI, MUR and NWO about 10 % each and AKA 6 %. Contributions of FCT, RCN and EWI are about 1.5 %. It should be noted that the budgets are not directly proportional to the participation in person months due to differences between the countries in personnel costs and coverage of overhead costs by grants.

### Sub Call B

242 pre-proposals were submitted to Sub Call B, from 11 countries and 36 consortia. From these pre-proposals 30 consortia were invited to submit full proposals to the Programme Board, which rated all proposals before a moderating panel made the final funding recommendation. The ERA-PG consortium granted 14 proposals of these 13 were public-private partnership. The overall budget for sub call B totalled 16.6 million euros. Six of the granted projects are headed by a German coordinator, five by a Spanish coordinator, two by a French coordinator, and one by a coordinator from the UK. The selected projects are listed with abbreviation, title, main applicant, consortium size and total granted budget in Table 3 above.

The total granted budgets for the projects in Sub Call B range from 0.4 million euros for FRRB (7 partners) to 2.4 million euros for CEREHEALTH (13 partners). The two very large consortia, GRASP GRAPE WINE with 16 partners and LEGREST with 14 partners receive total grants of about 1.6 million euros. The average total project budget is 1.18 million euros.

### The Future

The second call will be announced on the ERA-PG and national websites early in 2008, and will be similar in nature to Sub Call A of the first call. The trilateral partnership of France, Germany and Spain expect to launch a further public private partnership call but no date is set for this yet.

For more information about the second call visit <http://www.erapg.org/> or contact the UK Coordinator Sophie Laurie - [sophie.laurie@bbsrc.ac.uk](mailto:sophie.laurie@bbsrc.ac.uk)

Abbreviation	Project title	Main applicant	Size	Granted budget
ARABRAS	Identifying relevant candidate genes for improving plant growth under abiotic stress conditions in Brassica crops	Prof. M. Koornneef	7	897,677 €
BIOREGULATORS	Identification of molecular markers for the detection of bioregulators that enhance plant productivity and quality	P. Eckes	6	2,179,822 €
CEREHEALTH	Securing a sustainable production of food and feed? A functional genomic-guided strategy for improving biotic stress tolerance in cereals.	Dr. G. Strittmatter	11	2,446,286 €
COGS	Comparative genomics of shoot branching	Prof. O. Leyser	6	1,073,006 €
EUCANET	Sustainable Fiber: Eucalypt genomics research for improved wood properties and adaptation to drought.	Dr. J. Grima-Pettenati	8	620,29€
FIELD RESISTANCE IN RICE TO BLAST (FRRB)	Deciphering the genetic basis of field resistance to blast in European rice varieties to improve breeding for durable resistance	Dr. L. Marqués Falcó	7	433,222 €
FROSTY	New investigations of the CBF cold response pathway using natural variation, genetics, genomics and metabolomics	Dr. H.I. McKhann	5	827,519 €
GRASP GRAPE WINE	Genomic Research-Assisted breeding for Sustainable Production of quality GRAPes and WINE - GRASP GRAPE WINE	Dr. E. Zyprian	16	1.546.496 €
LEGRESIST	LEGRESIST: Exploiting Genetic Variability of Resistance Genes in major European Food Legumes to Improve Varieties for Sustainable Agriculture	Dr. P.J. Winter	14	1.587.381 €
MELRIP	Understanding the climacteric vs non-climacteric fruit ripening mechanisms in melon using transcriptomic, metabolomic and reverse genetic approaches	Dr. J. Garcia-Mas	7	922,522 €
MUEXPRESS	Isolation of key genes for kernel development through the identification, in a collection of 300 mutant lines, of Mutator insertions in genes expressed in the maize seed	Dr. G. Hueros	4	703,556 €
PROTEIN STORAGE	An integrated genomic and proteomic characterization of induced seed storage organelles for the optimal production of biopharmaceuticals in plants and plant cells (Acronym: ProteinStorage)	Prof. P. Christou	7	808,107 €
RCA GENOMICS	International reference center for the genomics and diagnosis of viruses with small circular DNA	Prof. H. Jeske	4	1.031.039 €
TRIESTER	TRIESTER: Trilateral Initiative for enhancing salt tolerance in rice	Prof. B. San Segundo	9	1.485.317 €

Table 3: List of granted projects in Sub Call B

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*University of Calabria*

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*University of Copenhagen,*  
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Dr Phil Newland *University of Southampton*

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**A Tribute to Simon Maddrell FRS**  
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Professor Julian Dow *University of Glasgow*

### CROSS SECTIONAL SESSION

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Dr Claire Grierson *University of Bristol*  
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#### WORKSHOP: TOOLS FOR SYSTEMS BIOLOGY

Dr Carol Wagstaff *University of Reading*

### CELL

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Professor Keith Lindsey *University of Durham*

#### Circadian Clocks

Dr Weiqun Lu *University of Manchester*  
Professor Richard Balment *University of Manchester*

#### Cross-Tolerance Towards Environmental Stress: Molecular Mechanisms and Ecological Case Studies

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Polar and Marine Research*  
Professor Craig Franklin *University of Queensland*  
Professor Lars Tomanek *California Polytechnic  
State University*

#### Glycosylation

Dr Susan Brooks *Oxford Brookes University*

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Hans Otto Poertner *Alfred Wegener Institute for  
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*The Society for Experimental Biology*

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Judith Bender  
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### Contact Information:

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**Jean Rosenberg** (Exhibition and sponsorship, [info@plantconferences.org](mailto:info@plantconferences.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 the Universities of Newcastle and Nottingham.

## Spotlight on the University of Newcastle upon Tyne

UNIVERSITY OF  
NEWCASTLE UPON TYNE



Research at Newcastle University concerns plant responses to the environment and its impact on plant product production and quality. Within the context of acclimation and adaptation to biotic and abiotic stress, there is a strong focus on redox biology and signalling. The fundamental mechanisms and evolutionary processes that underpin stress tolerance are examined using a range of biological systems that encompass plant-insect interactions and acclimation to atmospheric CO<sub>2</sub> enrichment, exposure to gaseous pollutants as well as chilling/freezing, drought and salinity. Experimental approaches range from *in silico* analyses of gene regulation, through to the examination of the physiological repercussions of stress adaptation in model and crop species. Our goal is to use the accrued knowledge of biotic and abiotic stress signalling and responses to improve crop yield via marker development, the acceleration of plant breeding programs, genetic engineering and the optimisation of crop agronomy and management. Applied research is also undertaken in key areas such as the improvement of non-edible oilseed plants as sources of bio-diesel, the generation of plant cell factories for molecular pharming and post-harvest storage technologies. Start-up and spin-out companies generated by the plant science research team include, BioFresh; launched in 2003 to exploit intellectual property allied to the use of modified atmospheres for the prevention of the spoilage of crops in storage/transit; BioProfiles (launched in 2005) and Genevision (launched in 2007) offering state-of-the-art DNA fingerprinting technology for the identification of plants and microbes. Basic research on plant biology is also interfaced with the group focused on Food Quality and Human Health at Newcastle (<http://www.ncl.ac.uk/afrd/research/integratedagric/food/index.htm>), whose aim is to understand and optimise how diets, foods and food components affect human health, and how production methods affect the quality of foods, food supplements and herbal medicines. Research into food quality focuses on the quantification of the effects of primary production (agriculture), processing, storage, quality control/standardisation, safety assurance, cooking etc. Other related areas include diet composition, functional foods, food supplements as well as the medicinal plants used by consumers, and the provision of evidence to support health claims.



