June 2007. Edition 7

GARNish

The official GARNet newsletter

Bio energy

extracting energy from plants

Also in this issue;

Spotlight on The University of Oxford and Oxford Brookes University 2010 Programme

GARNet 2007 at the John Innes Centre

Genespring workgroup, WeedsWorldWiki and iGEM

Editorial

Welcome, to this, the 7th issue of GARNish. So far 2007 has been a productive year for GARNet. At the start of 2007 we welcomed 3 newly elected members to the committee; Jim Beynon (Warwick HRI), Philip White (SCRI) and Miltos Tsiantis (University of Oxford). However, this sadly meant we had to say goodbye to Nick Harberd, Ian Furner and Ottoline Leyser. Many thanks to you all, particularly Ian and Ottoline (who started GARNet back in 1999) for their tireless and invaluable contribution which has made GARNet the successful organisation it is today.

It seems that Systems Biology continues apace in the UK in 2007, with the BBSRC Systems Approaches to Biological Research call and numerous other initiatives such as Mathematical Tools for Systems Biology. I hope that many of you will be successful in securing funding in this emerging field. However, if you are just starting out to investigate how theoretical approaches could further your research, you might like to attend the inaugural Mathematics in Plant Science Study group that will be hosted by GARNet and CPIB this December (17-20th). The study group aims to explore mathematical approaches to questions in Plant Science. Researchers are invited to submit a problem based in plant science, for leading theoretical academics to analyse during the 4 day study group. Problems can be from any area of plant science but need to be amenable to mathematical modelling and analysis. If you would like to learn more visit http://cpib.info/workshop.shtml

If you can't wait until December to see what the Centre for Plant Intergrative Biology is up to then head over for its launch on the 2nd July, http://www.cpib.info/.

The other hot topic of the year is, of course, Bioenergy, so if you would like to know more about the area and the role UK Plant Science can play see pg 7-9.

Did you predict that renewable energy would be so big? If so GARNet needs your crystal ball talents to highlight the topics/themes that the International Arabidopsis community should be pursuing in the next 5-10yrs. These suggestions will then be put forward for consideration at a meeting of the Multinational Arabidopsis Steering Committee in Beijing, where we will be discussing the future directions of Arabidopsis functional genomics beyond 2010 (see pg 5).

Contents

Front cover image kindly suppiled by Lucio lucianoaglioni@hotmail.it
Many thanks to all who contributed to this issue of GARNish, especially Iain Donnison, Beatrice Schildknecht, Miltos Tsiantis and John Runions

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

bbsrc
biotechnology and biological sciences research council

The second half of 2007 looks like it will jammed packed with events and conferences across the UK and further a field; the most important of which will obviously be GARNet 2007. This year the GARNet meeting will be held at the John Innes Centre 10th-11th September. It only costs the very modest price of £80 for a student or £100 for an academic to register so you should still have some change left to attend some of the other gatherings during 2007 including:-

ASPB
Chicago, USA; 7-11 July 2007

Systems Biology and the Biology of Systems
Buxton, UK; 13 - 14 September 2007

Plant GEMs 2007
Tenerife, Spain; 3-6 October 2007

Have a great summer, see you in Norwich,
Ruth

GARNet 2007

Make a date in your diaries now for the most important UK meeting of the year;

GARNet 2007, 10-11th September, John Innes Centre, Norwich.

This exciting meeting will cover a plethora of topics ranging from Systems Biology to Plant Pathology and will include a number of talks and workshops to help you access, use and analyse the ever increasing data mountain.

As always we have a great line up of speakers for you including:-

Malcolm Bennett- University of Nottingham, UK
"Towards a virtual root"
Mike Bevan – John Innes Centre, Norwich, UK
"Developing Brachypodium distachyon as a new model for temperate grass and bioenergy research"
Ralph Panstruga - Max Planck, Cologne, Germany
"Durable broad-spectrum powdery mildew resistance in crops and cereals: What can we learn from Arabidopsis?"
Jan Traas - ENS, Lyon, France
"The virtual flower: artefact or reality?"
Rodrigo Gutierrez - P. Universidad Católica de Chile
"VirtualPlant: A software platform to support Systems Biology research in the post-genomic era"
Jian Kang Zhu - University of California
"Salt and drought stress tolerance: role of proteins and small regulatory RNAs"

For a full meeting programme and speaker abstracts visit http://garnet.arabidopsis.info/garnet_meetingprogramme2007.htm

In addition to the informative evening workshops on tools and resources and funding, GARNet 2007 will also be offering hands on computer tutorials on two useful programmes for those of you grappling with the process of predicting networks and pathways from large datasets;
1. Taverna – a tool providing scientists with a graphical interface to facilitate the easy creation of workflows that enable automated mining and analysis of data from distributed web resources.
2. Pathway Editor – A visual editor designed for annotation, visualisation and presentation of wide variety of biological networks, including metabolic, genetic and signal transduction pathways.
These workshops will be limited to 10 attendees each, so register now to ensure you book your place.

We will also select a number of short talks from submitted poster abstracts, so if you have some outstanding data or ideas you would like to share with the community then register your abstract now.
So what are you waiting for?
Visit the GARNet website today and register for GARNet 2007. http://arabidopsis.info/garnet/garnet_meeting_2007.html

News and Views

iGEM 2007 - International Genetically Engineered Machine Competition in Synthetic Biology

written by James Brown, University of Cambridge

The iGEM competition is an open design challenge for student teams to design, engineer and assemble a simple biological system using standard, interchangeable components and operate it in living cells. The engineering of new biological systems is an exciting frontier, with new opportunities for collaboration between biologists, programmers and engineers. The iGEM competition throws together students from different disciplines, requires them to initiate a novel scientific program over the summer, and challenges them to learn and share different skills. The competition has provided a new educational model in an exciting new field. In Cambridge, we are unreservedly positive about the educational aspect of the competition. As well as learning challenging new scientific skills, the competition has allowed students to experience project brainstorming, management, teamwork, presentation and other organisational skills – in a way that is essentially outside the undergraduate curriculum.

The Biological Engineering Division of MIT's Computer Science and Artificial Intelligence Laboratory has pioneered the collection and use of modular biological components. They have established a Registry of Standard Biological Parts, which contains about 100 basic parts such as operators, protein coding regions, and transcriptional terminators. It also includes many devices such as logic gates built from these basic parts. These parts and devices, or "BioBricks", have been developed and used by student teams to build biological systems.