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<b>Research Area</b>	Plant Physiology

### Research Activities

In the natural environment, plants are subject to levels of ozone pollution that depress crop yields and exert far-reaching effects on native plant communities. The impacts of ozone on vegetation are poorly documented. Work in Jerry's laboratory focuses on improving fundamental understanding at the biochemical and molecular level of the mechanisms underlying resistance to ozone-induced oxidative challenge. Current work is focusing on the development of a detoxification algorithm for incorporation into flux-models employed for pan-European ozone risk assessment, with a special emphasis on the exploration of environmentally-relevant levels of ozone on upland plant communities. Also, particular attention is being paid to establishing the genetic basis for the sensitivity of wheat yield to ozone, in a bid to prospectively breed genotypes with enhanced tolerance to this ubiquitous pollutant. Jerry also advises on a range of commercial applications for ozone, and his company – biofresh (<http://www.bio-fresh.co.uk>) launched in 2003 – has successfully exploited the use of trace levels of ozone or ethylene to reduce spoilage and extend the shelf/storage life of fruit and vegetables.

The group is well-equipped and amongst other resources have at their disposal c. 50 controlled environment chambers equipped for laboratory-based ozone treatment, a field facility comprising 16 open-top chambers plus a recently-completed free air ozone exposure system (unique in the UK) that is being used to explore the effects of future upland ozone climates on conservation-important traditional hay meadows.

## Spotlight on the University of Newcastle upon Tyne



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**Research Area** Adaptation and acclimation of CO<sub>2</sub> assimilation and carbohydrate metabolism to extreme environments

### Research Activities

Understanding how plants adjust photosynthetic carbon acquisition and partitioning between competing metabolic functions in response to environmental stress is crucial for developing effective strategies to enhance growth and productivity in potentially limiting environments. One focus of research in this area is the photosynthetic specialisation of crassulacean acid metabolism (CAM) which improves carbon assimilation in water-limited environments. Expression of the CAM pathway is extremely responsive to environmental conditions and thus serves as a model system for establishing the functional significance of genes and enzymes that optimize physiological performance in arid, resource-limited habitats. Moreover, the day/night separation of carboxylation processes in the photosynthetic cells of CAM plants, poses fundamental questions in terms of metabolic control.

Experimental approaches in the lab integrate measurements of leaf gas exchange, biochemistry and gene expression. Current projects include:

- Characterising the physiological and metabolic consequences of CAM deficiency in mutants of *Mesembryanthemum crystallinum*
- Establishing the functional role and regulation of vacuolar sugar transporters
- Determining the role and regulation of starch degrading enzymes in CAM plants
- Establishing the molecular bases of divergent strategies of drought resistance in tropical trees of the genus *Clusia*.



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**Research Area** Biological roles of plant secondary metabolites in nutrition and agriculture

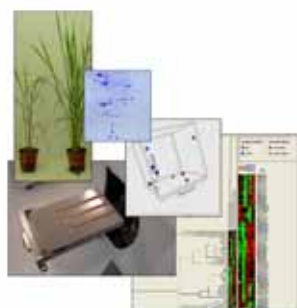
### Research Activities

Plant secondary metabolites are responsible for much of the impact of plants on human and animal health, and their accumulation is affected by a range of environmental factors, some of which depend on the agronomic management.

Kirsten's research focuses on links between agricultural methods, plant chemistry, food quality and health of humans and animals, in particular:

- Biological effects of plant secondary metabolites (natural pesticides) in the diet, in order to improve the beneficial impact of vegetables and other herbs on human health.
- Plant adaptation to low-input conditions regarding product quality and susceptibility to pests and diseases, in order to improve the balance of environmental and economic sustainability in agriculture and horticulture.
- The feedback mechanisms (conditioned taste aversion, nutrient sensing) that ensures innate preference for nutritious, non-toxic food, dependent on the present needs, in humans and other animals.

Presently an important activity is to coordinate efforts at Newcastle University to enhance the impact and exploitation of the research and training activities in industry and society and to facilitate the creation and success of multidisciplinary research projects.



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**Research Area** Plant genome/proteome analysis for food safety assessment

### Research Activities

Food crops are subjected to genetic manipulation or conventional breeding to improve their nutritional values, agronomic characteristics and texture. However, there may be associated unintended effects. Angharad and Kaveh's research aims to identify these effects, via detailed analysis of the plant material at the molecular level followed by bioinformatic analysis. The lab uses comparative profiling technologies (proteomics, genomics) to detect and identify the potential unintended effects that have occurred during the course of breeding and selection processes (non-targeted approach). Similar information is also obtained for GM plant lines with altered contents of specific compounds. Furthermore, if the GM plant lines have been generated by the insertion of specific gene(s), detailed studies are carried out on the GM and parental lines to determine changes in terms of target gene copy number and chromosomal location. The group also utilizes a range of different technologies to assess changes in gene expression between novel and parental lines. During last three years Kaveh has set up and managed the proteomics unit of The Institute for Research on Environment and Sustainability at Newcastle University. The unit intends to provide support facilities for protein identification and characterisation through i) High-Throughput Two-Dimensional Polyacrylamide-Gel Electrophoresis (2-DE); ii) Matrix-Assisted Laser Desorption Ionisation Time-of-Flight Mass spectrometry (MALDI-TOF); iii); and Surface-Enhanced Laser Desorption Ionisation Time-of-Flight (SELDI-TOF) Mass spectrometry. In addition to these studies the group is also studying the effect of biotic/abiotic stress on plant gene expression and thermoregulation of microbial gene expression.

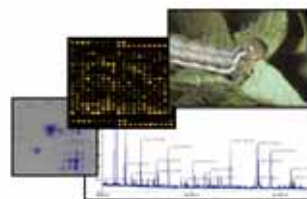
## Spotlight on the University of Newcastle upon Tyne



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**Research Area** Redox metabolism and plant stress responses

### Research Activities

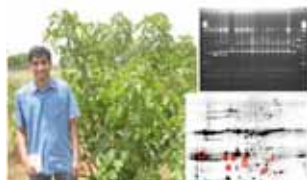
Farmers currently face regular crop losses due to environmental stress. Yield will become even more unpredictable because of the effects of climate change. Advances in our current understanding of how plants manage redox interactions and primary metabolism when faced with environmental changes are central to the development of strategies aimed at reducing the impact of environmental variability on crop yield and quality. Christine Foyer is a specialist in redox biology and antioxidant metabolism, and also in primary carbon and nitrogen assimilation, metabolism and interactions. The research conducted in the Foyer lab concerns the responses that enable plants to withstand environmental abiotic stresses particularly drought, chilling and CO<sub>2</sub> enrichment. A range of transgenic approaches as well as mutants are used to study redox regulation and signalling and the metabolic crosstalk that co-ordinates redox signals and carbon/nitrogen signalling in model (*Arabidopsis*, tobacco) and crop (maize, soybean, pea) species. The immediate aim of this work is to understand the role of redox processes in the acclimation of photosynthesis and respiration and associated carbon/nitrogen metabolism to environmental stress. The further goal is to identify stress-induced senescence and programmed cell death pathways in leaves and root nodules and to use this information together with systems biology approaches to develop crops that perform more predictably in extreme environmental conditions. Specific current research projects are: 1) The role of redox processes involving ascorbate and glutathione in the control of the cell cycle; 2) The role of cysteine proteinases and cysteine proteinase inhibitors in the regulation of stress-induced cell death and senescence; 3) Responses of maize to growth with CO<sub>2</sub> enrichment and drought stress; 4) Chilling-induced senescence in soybean nodules.



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**Research Area** Molecular and biochemical bases of plant-insect-insect interactions; Safety assessment of novel foods

### Research Activities

Plant productivity is limited by exposure to insect pests which cause direct damage and act as vectors for plant diseases. This situation is exacerbated by climate change which may have an impact on pest dynamics, and on the interactions of the pest with parasitoids/predators. Although information is currently available for genes induced in model plants as a consequence of stress, the pathways used are often poorly understood, due mainly to the function(s) of many of these induced genes being unknown. Previously Angharad's group have identified and expressed insect resistance genes (including those from plants as single gene traits or as fusion proteins) in a variety of major crops species and determined the efficacy of these transgenic plants on pests and their subsequent impact on non-targets, particularly natural enemies (Natalie Ferry). Currently the group (subgroup leaders: Ferry/Edwards/Emami) is using post-genomic technologies (transcriptomics, proteomics, metabolomics) to identify resistance genes and their end products in a range of economically important crops (including wheat, rice, potato, oilseed rape) that are up-regulated in response to stress. Enhancing resistance of wheat to insect pests, as part of a consortium funded via the Crop Science Initiative, is a major research focus of the group. Understanding of the molecular basis of resistance mechanisms, in terms of defensive compounds, can be used to define molecular markers at metabolite, protein or nucleic acid levels, to be used to rationalise the breeding process. This will significantly contribute to the realisation of 'low input' agriculture as an important component of sustainable agriculture.



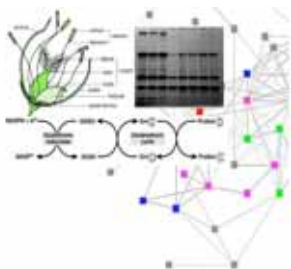
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**Research Area** Bioenergy, non Coding DNA and redox genes

### Research Activities

- Energy Biosciences: *Jatropha* as a model nonedible oilseed plant for biodiesel.**  
 A number of alternate and renewable energy resources are being investigated to address the limited supply, rising prices and adverse environmental impact of fossil fuels. Biodiesel in the form of esterified vegetable oil is one such renewable source. Non-edible oil seed plants such as *Jatropha curcas* are becoming increasingly popular as a source of biodiesel due to the advantage of being able to grow on marginal land. However, to make *Jatropha curcas* a commercially viable feedstock the Kohli lab has undertaken research into identification of pathways and processes relevant to qualitative and quantitative improvement of seed oil through appropriate modifications to specific genes and proteins including transgenic approaches. Areas of current focus include:-
  - Characterising natural accessions of *Jatropha* from various regions of the world.
  - Identifying, isolating and characterizing the fatty acid biosynthesis genes, the oleosin genes and the seed texture genes of *Jatropha*.
  - Reducing carcinogenic substances such as curcins and phorbol esters.
- Cryptic codes in non-coding DNA: Relationships between cis-regulatory element distribution and gene co-expression in rice**  
 Regulatory elements upstream of genes and in regions previously thought of as "junk DNA" can produce considerable phenotypic effects by controlling the expression of the genes they



## Spotlight on the University of Newcastle upon Tyne



### Ajay Kohli Research Activities Continued

operate on. Nearly half of all polymorphisms occur in regulatory regions making them an equally important driving force behind evolutionary development. Work in the Kohli lab is currently focussed on discovering how patterns of cis-regulatory element distribution affect co-expression of disparate genes. Auto-associative Neural Networks (ANN), Self Organising Maps (SOM), Multivariate data analysis (MVDA)-mediated bioinformatics and computational biology tools are being used to study the importance of variables in the patterns of upstream cis-regulatory element distribution. The in silico results from this work will be tested/validated in the lab through high-throughput expression analysis. A rice redox gene set has been chosen to test and validate the cis-element distribution-gene expression models that are generated from this work.

3. Rice redox genes as a model set for multi-networked complex systems in development, stress response and yield capacities (heterosis).

Redox genes are functional in various cellular processes and pathways. The role of redox genes in stress response, signal transduction and as ROS scavengers is well established. Additionally, glutaredoxin, an oxido-reductase, is involved in petal formation in *Arabidopsis*. Seed development and germination is affected by redox genes, while glutathionylation of fructose 1, 6-bisphosphate aldolase affects basic cell metabolism. An oxalate oxidase specifically affects lignin content in cereal husk, while redox genes controlling H<sub>2</sub>O<sub>2</sub> levels affect biomass through lignin and cellulose synthesis and deposition. Redox genes affect the redox status of ascorbate and ubiquinone, two of the most important molecules in the cell. The Kohli lab has targeted a set of 355 isogene loci of 35 genes belonging to 6 families of redox genes in rice. Starting with glutaredoxins as proof of principle, these are being analysed for expression patterns under different spatio-temporal and induction regimes, posttranslational protein modification and for protein-protein complexes to elucidate their role in different pathways.



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**Research Area** Medicinal Plants

### Research Activities

Research in the Okello lab focuses on the identification of new plant based preventions and therapies for a wide range of applications, particularly for neurodegenerative diseases such as dementia of the Alzheimer's type. Research objectives include: (i) identification of relevant plant species from traditional/ethnic/herbal practices as well as through chemotaxonomy, (ii) screening for key bio-actives in disease mechanisms – e.g. molecular targets such as antioxidants, anti-inflammatory agents, neuro-modulators, and enzyme inhibitors (iii) chemical characterisation of active components, (iv) determination of synergistic/antagonistic interactions in plant extract constituents, (v) effects on nutrition and health, (vi) controlled clinical trials in normal and patient populations (vii) development and standardisation of drugs, food and food supplements.



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**Research Area** Physiological and genetic basis of responses of wheat to abiotic stresses

### Research Activities

Current research is focused on a mapping population of 95 doubled haploid lines of wheat and near isogenic lines (NILs) being made for quantitative trait loci (QTLs) analysis of yield and other physiological and developmental traits important in determining yield and responses to abiotic stresses. Detailed analysis of plant growth, development and physiology is used to help identify candidate genes for QTLs. Current activities include:

- Localising a major QTL for grain yield on chromosome 7A long arm.
- Studying the responses of wheat to ozone fumigation and their genetic control.
- Preparing sets of NILs for about 20 regions of the wheat genome regulating yield and several agronomic, morphological, physiological and biochemical traits.

Stephen has collaborations with the Institute of Plant Physiology, Krakow, University of Tuscia in Italy and several research institutions in Serbia that provide phenotypic information from field and glasshouse trials, together with molecular marker information on some of the NILs. The groups' extensive experience in QTL analysis supports other research programmes within IRES.



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**Research Area** Nutritional quality of cereal-based foods

### Research Activities

Cereal foods are staples in the UK diet, but the vast majority are produced from refined (white) flours. Epidemiological evidence, however, suggests that there are considerable health benefits in consuming wholegrain foods compared with refined grain foods. Currently there are no dietary guidelines for whole grain consumption in the UK, the Seal laboratory are therefore working to provide evidence which can be used to underpin new guidelines. The group are also interested in the mechanisms by which whole grains exert their beneficial effects; these could include the different types of fibre present in the grains, their antioxidant and phytochemical content and the

## Spotlight on the University of Newcastle upon Tyne



### Chris Seal Research Activities Contd.

digestion rates of carbohydrate in the endosperm. Researchers believe that no one single factor is involved and that it is a synergistic effect of eating the 'whole grain package' which is important. Chris and his colleagues are currently running the largest wholegrain intervention worldwide - the WHOLEheart Study ([www.wholeheart.org.uk](http://www.wholeheart.org.uk)). The aim of this project is to see whether eating wholegrain foods causes (positive) changes in cardiovascular risk factors such as blood cholesterol, blood pressure, haemostatic and inflammatory status.

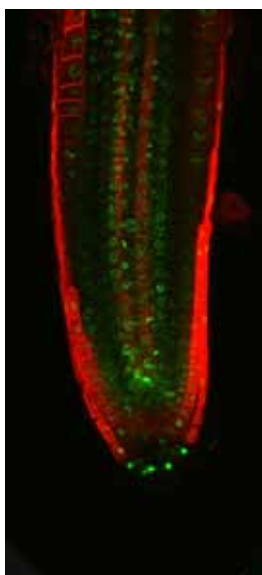
The composition of grains may also affect their nutritional value. Quite a lot is currently known about cereal fibres, but much less about the large array of phytochemicals and antioxidants found in the bran and germ layers. Studies are therefore being undertaken to explore how the concentration and composition of these compounds varies under different agronomic conditions and how they are released during digestion, with the aim to understand how these compounds may contribute to the nutritional value of grain and the healthfulness of wholegrain foods in particular.