While 13 teams competed in 2005, last year the competition ran with teams from 35 universities worldwide including UK entries from Cambridge, Imperial and Edinburgh. The teams constructed systems with functions that ranged from biological sensors, artificial navigation and multicellular patterning to implementation of a bacterial photographic film. So far there are a staggering 57 teams registered for iGEM 2007. The project culminates in a November Jamboree at MIT, providing an opportunity for the students and instructors to make contact with the other international groups competing and present their summer's work.

For more information about iGEM visit:
www.syntheticbiology.co.uk
www.igem2006.com

Picture 'iGEM from above' taken at the iGEM 2006 November Jamboree at MIT
Credit: Randy Rettberg, iGEM Program Director

ERA-PG Updates

All grants have now been awarded from ERA-PG and the projects are getting underway. A grant holders workshop will be held at PlantGEMs6, 3-6 October, Tenerife - http://www.plant-gems.org/pages/home.php. This will be an opportunity for awardees to become familiar with the range of projects funded, the scope of the programme, and for networking between consortium members. In the meantime plans are underway for the second call which it is hoped will be announced at the end of 2007. The main ERA-PG contract from the European Commission ends this year and the potential for creation of a legal basis for sustaining the collaboration outside of Commission funding is being explored, as well as considering the options for extension of the network in a new application to Framework Programme 7. Following on from an interesting workshop at the Plant and Animal Genome meeting in January this year, an informal steering committee on Plant Genomics has been formed including representatives from US, UK, Canada, Brazil, China, Japan and Australia. The committee will look at opportunities for bilateral and multilateral funding in Europe and beyond; a follow-up workshop will held at PlantGEMs6. Sophie Laurie BBSRC

Join the great experiment in Arabidopsis annotation - New WeedsWorld Wiki Launched -

We are pleased to announce the creation of WeedsWorldWiki, the online collaboratively-authored Arabidopsis community 'encyclopedia' or 'blackboard', which allows any registered user to add and modify the content of webpages through a simple and intuitive browser.

The success of this Wiki lies in the community that forms around it.

We would like your help in defining the foundation of this new Wiki.

Any ideas for content, layout, or structure are very welcome. So, please check it out, sign-in and contribute!! - review that stock, add links to your lab pages, courses, papers, protocols!! There are no hard and fast rules, but don't trash it!

If you have made a line homozygous, let people know. If you have described the phenotype of a mutant – put it here and add your name to it. If you have published on a line, or have just written a review / thesis / report on a phenotype – put links to the original references here. Add experiences, tips and tricks, even (small) pictures. The only limit is your enthusiasm.

WeedsWorldWiki is designed to be your resource – it is what you make it to be. If you have any problems or questions, email us at bioinfo@arabidopsis.info. Go on - try it!!

See an example stock: NW20 http://arabidopsis.info/wiki/index.php/NW20.

WeedsWorldWiki - arabidopsis.info/wiki/ - 534,388 pages as of 7 June 2007

Arabidopsis Resources

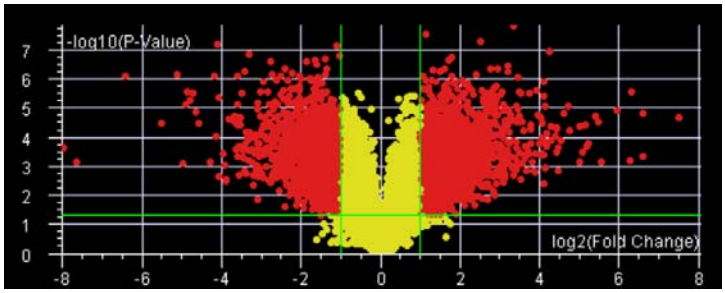
Genespring Workgroup at NASC

http://arabidopsis.info
written by Neil Graham
Nottingham Arabidopsis Stock Centre, School of Biosciences, University of Nottingham,
Sutton Bonington Campus, Loughborough. LE12 5RD

NASC have recently obtained a grant from the BBSRC to implement the Genespring workgroup database (Agilent technologies). This will allow users to easily access all the data within the NASCArrays database (currently >3000 slides) and perform detailed statistical analysis on the data. Similar implementations of Genespring workgroup have been used by NERC, Finland and Switzerland transcriptomic groups and numerous pharma companies.

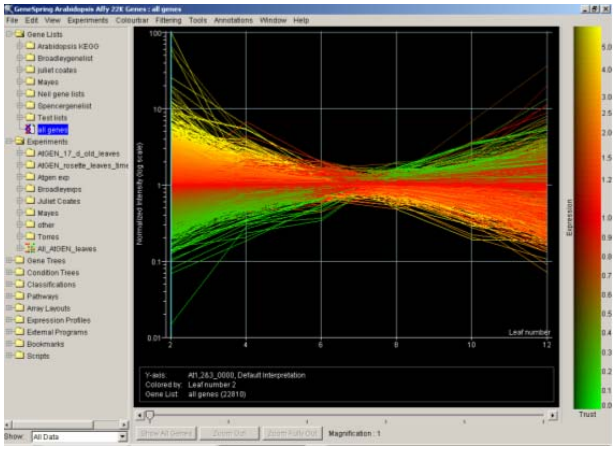
Genespring GX features

Genespring GX is a powerful visualisation and analysis tool for use with a wide range of expression data including Affymetrix, Agilent, spotted-arrays and real-time PCR data.



Data can be visualised in a number of ways, including:
- Line graphs
- Chromosome maps
- 2D and 3D scatter plots
- Volcano plots
- Overlaid on pathway diagrams (KEGG etc)
- Grouping by GO ontologies

Data can be analysed using range of techniques, including:
- Volcano plots for differentially expressed genes
- One and two-parameter ANOVA
- Clustering (Hierarchical, K-means, self organising maps etc)
- Promoter motif identification
- Class prediction



Genespring GX workgroup features

Genespring workgroup allows direct access to all experiments in the NASCArrays database. Whole experiments, individual or groups of .CEL files can be downloaded and analysed. Personal data (experiments, gene lists, analysis results) can be shared with the entire community or selected users.

Access

Access to Genespring workgroup can be done in a number of ways:
1. Full Genespring GX functionality (5 concurrent seats). Genespring can be installed on any computer and access is granted if a seat is free.
2. Genespring workgroup viewer (100 concurrent seats). Allows existing data / experiments to be viewed and limited analysis tools. All Genespring viewing tools and filtering tools (volcano plots etc) are available to generate new gene lists.
3. Web viewer. Allows viewing of genes lists / data via a web browser.