## Spotlight on the University of Nottingham



The University of Nottingham represents an International Centre of Excellence for Plant and Crop Science with the largest University-based communities of scientists in the UK, currently totalling 26 research laboratories and over 150 researchers. Its researchers originally pioneered the use of transgenic technologies and gene silencing to create the first GM product for sale in Europe. Nottingham plant scientists have also been at the forefront of international research studying the model plants *Arabidopsis thaliana* and tomato, identifying many of the key genes that regulate their development, coordinating their genome sequencing efforts and, through the Nottingham *Arabidopsis* Stock Centre (NASC), providing underpinning resources to the international scientific community. Nottingham researchers have access to excellent growth facilities that include 35 available CE compartments; 880 m<sup>2</sup> of transgenic greenhouse space; 1879 m<sup>2</sup> of experimental glass house space; and a 450 ha University farm, 20 ha of which is managed organically, with substantial trial plots and a 30ha area dedicated to field research. Plant Scientists are accommodated in a new custom designed research building containing an excellent infrastructure which includes a genomics facility, advanced confocal microscopy equipment and the NASC Affymetrix expression profiling service.

Research extends from fundamental studies of model species such as *Arabidopsis* and tomato, to the physiology of temperate and tropical crops under field conditions. Research is structured into 6 thematic areas; *Plant Development*; *Crop Physiology*; *Biotic and Abiotic Stress*; *Biotechnology & Breeding*; *Genomic Resources*; and the new area, *Integrative Systems Biology* ([http://www.nottingham.ac.uk/biosciences/plantsci/research/plant\\_and\\_crop\\_sciences.php](http://www.nottingham.ac.uk/biosciences/plantsci/research/plant_and_crop_sciences.php).) Innovative projects in plant science-related areas are also conducted by Environmental Scientists in the areas of climate change, soil pollution, soil structure and modelling. There is extensive collaboration between these areas and other groups within the University, and external academic and commercial organizations. This is exemplified by the new £9.2m BBSRC/EPSC sponsored Centre for Plant Integrative Biology ([www.cpiib.eu](http://www.cpiib.eu)). CPIB builds on the world-class research strengths and collaborations across four RAE 5-rated schools (Schools of Biosciences, Computer Science, Mathematical Sciences and Mechanical, Materials and Manufacturing Engineering).



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**Research Area** Hormone regulated root growth and development

### Research Activities

Malcolm's research program falls into three main areas: *Root Developmental Biology*, *Integrative Systems Biology* and *Plant Biotechnology*. His laboratory originally pioneered genetic studies which investigated the regulation of root growth and development by auxin transport. Early work by his group led to the isolation and characterisation of AUX1, the first auxin transport protein to be described in plants and a key regulator of root gravitropism. Subsequent research has demonstrated the importance of auxin transport during lateral root initiation and emergence. Recently Malcolm's group has adopted an integrative systems biology based approach to study hormone regulated root growth. He is the Biology Director at The Centre for Plant Integrative Biology (CPIB), the BBSRC/EPSC Centre for Integrative Systems Biology that aims to create a virtual root model. CPIB embraces disciplines such as mathematics, engineering, computer science, as well as plant science, enabling Malcolm to study root development at multiple physical and temporal scales (e.g. molecular, cellular and organ levels) and has enabled his research to become more quantitative, integrative and predictive. Several members of Malcolm's lab employ their expertise in molecular genetics, plant transgenics and metabolite profiling technologies for biotechnological applications relating to human nutrition. This work has led to the isolation of several genes that influence the abundance and bioavailability of phytochemicals such as glucosinolates and folates with anti-cancer properties or nutritional importance.

## Spotlight on the University of Nottingham



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**Research Area** Agroforestry

### Research Activities

Work on semi-arid agroforestry systems is a core element of Colin's research. The objectives are to establish the principles underlying resource capture (water, nutrients, light) and resource use efficiency with a view to improving long-term productivity and sustainability. The results have been used to test process-based resource use models. Studies in Malawi have established the physiological and agronomic basis for the substantial yield benefits obtained when tree prunings are incorporated into the soil before planting annual crops. Studies in Kenya and Uganda have examined the role of physiological and phenological traits in determining competitive interactions in systems containing exotic tree species.

A second major theme concerns the impact of gaseous pollutants, particularly ozone, sulphur dioxide and carbon dioxide, on plant growth and reproductive development. The group has shown that specific reproductive processes are highly susceptible to injury and that realistic single or multiple ozone exposures during flowering may reduce seed yield and quality and seedling vigour. Phytoremediation is an expanding theme in which the lab have examined the suitability of phytoextraction for remediating arable soils contaminated with sewage sludge. The objectives were to determine: the relative effectiveness of hyperaccumulators and high biomass crops, including trees; the role of chelate and/or herbicide-assisted extraction; and the suitability of the arsenic hyperaccumulating fern, *Pteris vittata*, for remediation of contaminated land. Current research is examining the human health risks associated with consumption of leafy vegetables grown on soil contaminated with heavy metals in peri-urban agriculture in Uganda and the potential of bamboo, irrigated with waste water too contaminated for use with food crop, to provide valuable commodities.



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**Research Area** Plant and crop mineral nutrition

### Research Activities

Martin's research interests are in applied and fundamental aspects of plant and crop mineral nutrition. At an applied level, this research seeks to improve the nutritional quality of crops (biofortification) using agronomic and genetic approaches. Work in this area is currently focused on the elements calcium (Ca), magnesium (Mg), selenium (Se) and zinc (Zn). Martin co-ordinates a current Defra/industry-funded LINK project on Se-biofortification of wheat, which aims to develop efficient dietary Se delivery systems (<http://bagels.ukcrop.net/>). This project spans the food-chain from soil science through to test-baking. In addition on going research in the group on vegetable and oilseed brassicae, cereals and potatoes (in collaboration with scientists at Rothamsted, IFR/UEA, SCRI and Warwick HRI) is yielding novel insights into the genetic control of mineral composition. At a fundamental level, metal hyperaccumulators (i.e. plant species which accumulate very high concentrations of particular elements in their leaf tissues, in their natural environment) are excellent biological systems for elucidating molecular mechanisms controlling mineral element homeostasis and hence accumulation. For example, Zn hyperaccumulation has probably evolved twice in plants; once in the genus *Arabidopsis* (one species) and once in *Thlaspi* (*Noccaea*; several species). Martin is exploiting the recent evolutionary heritage of *Arabidopsis* and *Thlaspi* to unravel hyperaccumulator gene function using comparative genomics. Recent successes include robust cross-species transcriptomic profiling (<http://affymetrix.arabidopsis.info/xspecies/>), and the development of a genomic library for *Thlaspi caerulescens*, with colleagues in NASC (Sean May, Neil Graham), SCRI (Philip White) and Warwick HRI (John Hammond).