Implementation and training

The implementation on the workgroup has been initiated and we anticipate it being live by the 2007 GARNet meeting. Training sessions will be initially held at NASC and at selected meetings. For more information see http://arabidopsis.info or email affy@arabidopsis.info

Arabidopsis Resources

The 2010 Programme

http://www.arabidopsis.org/portals/masc/index.jsp
written by Joanna Friesner - MASC Coordinator University of California, Davis, Davis, CA 95616. jdfriesner@stanford.edu

In the year 2000, concluding a 10 year effort, the Multinational Coordinated *Arabidopsis thaliana* Genome Research Project ended with the release of the complete *Arabidopsis* genome sequence. As a follow-up to the sequencing effort the National Science Foundation established the 2010 project to maximally leverage the newly available genomic data. The goal of the project was to determine a function for every *Arabidopsis* gene by the year 2010. Since its inception the project has funded proposals in two main areas: proposals that address gene function directly and proposals that develop enabling tools and resources for functional genomics research. Since the first awards were granted in 2001, 119 diverse projects have been funded ranging from studies of gene families, development of research tools, analysis of natural variation, transcriptomics, widely-used reverse genetics resources such as sequence-indexed insertion lines, and many others. All current and past projects, including project descriptions can be found at the NSF AT2010 award page: http://www.nsf.gov/bio/pubs/awards/2010awards.htm.

In 2005 at the mid-point of the 2010 project, a workshop was held to assess the status of the Project, to recommend the objectives for the remaining five years, and to ensure the project can reach its original goals by 2010. The workshop report can be found at http://www.arabidopsis.org/portals/masc/masc_docs/AT2010WorkshopFinal.pdf. Based in part on recommendations from the workshop, the NSF revised the scope of the Project for the 2006 fiscal year to focus on :-

(1) Projects that include genome-wide analyses for benchmarking the function of all genes in the genome (*e.g.* gene expression patterns at high spatial and temporal resolution and interacting partners under defined, physiologically relevant conditions)

(2) Projects that will develop experimental and computational methods, tools, and resources for enabling a broad community of scientists to conduct functional genomics research on *Arabidopsis* (including biological resources and informatics tools that will complement existing resources that are cost-effective and can be readily adopted by the community).

(3) Research on exemplary networks that use high throughput methods and integrate modeling with experimental data to understand the gene circuitry underlying basic plant processes.

In 2006, 16 new or continuing projects were funded, and as in the past, accessibility of data and resources generated by the projects to the research community is of high priority. One newly funded project (AT2010: A Comprehensive Resource for Analysis of *Arabidopsis* Gene Function) will generate a complementary tool for gene silencing through the use of artificial microRNAs (amiRNAs) which have several advantages including the simultaneous silencing of duplicated genes or entire gene families and the ability to be used in accessions other than the standard strains used for insertion mutagenesis. Furthermore, amiRNAs can be designed with constitutive, inducible or tissue-specific promoters which will allow gene silencing to be achieved in a more controlled manner. Another newly-funded proposal (AT2010: Functions of *Arabidopsis* Small RNAs) focuses on small RNA-directed pathways and will perform sequence-based small RNA profiling in *Arabidopsis* including mutant lines, various developmental stages and treatments, and related species to examine the importance and evolution of small RNA pathways in plants. A third project funded in 2006 (AT2010: Towards a Comprehensive *Arabidopsis* Protein Interactome Map) will address protein-protein interactions, an area of *Arabidopsis* research that is currently under-represented. The project proposes to determine the interactions of 6,400 integral membrane proteins and proteins predicted to be involved in signaling or protein modification (AGI codes available at http://www.associomics.org/2010-final-v8.xls). Additional projects funded in 2006 can be viewed at the NSF AT2010 award page.
http://www.nsf.gov/bio/pubs/awards/2010awards.htm.

The abundance of knowledge, and community resources generated so far by the 2010 project have helped facilitate rapid advances in elucidating the function of many *Arabidopsis* genes. With the end of the Project rapidly approaching, the NSF and members of the international research community are preparing for the next phase of *Arabidopsis* research in the 'post-2010' era. At the annual meeting of the Multinational *Arabidopsis* Steering Committee in June, 2007, coordinated discussions about future research directions using this invaluable reference plant will begin. It is clear that cooperation and collaboration were key factors in the past success of the *Arabidopsis* Genome Project, and for the success of the current 2010 Project and other large-scale international *Arabidopsis* functional genomics projects. To maximize the return from such efforts, future projects must similarly be integrated and coordinated.

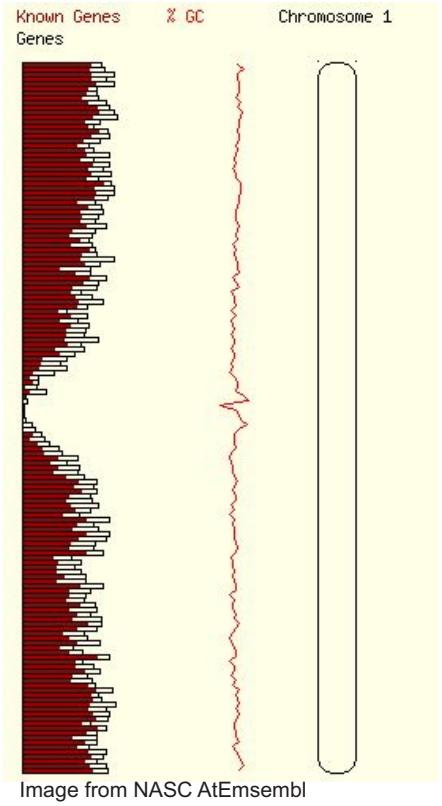


Image from NASC AtEmsembl

Beyond 2010:
The focus of future Arabidopsis research

A genome sequence by 2000… gene functions by 2010… what targets for 2020? The UK's representation on MASC gives us the opportunity to influence the international Arabidopsis research programme. To ensure that the programme is aligned with UK goals, GARNet would like to know what areas and concepts YOU think should be considered as a focus for research in the 'post-2010 era'. For example, can synthetic biology provide us with parts and devices that will help us to explain and control the complexity of biological systems?

Alternatively, should future research focus more on validation in nature than under controlled laboratory conditions?

Please consider what would be most productive for the whole community and e-mail your ideas to ruth@arabidopsis.info

17th *New Phytologist* Symposium

Systems Biology and the Biology of Systems: how, if at all, are they related?

The Palace Hotel, Buxton, UK

13-14 September 2007

Invited speakers

Andrew Bangham (University of East Anglia, UK)
Gerhard Buck-Sorlin (IPK Gatersleben, Germany)
Stefan Jansson (Umeå Plant Science Centre, Sweden)
Jan Kim (University of East Anglia, UK)
June Medford (Colorado State University, USA)
Andrew Millar (University of Edinburgh, UK)
John Sheehy (IRRI, Philippines)
Andy Taylor (SLU, Uppsala, Sweden)
Michael Wilkinson (University of Wales, UK)
Xinyou Yin (Wageningen University, The Netherlands)

Organization

Sid Thomas, Helen Ougham, Alan Gay & Janet Taylor (IGER, Aberystwyth, UK)
Helen Pinfield-Wells (*New Phytologist*, Lancaster, UK)

Contact

Helen Pinfield-Wells newphytsymp@lancaster.ac.uk

New Phytologist Central Office
Bailrigg House
Lancaster University
LA1 4YE, UK.
Tel: +441524 594691
Fax: +441524 594696

Further details and registration information at

New Phytologist

www.newphytologist.org

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Energy Crops and Biomass

What is Biomass?

Essentially, biomass is a form of stored solar energy. Plants capture the sun's energy via photosynthesis and convert this energy into plant material for growth. It is possible to release this stored energy by thermal conversion such as combustion, gasification or fast-pyrolysis; or by biological conversion using micro-organisms and/ or enzymes to generate biofuels (pg 9) including alcohols and 'biogas'.
There are many different sources of biomass and numerous ways in which the energy within them can be realeased. This article will focus on UK grown plant material.

Why use biomass as fuel?

Energy consumption is steadily increasing across the globe and only a small percentage of our energy (3% in the UK) is obtained from renewable sources. Current concerns over carbon dioxide induced changes in climate are increasing the need to develop energy sources with reduced CO_2 emissions. Plant biomass provides a viable alternative to fossil fuels as it can be a carbon neutral energy source. In theory the CO_2 released by burning plant biomass is balanced by that absorbed during photosynthesis, so that it does not contribute to greenhouse gas (GHG) emissions. In reality biomass production from first generation crops such as oilseed rape and cereals does impact on the environment, either through the GHG generated during the production of nitrogen fertilizers that are often used to grow the biomass, or in fossil fuel usage during production, harvesting and transportation of the biomass. Dedicated energy crops such as Miscanthus and short rotation coppice (SRC) willow can however produce higher yields of biomass more sustainably with a significantly positive energy balance. Although a number of other renewable energy technologies can produce electricity, biomass is the only current technology which can generate liquid fuels for transport and platform chemicals for industry to directly substitute for oil.

Use of Biomass

There are two distinct markets for combustion of biomass in the UK

1. Small scale (domestic) – Logs/wood pellets/wood chips are burnt in wood burning stoves and the energy generated is used to heat space and/or water.
2. Industrial Scale – Electricity generation via combustion of plant biomass to generate steam. This includes the co-firing of biomass with coal at concentrations typically of up to 10%. This approach is used at the UK's largest power plant Drax which generates approximately 7% of the UK's total electricity.

In addition oilseed rape is used to make biodiesel and cereal grain used to make bioethanol (pg 9) for transport fuels. However, these processes are not sustainable in terms of the energy balance. In the future lignocellulosic, feedstocks comprising cereal straw or stover and dedicated energy grasses such as Miscanthus, are seen as the most likely feedstocks for ethanol and next generation transport fuels. Forage crops such as perennial ryegrass are also seen as an option particularly for hydrogen or methane (biogas) production. Provided the technology exists to break down complex plant cell walls, even woody crops such as SRC willow may provide feedstocks for transport fuels.

Main Sources of UK Biomass

1. Forestry materials, where the fuel is a by product of other forestry activities, but supplies are limited.
2. Dedicated energy crops, such as SRC willow or popular and energy grasses e.g. Miscanthus and reed canary grass.

These energy crops offer the advantage of a shorter generation time compared to forestry species. Biomass yields are typically about 12 ton on average across the UK however this is expected to increase with breeding as these crops have received little to no previous genetic improvement. Energy grasses are harvested annually and SRC every second to third year but this requires more specialist machinery.

Energy Crops and Biomass

Future Priorities for Bioenergy research

The three primary targets for improving biomass crops are greater yield, increased efficiency of conversion into energy and improved sustainability of the crop. In other words, we need to increase the yield of biomass per hectare and the yield of energy per tonne of biomass, hopefully achieving both objectives in an ecologically and financially sustainable manner. Increasing the amount of energy released from a given quantity of biomass, can be achieved by tailoring the chemical composition of the crop. There are obvious parallels between the improvement of biomass composition quality in energy crops and quality improvements to food and feed crops. Moreover, it is also important that improvements made to yield, are not linked to unintended negative effects on conversion efficiency. Future basic research into bioenergy crops therefore needs to be targetted at:-

- Improving our understanding of assimilation and biomass partitionning in plants for future manipulation.
- Increasing the overall yield of bioenergy crops via improvement of carbon flux and sequestration.
- Increase generation time by improving growth rates and optimisation of flowering time.
- Optimisation of plant architecture, including enhancing light capture.
- Increase the chemical composition of the biomass, in particular cell walls, to increase the conversion efficiency of the biomass for either thermal or biological conversion routes.
- Maintain yield by increasing biotic and abiotic stress tolerances.
- Increase the sustainability of bioenergy crops by reducing the dependence on inputs, in particular nitrogen fertilizers and water.
- Quantification and prediction of how growing bioenergy crops will affect the landscape; biodiversity (above and below ground) and farming practice.

There will be clear opportunities for the translation of knowledge gained in model plants such as Arabidopsis, rice and most recently Brachypodium, to help improve energy crops. In addition to this research, improvements will also need to be made to the thermal and biological conversion processes to maximize energy yields. It will therefore be important that biologists work in tandem and in collaboration with engineers, chemical engineers and microbiologists to ensure that the next generation of energy crops are compatible with current conversion processes.

Is Biomass a viable option for the UK?