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**Research Area** Effects of nitrogen enrichment

### Research Activities

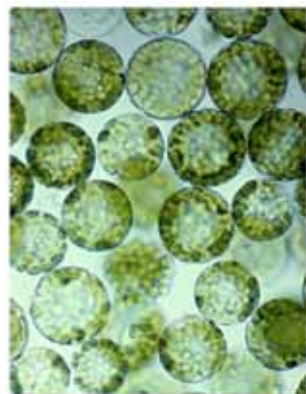
Nitrogen enrichment has been identified as a major potential driver of biodiversity and ecosystem change at mid to high latitudes. Peter and his collaborators are examining the impacts of enhanced nitrogen deposition in a wide range of 'low-productivity' ecosystems. At the northern tree-line in European Russia he is using chronological changes in wood chemistry and isotopic signatures to seek responses to increased regional nitrogen loads. Peter is also examining the effects of temperature increase and nitrogen fertilization on tree seedlings (e.g. *Picea obovata*) grown in tundra soils. Dispersion and deposition of ammonia around major animal colonies in the Namib Desert and at Cape Hallett in Antarctica is being quantified and its effects on lichen communities examined using <sup>15</sup>N natural abundance signatures and physiological changes. One such change is pronounced up-regulation of phosphomonoesterase (PME) activity. In British heathlands, relationships are being examined between nitrogen deposition and N/P ratios and PME activity in *Cladonia portentosa*, a common ground-dwelling mat-forming lichen. This group of lichens

## Spotlight on the University of Nottingham



### Peter Crittenden Research Activities Contd.

appear to be a relatively precise indicator of nitrogen deposition in more remote northern regions. Such lichens also have among the highest PME activities yet recorded among plant/microbial systems and work is in progress to characterize the extracellular enzyme(s) involved. Closer to home, Peter is also working on heathlands in the East Midlands region focusing on effects of patch fragmentation and nitrogen enrichment on plant community composition and ecosystem sustainability



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**Research Area** Plant genome/proteome analysis for food safety assessment

### Research Activities

Robust tissue culture systems are essential for micropropagation of elite germplasms and for plant genetic manipulation by exposure of somaclonal variation, somatic hybridisation and transformation. Mike's research focuses on the multiplication of endangered woody plants, such as the Chilean tree *Gomortega*, the securing of novel floral "sports" in chrysanthemum and protoplast fusion to generate somatic hybrids in ornamental species of tobacco. Transformation using *Agrobacterium* and biolistics for gene delivery is being exploited to manipulate leafy vegetables such as lettuce and chicory to synthesize novel pharmaceutical products (collaboration with the University of Bristol), and the manipulation of gibberellin biosynthesis to modify plant stature (collaboration with Rothamsted Research). Other investigations are targeting the cryopreservation of banana and the development of culture systems for bambara groundnut and other under-exploited legumes, such as Jicama. In an EPSRC funded project with the School of Physics and Astronomy, also involving colleagues in the Food Sciences Division, the effects of magnetic fields and altered gravity on the development of plant cells and microorganisms are being investigated.



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**Research Area** Phytoplasma diseases of plants

### Research Activities

Phytoplasmas are cell wall-less bacteria that are obligate parasites and pathogens of insects and plants, and are known to cause disease in hundreds of plant species worldwide, causing symptoms such as virescence, phyllody, yellowing, witches'-broom, leaf roll and generalised decline. To help combat these bacteria the group are improving current phytoplasma diagnostic techniques as part of a DEFRA Plant Health Fellowship in collaboration with Rick Mumford and Neil Boonham (Central Science Laboratory, York). This work has involved the development of the terminal restriction fragment length polymorphism (T-RFLP) technique for diagnostics and strain identification and the development of new universal primers that are able to amplify the *secA* gene from all phytoplasmas tested, which will result in improvements to phytoplasma classification systems. Ongoing work is focusing on developing monoclonal antibodies into a phytoplasma diagnostic system and developing real-time PCR techniques based on new primer combinations. In addition, the group is conducting experiments to analyse changes in gene expression in phytoplasma-infected plants using tomato as a model system. In other phytoplasma work (involving collaboration with the Coconut Research Programme, OPRI, Ghana) researchers have been investigating the possibility that phytoplasmas are transmitted through seed, and examining the nature of resistance and tolerance to phytoplasmas in coconut. This work is aimed at improving the effectiveness of replanting programmes with resistant germplasm to combat coconut lethal yellowing type diseases and address the 'Millennium Development Goals' by reducing poverty in coconut growing communities of Ghana and worldwide.



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**Research Area** Plant-insect-insect interactions

### Research Activities

Trees form the matrix upon which forest communities are built, and their characteristics and distribution shape the niches of the species living on and around them. Markus' research tackles this from an explicitly spatial perspective, identifying patterns within forests and the processes that underpin them. Studies are being conducted in a range of locations, from boreal to tropical. The major research themes are:

- How local-scale interactions between trees generate spatial patterns and dynamics within forests, and whether these influence the ability of different tree species to co-exist in a given location. Current data is derived from mapped forest plots in the UK and Russia.
- Whether the characteristics and distribution of woody plant species influence insect herbivore communities, with particular regard to their composition, diversity and impact. A long-term study

## Spotlight on the University of Nottingham

### Markus Eichhorn Research Activities Contd

in Sabah, Malaysia, is considering the interaction between dipterocarp tree seedlings and their insect herbivores, with a recent focus on the impact of herbivory under differing resource conditions.

- c) The manner in which variations in local-scale interactions within forests along environmental gradients are responsible for vegetative transitions. Collaborative datasets from Alaska and Russia are being utilised to investigate the link between local interactions and metacommunity processes on large scales.



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**Research Area** RNA metabolism and plant biotechnology

### Research Activities

Rupert's research group studies the prevalence and role of post-transcriptional nucleotide modifications found within some mRNAs. His primary interest is base modification of adenosines at internal sites within messages. Whilst this modification does not change the coding capacity of the mRNA, inhibition of the enzyme which carries out the methylation results in embryo lethality. Rupert's Group is developing novel antibody-based techniques to identify messages containing modified nucleotides and to quantify global levels of mRNA methylation in different plant tissues and during development. Similar modifications are found throughout the plant and animal kingdoms and it is likely that the insights gained from the Arabidopsis studies will have wider implications. In addition to his work on RNA metabolism, Rupert has a long standing interest in manipulating plant metabolism and has previously engineered potato, tomato and tobacco plants to produce various bacterial N-acetyl homoserinelactone signal molecules. These plants interfere with normal bacterial density dependent behaviour and alter susceptibility to certain pathogens. More recently in collaboration with Dr. Chris Hayes in Chemistry, he has demonstrated the potential for diverting the tomato fruit carotenoid pathway for the production of high levels of novel anti-cancer taxanes.



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**Research Area** Ethylene signalling in fruit ripening and the mechanism of post-transcriptional gene silencing

### Research Activities

Research studying ethylene-regulated fruit ripening and gene silencing led to the creation of one of the first GM products sold in Europe in the 1990s. More recently the group have employed fluorescently tagged proteins to study the interaction between tomato ethylene receptors and multiple CTR proteins in the ER. Using yeast 2-hybrid screening and analysis of stably transformed plants, researchers have identified a new protein, INT106, involved in hormone signalling. In addition, the lab has also identified a HD-Zip homeobox protein that binds to the ACC oxidase gene 1 promoter and regulates ethylene biosynthesis. In a new collaboration with Yiguo Hong at Warwick, Prof Grierson has shown that silencing this gene delays ripening (Figure: silenced on the left, control on the right) and that this gene also plays a role in flower development. Other investigations into gene silencing caused by inverted repeats (IRs) in transgenes, have shown that small interfering RNAs (siRNAs) are generated from the 5' region (inverted repeats and downstream region) of the transgene, whereas siRNAs are normally produced from the 3' region of the transgene without IRs. Examination of the mechanisms that causes degradation of polygalacturonase mRNA during gene silencing has revealed that the cleavage site of PG mRNA is linked to the generation sites of siRNAs from the transgene. The lab has also shown that silencing can be enhanced by grafting and that, contrary to an earlier report, both sense and antisense silencing can be transmitted by grafting.



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**Research Area** Integrative systems biology

### Research Activities

Charlie's principal research activity concerns the BBSRC/EPSC Centre for Plant Integrative Biology, which aims to produce predictive, multi-scale models of Arabidopsis root growth and development. He also aims to translate this experience into modelling related processes in crop species. Research through collaboration and sharing is key to the Centre's success. His specific research interest concerns the representation and integration of data relating to the different physical scales (molecular-to-cell and cell-to-organ scales) and mathematical model integration. Other plant related research collaborations involve developing the informatics and systems biology of stress responses in wheat and tea, and the regulation of tomato fruit ripening.