Biomass will ultimately play a major role in supplying renewable energy, transport fuels and other industrial products to the UK. It is therefore important that we continue to develop a range of mechanisms to reduce GHG emissions and provide renewable alternatives to fossil fuels. The UK actually has a considerable biomass resource; 20 million tonnes annually could be utilised as a source of renewable energy, A recent review by the Biomass Task Force concluded that up to 1 million hectares of UK land could be dedicated to specialist bioenergy crops by 2020 (http://www.defra.gov.uk/farm/crops/industrial/energy/biomass-taskforce/pdf/btf-finalreport.pdf). Whether or not this is achieved in the next decade, is likely to be determined by a number of factors including; social acceptance of changing land use, environmental impact and land use competition for the production of food/fuel/energy/industry. One potential alternative to this competition for land could be to develop/use multi-use crops in bio refineries that produce a marketable end product, as well as heat and energy.

The UK has great research strengths in plant science and engineering however, there are currently only a few networks focused solely on bioenergy including:-

SUPERGEN Bioenergy (www.supergen-bioenergy.net)
TSEC- Biosys (http://www.tsec-biosys.ac.uk)
RELU-Biomass (http://www.relu-biomass.org.uk)
Genetic Improvement Networks: Miscanthus based at IGER, Willow based at RRes.

Although many plant science groups across the UK are working on bioenergy based topics (http://ukerc.rl.ac.uk/Landscapes/Bioenergy.pdf) they are often fragmented and not part of core activities. Only by forming a coherent bioenergy strategy and increasing funding, via initiatives such as that by the BBSRC (http://www.bbsrc.ac.uk/science/initiatives/bioenergy.html), will the UK build enough capacity to benefit from the rapidly expanding international bioenergy and biomass markets.

Images in this article were kindly suppiled by IGER. Many thanks to Iain Donnison for all his help in producing this article.

Renewable Transport Fuel Obligation

In November 2005, the UK Government introduced the Renewable Transport Fuel Obligation Programme (RTFO). The RTFO places an obligation on fuel suppliers to ensure that, by 2010, 5% of all road vehicle fuel is supplied from sustainable renewable sources. This will equate to approximately 2.5M tonnes of biofuels by 2010, a 20 fold increase on current UK sales (HCGA). It is expected that the RTFO will come in to force in April 2008 and will help to bring the UK into line with the European Union biofuels directive, which sets targets for all EU countries for biofuel usage of 2% by the end of 2005 and 5.75% by the end of 2010.

So how will it actually work:-
The RTFO will be implemented through a certification scheme; for each litre of biofuel supplied, the obligated party will receive an RTF certificate.
If an obligated party fails to meet its RTFO (obtain enough certificates), they will either have to buy more RTF certificates from a third party to cover the shortfall, or pay a penalty buy out price to the Government.
The RTFO will only apply to those companies, generally oil refiners and importers, who supply liquid fossil fuels into the UK market. This means that the fuel can come from anywhere across the globe.
The obligated parties will need to provide publicly available information on the carbon and sustainability content of the biofuel used. It is hoped this will encourage suppliers to source fuel with 'real environmental' benefits rather than using the cheapest biofuel available.

Biofuels - in a nutshell

written by Dr. Martha Simpson-Holley
The National Non-Food Crops Centre Biocentre, York Science Park Innovation Way, Heslington, York. YO10 5DG

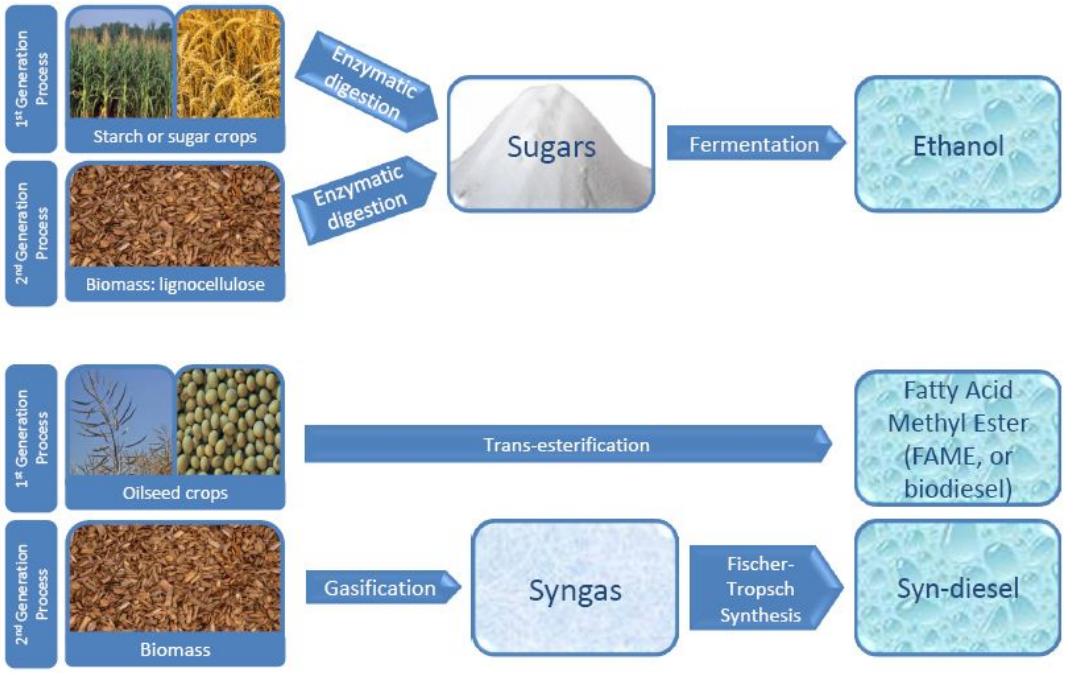
The National Non-Food Crops Centre (NNFCC) is the UK's independent authority on plant-derived renewable materials and technologies. We can be found on the web at www.nnfcc.co.uk.

Biofuels: why do we need them?