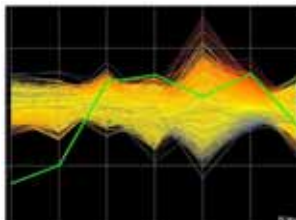
## Spotlight on the University of Nottingham



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**Research Area** Plant and crop developmental genetics

### Research Activities

Research programmes focus on the genetic control of germination and seedling establishment, and genomic and post-genomic approaches to understand and manipulate plant development. Emphasis is placed on the transfer of molecular genetic information from studies in model species, to address important agricultural problems. Current projects include an analysis of the genetics of the embryo-seedling transition in *Arabidopsis thaliana*, systems biology approaches to understand early root growth (as part of CPIB), functional genomics approaches in *Arabidopsis* and wheat to define new genes of agricultural importance, molecular genetic and physiological analysis of seed development in wheat, including the agriculturally important disorder pre-harvest sprouting, and analysis of the genetics of germination in barley.



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**Research Area** Functional genomics and single cell transcriptomics

### Research Activities

In a joint project with the University of Bristol and Rothamsted Research, Chungui has been investigating the effect of nitrogen supply on the wheat transcriptome and examining how organic and inorganic fertiliser can significantly influence gene expression. More recent studies have concentrated on the use of wheat microarray data (produced at the University of Bristol) to identify the potential synergism or antagonism between signalling pathways, and storage protein metabolism. Wheat genes, whose expression is affected by cold temperatures, are also being mapped onto a virtual cell network so that the molecular mechanisms of cold stress response can then be investigated from the output of the transcriptomics analysis.

In collaboration with CPIB, Chungui has been applying transcriptomic profiling at the single-cell level (cell sorting and microcapillary). It is hoped that this technique will provide a powerful tool for functional genomic characterisation of signalling pathways at the cellular level.

In addition to these studies Chungui also has interest in plant chemical genomics and aims to create a chemical library enriched in plant-bioactive compounds. The bioactivity and phenotypic information garnered for this library, together with chemical structure information, will be systematically analysed in future projects.



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**Research Area** Functional genomics and single cell transcriptomics

### Research Activities

Several important processes, including abscission, seed germination and fruit softening, are dependent upon the modification of cell walls. These processes are under the control of hormonal signals and require the controlled secretion of cell wall modifying enzymes to the apoplast. Rab GTPases control secretory processes in mammalian systems and it is clear that they also perform this function in plant systems, though different classes of Rab GTPases have undoubtedly taken on slightly different roles in plants. This means that they would be expected to control trafficking of cell wall modifying enzymes to the cell wall and also the trafficking of hormone receptors to and from the plasma membrane. There is also evidence to suggest that the Rab11/RABA GTPases may play a more direct role in signalling processes. Grantley's lab, in association with Greg Tucker's lab, has been active in using gene silencing techniques to investigate the role of these GTPases in tomato. Silenced lines show reduced softening of fruit and particularly reduced over-softening and spoilage. As expected, this is associated with reduced pectic hydrolase levels. Some of the silenced plants also show effects associated with disturbed hormone levels and/or hormone perception. The effects of Rab gene silencing on other plant organs and other physiological processes is being determined. Investigations on the level of functional Rab gene redundancy in these processes are also continuing.

## Spotlight on the University of Nottingham



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**Research Area** The physiology of crop photosynthesis

### Research Activities

Erik's research concerns the regulation of photosynthesis in rice crops and plants. The group study the physiology and biochemistry of leaf photosynthesis, the response to environmental factors such as excess irradiance and drought and also the way in which these processes scale up to the canopy level. Researchers use a number of physiological and biochemical techniques including classical gas exchange and chlorophyll fluorescence techniques. In addition, the laboratory is exploiting the rapidly expanding range of mutant collections available for rice. Current work includes:

- 1) Screening rice mutant populations for alterations in photosynthesis, light-use efficiency and leaf morphology.
- 2) Analysing historical rice cultivars which show trends in photosynthetic capacity since the 'green revolution' in order to elucidate relationships between leaf photosynthesis, biomass production and water use efficiency.
- 3) Analysing mechanisms at the cellular and leaf level by which rice plants deal with excess irradiance and high light stress: using rice as a genetic model for plant and crop photosynthesis.

Applications: Assimilation under high irradiance is particularly relevant in tropical areas where there is a need to improve biomass production rates and yield in rice. To do this Erik collaborates with scientists from the International Rice Research Institute, including the recently formed C4 rice consortium, and also laboratories in China.



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**Research Area** Molecular genetics of crop plants and crop improvement

### Research Activities

Sean's group is interested in exploiting molecular genetic approaches in both temperate and tropical crops to advance the understanding of genetic traits of agronomic importance. The work ranges from population genetic studies to understand gene-flow and population structure through to focused marker-assisted breeding programmes. They currently have active research in wheat, oil palm, tea, rice, bambara groundnut, avocado and the agricultural weed, Restharrow. Previous work includes studies in date palm and 2-spot ladybird.

Climate change represents a real challenge for crop breeders and understanding the genetic basis for agronomically important traits in crop plants is one of the keys to producing improved varieties (in the context of a good conventional breeding programme). In the future, understanding the control of recombination and having the ability to increase genetic exchange between parental lines will be critical for increasing the rate of breeding progress.



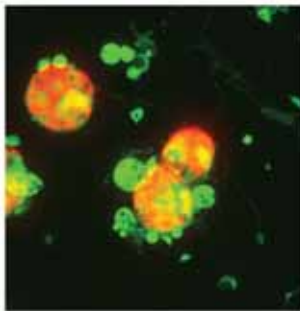
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### Research Activities

NASC distributes, collects and preserves seed and DNA resources of Arabidopsis and related species (but has also expanded to embrace tomato). It has knockouts or RNAi knockdowns available for almost all known Arabidopsis genes as germplasm or clone resources. In 2007 alone NASC sent out 50,000 tubes of seed from a collection of over half a million stocks. In addition, NASC collects, generates and distributes transcriptomics data (especially Affymetrix) in the form of a primary repository (NASCCarrays), which represents the majority of plant transcriptomic experiments in the public domain. NASC also have a mature integrated genome browser AtEnsEMBL ([atensembl.arabidopsis.info](http://atensembl.arabidopsis.info)) as part of ukcrop.net which incorporates both TAIR and MIPS genome annotations and links through to all other databases and resources (as well as to external data such as Brassica gene information).

Most of NASC's data is available through SOAP and BioMOBY web services. Funding for developing and training users in implementing web services has been granted to NASC for 4 years as part of the AGRON-OMICS EU project. If you need help in using these, please ask NASC or contact the MASC bioinformatics sub-committee. BBSRC funding has been renewed in 2007 to cover a further 5 years of the NASC seed service and a further 3 years for the GARNet transcriptomics and bioinformatics service. As part of this renewal, NASC now has a public version of Genespring workgroup for community use in analysing transcriptomic data.

## Spotlight on the University of Nottingham



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**Research Area** Plastid and leaf development

### Research Activities

Kevin's research is focused on the general area of plastid development and plastid division, in particular the system of tomato fruit ripening in which green chloroplasts differentiate into red chromoplasts. Plastid replication during this process appears to involve a novel form of plastid division, namely plastid budding. Tomato mutants which change the differentiation process, such as *suffulta*, are being characterised and the underlying genetics revealed. A role for thin membranous tubules emanating from plastids (termed stromules) are also being investigated; in relation to plastid density sensing.

Kevin is also interested in development of leaves and petals in various different systems including *Arabidopsis* and *petunia* and recently has teamed up with Erik Murchie in Crop Sciences to examine the development of rice leaves with a view to identifying anatomies in mutant rice lines which tend towards those found in C4 type grasses.



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**Research Area** Gametophytic self-incompatibility

### Research Activities

The main area of research in the Robbin's group is gametophytic self-incompatibility with a ribonuclease-based mechanism. This is one of the most widely distributed genetic mechanisms that prevents self fertilization in angiosperms. Self pollen is rejected following a highly specific recognition between pollen and pistil. In the Solanaceae and Rosaceae families the stylar factor is a secreted ribonuclease and the pollen factor is an F-box protein (SLF/SFB). Researchers are studying self-incompatibility in both the Solanaceae (*Petunia hybrida*) and Rosaceae families (*Prunus avium* and *Pyrus communis*). *Petunia* is used as a model system to understand the mechanism of self-incompatibility utilising techniques such as transgenic manipulation and transposon mutagenesis. Work in the Rosaceae is mainly carried out in collaboration with East Malling Research and has a practical application for fruit breeding and horticulture.



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**Research Area** Abscission and cell separation processes in plants

### Research Activities

Most plant cells are surrounded by a rigid wall that provides both protection and support. The wall comprises a matrix of complex carbohydrates and proteins bonded together to provide considerable tensile strength whilst at the same time having the flexibility to be distended so that growth and development can take place. Although the architecture of the cell wall provides developmental flexibility there are times during the life cycle of a plant where extensive modifications are necessary to reduce, or remove entirely, the constraints that it imposes. Jerry's group is particularly interested in the events that are associated with wall remodelling during organ abscission and pod dehiscence. Two approaches are being taken to identify these. The first is a mutant strategy to identify genes that play a key role in the shedding of reproductive structures in *Arabidopsis*. Recent work has identified an F box gene, termed *HAWAIIAN SKIRT* that regulates the timing of abscission and also affects plant growth. The second approach is to generate a transcript profile from separating abscission zone cells and to use this resource to identify novel genes involved in the shedding process. Intriguingly, a reporter analysis of some of these abscission-related genes has revealed that they are also expressed at other sites where cell separation takes place such as the margins of the root cap and in cells adjacent to emerging lateral roots. The group is also exploring possible applications of this knowledge to the manipulation of crop growth and development.



## Spotlight on the University of Nottingham



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**Research Area** Micro-encapsulation of fungicides

### Research Activities

Steve's research is based on optimisation of the application of fungicides to control diseases of cereal crops, by the process of micro-encapsulation. This work is done in collaboration with Micap plc, and uses waste yeast as a vehicle for encapsulation of active ingredients. The objective of these studies is to achieve sustained and gradual release of active molecules to extend the window of opportunity for disease control. The initial target is to use the triazole fungicide tebuconazole as a seed dressing to control foliar diseases of wheat, such as powdery mildew and Septoria. In conventional formulations, such as Folicur, tebuconazole is too phytotoxic to permit application at a rate sufficiently high enough to provide control of such foliar pathogens. Preliminary data have indicated that this problem can be alleviated by the micro-encapsulation process; sufficient active ingredient can be applied to bring about effective and improved crop protection. The group is currently examining the release characteristics of fungicides from yeast cells by GCMS and aims to optimise the process by appropriate formulation of the fungicide. Future goals include extending this research to control other plant diseases, where sustained release of active fungicide molecules could provide an advantage in effective crop protection.



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**Research Area** Genetic and molecular basis of fruit quality

### Research Activities

The first Angiosperm fruits appear in the fossil record in the Cretaceous period. These early fruits were dry and split down one side to release their seeds. Fleshy fruits evolved from dry forms and both dry and fleshy types form a major part of the human diet. Research in the Seymour lab has three main strands.

- (1) Active involvement in resource development along with other members of the vibrant international Solanaceae community.
- (2) Development of dynamic models of the regulatory network controlling fruit ripening.
- (3) Exploiting the information generated in (2) to improve fruit quality, in collaboration with global players in the fresh and processed produce industries.

The model system of choice for studying fleshy fruits is the tomato with its ever-growing collection of molecular and genetic resources. Graham is spearheading (with colleagues at Imperial, SCRI and Sanger, the UK) contribution to the International Tomato Genome Sequencing Project, and in collaboration with Sean May at the Nottingham Arabidopsis Stock Centre (NASC) plans are being developed for a Tomato Stock Centre to supply the International Community with clones, vectors and other tomato specific resources. In collaboration with Ken Manning at Warwick the Seymour lab has identified a major regulator, *LeSPL-CNR*, necessary for fruit ripening. Dynamic models that will describe the molecular circuits involved in ripening are now being developed within the Centre for Plant Integrative Biology based at Nottingham, which is led by Charlie Hodgman. Delivery of this information through to commercial practice will involve harnessing the substantial untapped natural variation within *Solanum* spp.



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**Research Area** Crop physiology and sustainable agriculture

### Research Activities

Research activities encompass two main areas: crop physiology and sustainable agriculture. Debbie's research has focused on understanding the mechanisms underlying yield and quality in crop plants, and predicting how these may be influenced by management practices. For example, work investigating the response of wheat yield to reduced plant population led to revised recommendations of optimum plant populations for UK growers. Research into lodging of wheat has led to the development of a validated model which accurately predicts the lodging risk based on crop traits (e.g. height at centre of gravity, stem diameter, root plate spread). This is being used to advise growers on management practices to minimise lodging risk. Ultimately, the aim of this work is to find genetic markers for important lodging traits to facilitate the breeding of more lodging resistant varieties.

A five year study on the long term impacts of organic conversion strategies has also recently been completed. Within this research programme the impact of organic conversion strategies on subsequent crop yield, weed burden and soil physical and chemical properties was investigated, together with the economic aspects of conversion such as rotational gross margins and cash flow considerations (in collaboration with Dr Paul Wilson, Farm Management and Economics).

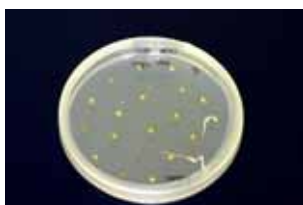
## Spotlight on the University of Nottingham



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**Research Area** Membrane trafficking, auxin transport and root gravitropism

### Research Activities

Ranjan's main focus of research is membrane trafficking in *Arabidopsis*. He has been using a variety of cell biology, genetic and chemical genetic approaches to pursue his interests. Ranjan has recently discovered a novel class of accessory proteins in plants that facilitate the assembly of polytopic membrane proteins in the ER. AXR4 represents one such ER protein that regulates the trafficking of the auxin influx carrier, AUX1. Currently, Ranjan's group is involved in identifying other novel ER accessory proteins in *Arabidopsis*. He is very excited about one of his candidate genes; *RASTA BANDH (RAN1)*. Knockouts in RAN1 appear to have an embryo lethal phenotype. RAN1 belongs to a small multi gene family and Ranjan is currently establishing the developmental role of these proteins in *Arabidopsis*. Ranjan is also interested in understanding the regulation of polar membrane targeting. He has been using smart screens to identify novel trafficking mutants that can alter targeting of apical or basal marker proteins. Ranjan is also actively involved with the newly formed Centre for Integrative Systems Biology (CPIB) heading the team that is creating a protein atlas of *Arabidopsis* root cells.



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**Research Area** Manipulating ABA biosynthesis to save water in irrigated crops

### Research Activities

Ian's research is primarily based on investigating and enhancing plant responses to environmental (abiotic) stress. Most of the work has been aimed at improving water-use efficiency, although some collaborative research with Jerry Roberts and Colin Black, in the Plant Sciences Division at Nottingham, has involved other stress factors e.g. soil compaction and nutrient stress. The role of the plant hormone Abscisic acid (ABA) in co-ordinating attempts by the plant to ameliorate the adverse effects of stress provides the central focus of the various research programmes. In collaboration with Andrew Thompson's research group at Warwick-HRI, the group demonstrated for the first time that it is possible to increase ABA biosynthesis using constructs encoding one key enzyme in the pathway, NCED (9-cis-epoxycarotenoid dioxygenase). One unwanted side effect of constructs designed to elevate ABA levels throughout the plant was to strongly increase seed dormancy. This can be overcome by inhibiting ABA biosynthesis in transgenic seed using chemicals e.g. norflurazon, to block the production of the carotenoid precursors of ABA. Using the correct dose and exposure time, seedlings can recover from this treatment to produce normal green transgenic plants. Increasing ABA levels in these transgenic plants results in reduced stomatal opening at times of peak demand, resulting in more water being retained in the soil for later use. Careful gravimetric studies, in which 'high-ABA' and control plants had water added as required to return the soil to field capacity each day, have revealed that the transgenic plants use 25% less water to produce the same amount of dry matter as non-transgenic control plants. This capacity to modify plants to make them less profligate in their use of water is currently being investigated in a number of irrigated crop species.