There are two reasons why we need an alternative to oil-derived transport fuels. The first is that oil is running out: proven reserves will last approximately 41 years (www.bp.com). The second is climate change: if we don't reduce global greenhouse gas (GHG) emissions, climate change will cost billions of pounds and millions of lives.
Biofuels are liquid fuels manufactured from plants. Plants are renewable and can be grown repeatedly, removing the problem of dwindling resources. Plants also remove carbon dioxide from the atmosphere; the carbon dioxide produced by burning one batch of biofuel is reabsorbed during the manufacture of the next. Biofuels are not completely carbon neutral and produce some GHG emissions, but can offer significant GHG savings over fossil fuels.
In this article we ask which biofuel production methods and crops are best, and if we can manufacture enough biofuel to reduce climate change using UK biomass. The answers put forward are the result of research carried out by the NNFCC and our partners (www.nnfcc.co.uk).

Which biofuels are best?

Two biofuels are currently available: bioethanol and biodiesel. They can be manufactured using 1st or 2nd generation processes (figure below). These processes use different feedstocks and achieve different savings in GHG emissions. 1st generation processes are simpler than 2nd generation processes: bioethanol is produced by fermentation of plant-derived sugars; biodiesel is produced by transesterification of plant oils or waste oils. These feedstocks are derived from 'food' crops: wheat, corn and sugar cane for ethanol; oilseed rape, oil palm and soybean for biodiesel. These crops tend to be fertiliser-intensive, with the exception of sugar cane and oil palm. Fertiliser is derived from fossil fuel and can produce nitrous oxide, so its use in biofuel production decreases their GHG savings. Fertiliser over-use has other environmental consequences such as eutrophication. The emissions savings achieved by 1st generation processes vary: corn ethanol achieves around 18% savings compared with petroleum, wheat bioethanol and rapeseed biodiesel can achieve savings of >50%. The use of by-products and crop residues as fuel or animal feed can increase the GHG savings.



1st generation processes are becoming established in the UK. They can provide biofuels at a cost which, although not competitive with fossil fuels, is made more viable by Government-imposed tax rebates: petrol and diesel are currently taxed at 48p/litre; biofuels have a 20p/litre tax rebate. In addition, the UK biofuels industry is bolstered by the imminent introduction of the Renewable Transport Fuel Obligation (RTFO), which requires the inclusion of 2.5% biofuel (by volume) in UK road fuels by 2008, and 5% by 2010. The RTFO requirements can be satisfied using 1st generation processes and UK feedstocks without affecting food production. In reality feedstocks used for 2nd generation processes are technically advanced. They bring higher capital investment costs than 1st generation processes. Once established, these processes could produce more biofuel, with better GHG emissions savings (up to 90%, http://ies.jrc.cec.eu.int/wtw.html). 2nd generation processes do not use 'food' crops: in theory they can use any biomass. This could reduce fertiliser use and increase the sustainability of biofuel production. Feedstocks include high-yield, low input energy crops such as short rotation coppice or Miscanthus, in addition to food waste, crop residues and municipal solid waste. 2nd generation processes cannot provide an unlimited fuel supply. We estimate that without affecting food production, UK agricultural resources can supply 10-20% of our road transport fuel in 2010. The lower figure is conservative: high yielding crops, crop surpluses and waste biomass would increase production capacity. The replacement of 10% of fuel with biodiesel could save around 11 billion kg CO2: 1.7% of the UK's total GHG emissions in 2006.

Balancing biomass with energy demand: eyes too big for our stomachs

The UK's biomass resources cannot fulfil all of our energy demands. For example replacing more than 20% of transport fuel with biofuel might exhaust the UK's spare biomass; other energy sources would have to supply all our electricity and heat. Therefore, biomass energy and fuels can form only part of our strategy for managing climate change.
The shortfall between UK biomass resources and energy demand can be managed in different ways; the development of low input, high yielding energy crops is desirable. Novel biomass crops might include algae, which could produce high yields of biomass. Other strategies for meeting energy demand may include importing feedstocks and biofuels, using other forms of renewable energy, increasing fuel efficiency, sequestering carbon from fossil fuels, and changing the way we travel, live and work. A combination of these approaches will be required on a global scale to stop climate change in its tracks.

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.

University of Oxford

UNIVERSITY OF OXFORD
Department of Plant Sciences

Research in the Department of Plant Sciences is organised into three main groupings: Biochemistry and Cell Biology (BCB), Comparative Developmental Genetics (CDG), and Ecology Evolution and Systematics (EES). The department is very excited about the forthcoming move of Nick Harberd and his group from JIC Norwich – Nick will be taking up the Sibthorpian Chair from October 2007. At the same time, Jane Langdale will take over as Head of Department from Chris Leaver who will retire in December 2007, after leading the department for the past 17 years. Further appointments at both Professorial and Lecturer level are expected within the next year, and the department is constantly seeking to recruit highly motivated graduate students, post docs and research fellows. http://dps.plants.ox.ac.uk/external/.

Name Nick Brown
e-mail nick.brown@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Ecology/Environmental change

Research Activities

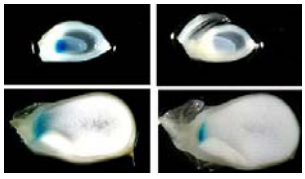
Nick Brown's research focuses on the impacts of both natural and human-induced environmental change on natural ecosystems. He is co-ordinating a collaborative project with the University of the West Indies and the Forestry Division measuring and mapping plant diversity across Trinidad and Tobago. The aim of this work is not only to identify areas that are of high conservation value but also to examine rates and patterns of change over the last 50 years and to build models to predict responses to future climate change.

Nick is also working with colleagues from the departments of Geography and Archaeology on a project that is exploring the industrial ecologies of three major kiln sites in south China from the 8th to the 14th centuries AD. The study is concerned particularly with deforestation in medieval China and its effects on the dynamics of stoneware and porcelain production throughout Zhejiang province. By applying palaeoecology techniques (e.g. pollen analysis and charcoal analysis) to lake sediment cores from the region, the group will be able to study the relationship between vegetation composition, fuelwood output and the rise and fall of production in these three centres.

Nick is part of the forestry research and policy group Forestry Horizons, which is exploring ways to increase both the productive and conservation values of private forests in England. The group are undertaking research on the current and future roles of forestry, with the aim of defining an optimum forestry strategy for England with an emphasis on broadleaves.