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**Research Area** Improving the quality of fruits and their products

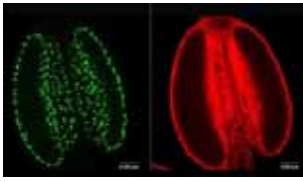
### Research Activities

Over softening is a major cause of loss during the transportation and marketing of fruit. This is particularly true for tropical fruits such as mango. Softening is largely due to degradation of the complex wall surrounding the fruit cells. The cell wall is also of major importance during the processing of fruit since it contributes to the cloud formation in juices and viscosity of pastes. A co-ordinated research programme is underway at Nottingham to investigate the molecular basis of softening in a wide range of fruit including tomato, melon, mango, citrus and strawberry. The use of gene silencing and other techniques, such as application of 1-MCP, are being used to enhance shelf life and improve quality.

Fruit and vegetables are key providers of several essential dietary components. In particular they contain antioxidants such as vitamin C, carotenoids (beta-carotene, lycopene) and flavonoids as well as other micronutrients such as folate. These antioxidants are thought to help protect us from several diseases including heart attack, strokes and some forms of cancer. Studies are underway at Nottingham ultimately aimed at:-

1. Identifying key regulatory genes involved in the production of these micro-nutrients within the plant.
2. Increasing levels of beneficial micro-nutrients in plants by enhanced breeding. Particular emphasis is being placed on folate and vitamin C.
3. Assessing the possible importance of these micro-nutrients in the Human diet. In particular with reference to cardiovascular function.

## Spotlight on the University of Nottingham

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Plant reproductive development

**Research Activities**

Zoe has used mutants that are defective at various stages of pollen and anther development to study and clone genes critical to these pathways. She has used fluorescently labelled proteins to analyse expression, Y2H screens to identify interacting proteins and transcriptomic approaches to identify down-stream regulatory targets. Laser capture microdissection (LCM) has also been used to analyse gene expression in specific cell types in the anther. Her group has concentrated on two stages of pollen development, those of tetraspore release/microspore development, during which the tapetum plays a prominent role and the *MALESTERILITY1* (*MS1*) gene is expressed, and dehiscence when the *MS35/MYB26* gene is expressed.

*MS1* contains a PHD-finger motif found in known transcription factors and is involved in the regulation of pollen wall biosynthesis genes and tapetal programmed cell death. Investigations into the *MS1* pathway are also being extended to orthologues of the *MS1* pathway in crop species, principally rice.

*MYB26* is a key regulator of secondary thickening in the anther endothecium, which is required for anther opening. Zoe is using this to study anther dehiscence and the regulatory network for secondary thickening. These processes are of commercial importance to seed and biotechnology companies, to control breeding strategies and for the manipulation of secondary thickening pathways.

Zoe is also the UK-coordinator of a BBSRC China Partnership on "Integrating molecular networks for male reproduction in Arabidopsis and rice" comprising 5 different UK groups and 5 Chinese Universities.

2008



**GARNet SEB Symposium 2008**  
**University of Nottingham, UK**

**8-10th September 2008**

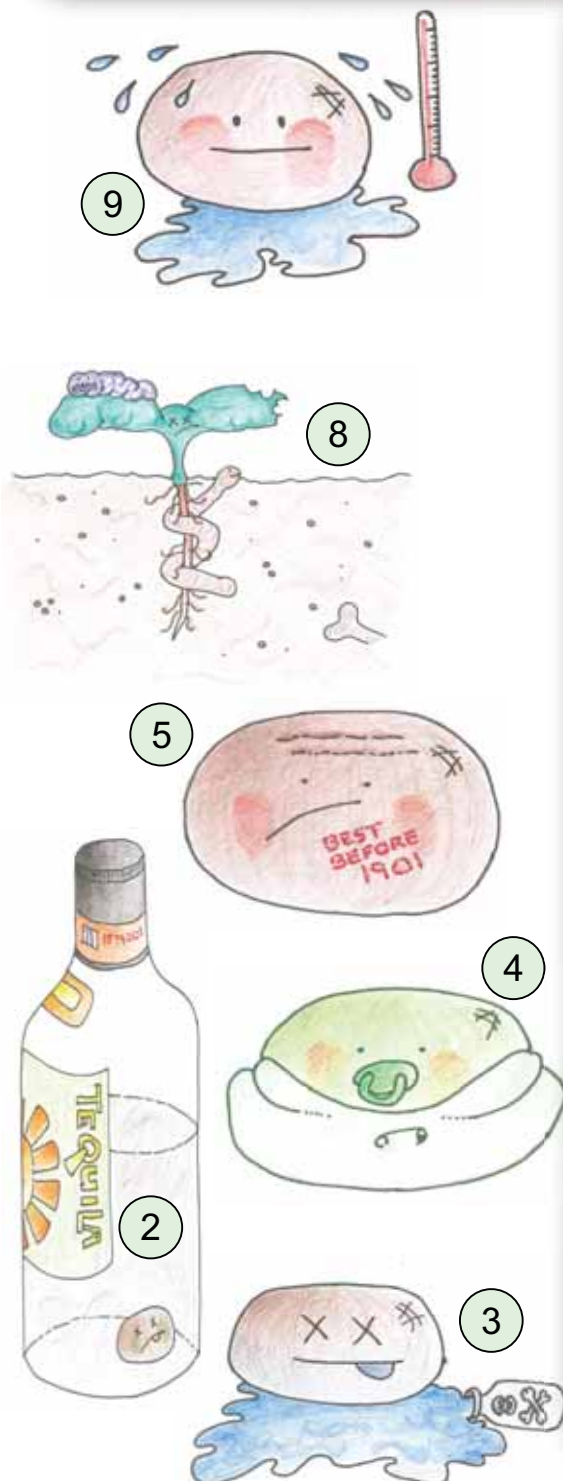
# The top 10 ways to kill arabidopsis .....by accident (honest guv)



Occasionally, people write into NASC (arabidopsis.info) complaining that they have problems with seed germination. Whilst we always take this very seriously and perform germination tests in-house, we do tend to find that many problems are due to 'operator-error'.

Here are our personal favourite top 10 reasons why you may be killing the seeds you love. We hope that this article can save the lives of innocent seeds everywhere. (Position 11 is dedicated to those users who receive empty tubes and complain about missing seed ...when they order DNA stocks !)

Graphics - Nicola Leftley, concept and text - Sean May, NASC Jan 2006.



**10. Gassing !** - If your mutant needs supplements (e.g. vitamins, amino acids) - have you forgotten to add them ?

**9. Too hot !** - Arabidopsis is not a tropical plant (< 30°C).

**8. Has it germinated already and been eaten ?** Use intercept or other pest control to kill those worms and grubs.

**7. Mould alert !** - don't store your seeds in a damp dark place - keep out of the fridge !

**6. Drowning ?** Arabidopsis is not sub aquatic - it likes to breathe and doesn't get on very well with algae !

**5. HOW long have you had the seed out of storage ?!**

**4. You didn't wait for the seed to mature on the plant did you ?** If it's green, it's not ready.

**..for those that sterilise for tissue culture:**

**3. Bleach sensibly** - if you forget to time it properly, you can forget germination.

**2. Use alcohol in moderation.**

**..and our favourite...**

**1. Don't bury your seed !** - they're only little plants and will never find the surface if you dig a hole and throw them in !!!