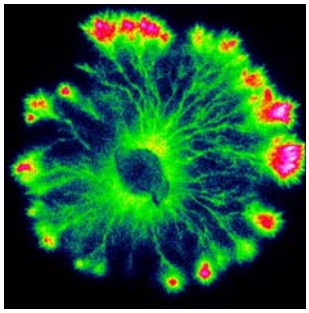
Name Hugh Dickinson
e-mail hugh.dickinson@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Developmental genetics of plant germlines

Research Activities



Unlike in animals, plant reproductive cell lines (germlines) are established late in development, and within a genetically independent plant structure – the haploid gametophyte. Interest in the Dickinson laboratory is focused on the genetic systems which confer reproductive fates on cells developing within the anthers and ovules, and the epigenetic changes that accompany meiosis and the formation of sperm cells and eggs. Current work on Arabidopsis centres on the interplay between the gene networks responsible for producing the outer, polarised envelope of anthers, and those which generate the germlines within them. Also of interest are the asymmetric epigenetic imprints or 'marks' which are conferred on genes as they undergo male and female development, and which later control expression post-fertilisation. In a current maize project it has been possible to make lines carrying 'imprinted' reporter constructs which mimic imprinted genes in their monoallelic expression. This project has led to the discovery that the control of imprinted sequences in plants differs from animals, in that it is effected by short regions upstream of each gene, but resembles animal systems in that expression is regulated by upstream islands of methylation. The features of genes which single them out for differential 'marking' in the male and female germlines are currently under study. Other projects under way are concerned with the extent to which imprinting regulates early seed development using genomic approaches and through the study of imprinted genes of known or predicted function, and the nature and function of the small RNA pathways operating in the male gametophyte and germline.

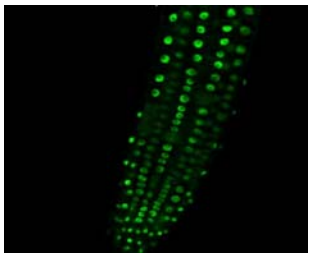
Spotlight on the University of Oxford



Name Marck Fricker
e-mail marck.fricker@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Imaging signalling and transport in complex systems

Research Activities

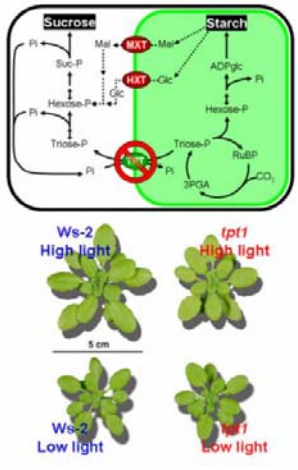
The primary research focus of the Fricker lab has shifted dramatically in the last few years. The group maintains a strong interest in quantitative fluorescence techniques to measure physiological parameters, such as pH, calcium and glutathione, and maintains expertise in confocal laser scanning microscopy of fluorescently-tagged proteins in intact living tissues. However, researchers have recently developed a novel scintillation imaging technique to map solute transport dynamics in fungal mycelial systems, which has opened up a completely new area of research. Analysis of these complex transport events has required the development of new analytical software tools such as Fourier- and Hilbert-based phase-mapping techniques to analyse the oscillatory component; mass-distribution analyses to map resource allocation and a new planar spatial network analysis system to characterise the topological network. To further understand the mechanism of amino-acid transport, the group is now linking these macro-scale approaches with confocal imaging to measure the rate of solute movement through the dynamic tubular vacuole system at sub-hyphal scale using a combination of confocal microscopy, fluorescence recovery after photobleaching (FRAP) and mathematical modelling.



Name Nick Harberd
e-mail nicholas.harberd@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/nicholas-harberd/index.htm
Research Area Plant growth and development

Research Activities

Currently based at the John Innes Centre, Norwich, the Harberd laboratory is re-locating to the Plant Sciences Department in Oxford in the autumn of 2007. Research in the Harberd group focuses on plant growth regulation. *Arabidopsis* is the 'primary' laboratory model, and other species are studied as appropriate. The group is especially associated with the discovery and characterisation of a family of plant growth-regulatory nuclear proteins known as the DELLAs. In 1997, the group reported the cloning of *Arabidopsis GAI* (the first identified DELLA-encoding gene). Subsequent highlights included the demonstration that 'green revolution' wheat dwarfing alleles are mutant forms of DELLA-encoding genes. The DELLAs are central components of the mechanism by which the plant growth-promoting hormone gibberellin (GA) stimulates plant growth, and the group (together with other laboratories) has advanced understanding of how this mechanism works. Essentially, the DELLAs are plant growth repressors. GA binds specifically to a soluble GA-receptor, thus stimulating interaction between the GA-receptor and the DELLAs. This interaction targets the DELLAs for destruction by the 26S proteasome. Thus GA stimulates plant growth by promoting the destruction of the growth-repressing DELLAs. In addition, the group has recently shown that the GA-DELLA mechanism is key to the growth response of a variety of endogenous and environmental signals, indicating that the DELLAs play a fundamental integrative role in plant growth regulation. Current and future research will include a comparative approach to understanding how the GA-DELLA and other plant growth and developmental regulatory mechanisms arose during land-plant evolution.

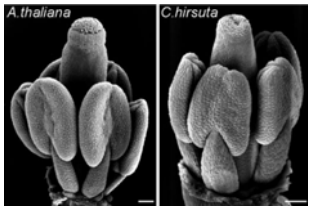


Name Nick Kruger
e-mail nick.kruger@plants.ox.ac.uk
Website http://www.plants.ox.ac.uk/Nick_Kruger
Research Area Regulation of central carbon metabolism

Research Activities

Carbohydrates are the major respiratory substrate in most plants, providing both energy and metabolic precursors for growth. However, our understanding of how the carbohydrate synthesis and degradation pathways are regulated to meet the requirements of the plant in response to changing environmental and developmental demands is still extremely limited. This restricts the potential for improvement of plant performance through rational genetic engineering of these important processes. Current work in Nick's group focuses on addressing the significance of two unusual features of central carbon metabolism and its organisation in plants: one is that the pathways are highly compartmented, with many of the enzymes being found in both cytosol and plastids; the other is that each step can be catalysed by multiple isozymes. Metabolic characterisation of *Arabidopsis* knockout lines in which functional expression of specific combinations of genes has been perturbed is being used to understand the precise metabolic and physiological role(s) of particular isoforms, and to establish the significance of processes occurring in specific subcellular compartments. To describe the metabolic impact of such manipulations, system-wide steady-state stable-isotope labelling approaches are being developed, in close collaboration with George Ratcliffe, to quantify flux through the reactions of primary metabolism. This work exploits NMR spectroscopy to resolve ^{13}C-isotopomers in a range of metabolites and to quantify their specific abundance in complex mixtures. This approach allows resolution of *in vivo* fluxes throughout the metabolic network including different subcellular compartments which will underpin the group's future studies on plant carbohydrate metabolism.

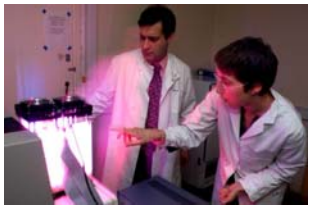
Spotlight on the University of Oxford



Name Angela Hay
e-mail angela.hay@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Comparative plant development

Research Activities

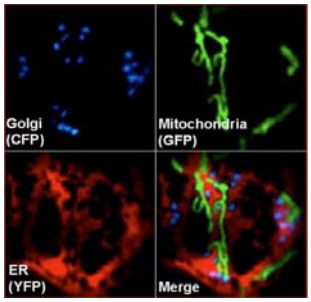
Angela's research interests include developmental genetics and the evolution of developmental mechanisms. Evolution has produced a wealth of variety in flowering plants, particularly in their floral structures. A key question in biology is how molecular changes in developmental pathways lead to morphological changes during evolution. Angela's research aims to identify the genetic differences that underlie divergence in floral structure between two closely related species; *Arabidopsis thaliana* and its wild relative *Cardamine hirsuta*.

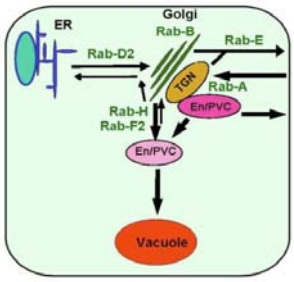


Name Harriet McWatters
e-mail harriet.mcwatters@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Circadian clocks

Research Activities

Circadian clocks are a fascinating adaptation to a rhythmic environment. All multicellular organisms, and some unicellular ones, possess a clock. This strongly suggests that the ability to tell the time and predict change is highly advantageous to a wide variety of organisms. Harriet McWatters' particular interest is the process by which these clocks are co-ordinated with the environment, on a daily or seasonal timescale. Recently, she has begun to ask questions about the way the plant can use information from changes in its own physiology, such as alterations in cell membrane rigidity or the increase in sugar level following the onset of photosynthesis, to tell the time. Her research is conducted at several levels from the gene through the individual plant to the population. Her laboratory is the first to use gene expression as the basis for studying quantitative traits leading to the identification of 4 QTLs responsible for phase differences between *Landsberg erecta* and *Cape Verde Island* ecotypes. Recently, Harriet has also shown that ELF4 is required to maintain the feedback loop between CCA1/LHY and TOC1 that forms the heart of the Arabidopsis clock.





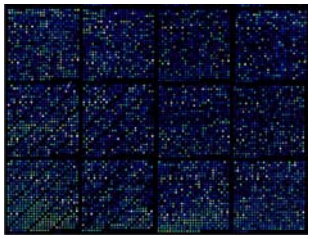
Name Ian Moore
e-mail ian.moore@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Molecular genetics of intracellular membrane trafficking in *Arabidopsis*

Research Activities

Ian Moore's laboratory investigates the intracellular membrane trafficking pathways of plant cells. They are responsible for the biogenesis of some of the most biologically interesting and commercially important structures in plants, including the cell wall, cell plate, plasma membrane, and an array of vacuoles. They are also important in determining cell polarity and responding to biotic and abiotic stress.

The laboratory has adopted two approaches to the elucidation of plant membrane trafficking pathways. One focuses on the Rab family of GTPases which are important determinants of membrane identity and vesicle targeting. Phylogenetic analysis indicates that higher plants have evolved a unique complement of Rab GTPases and suggests that the 57 *Arabidopis* Rab GTPases fall into between 12 and18 subclasses each of which is envisaged to perform a distinct trafficking function. Rab GTPases that act in the major trafficking routes between endoplasmic reticulum, Golgi apparatus, plasma membrane and vacuoles have been identified using membrane trafficking assays based on quantitative fluorescence imaging of specific marker proteins. Recent work has focussed on Rab GTPases that have plant-specific functions in endosomal sorting and cytokinesis. A second line of investigation has led to the identification of over 60 membrane trafficking mutants in *Arabidopsis* using EMS screens based on fluorescent secretory markers. The laboratory has also developed the widely used pOp/LhG4 and pOp6/LhGR systems for spatial and chemically-inducible temporal control of transgene expression in *Arabidopsis*, tobacco and maize. The group will shortly be releasing a range of additional resources for tissue-specific inducible expression of transgenes.

Spotlight on the University of Oxford



Name Haruko Okamoto
e-mail haruko.okamoto@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Plant heterotrimeric G-protein signalling in response to a changing environment

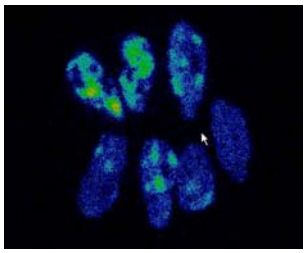
Research Activities

Heterotrimeric G-proteins have been implicated in many of the pathways mediating plant responses to environmental signals such as drought, ozone and light. Haruko's laboratory has been concentrating on dissecting the molecular basis of heterotrimeric G-protein signalling. The genome of the model plant Arabidopsis encodes just one gene of each of the G alpha and G beta subunits thus providing a uniquely simple system to work on. T-DNA insertion mutants as well as plants overexpressing G alpha and G beta subunits have been analyzed for their physiological characteristics in response to a range of environmental signals, in particular light. The main focus of Haruko's work is to understand the molecular basis of heterotrimeric G-protein signalling in Arabidopsis by employing molecular biology techniques, biochemistry, cell biology and genetics. Light signalling pathways, mediated by a range of photoreceptors, such as cryptochromes and phytochromes, have been identified as one of the many pathways in which heterotrimeric G-proteins function and therefore light signals are used as a primary input to understand the G-protein signalling process.

Name John Pannell
e-mail john.pannel@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Evolutionary ecology and population genetics of plant sexual systems

Research Activities

John Pannell's research is broadly centred on the areas of ecological genetics and plant evolutionary ecology. He has a special interest in the evolution of plant sexual systems, particularly transitions between hermaphroditism and dioecy, where individuals specialise either as males or females. Over the past decade, he has been elucidating how males can be maintained in populations with hermaphrodites, principally through detailed ecological, phylogenetic and population genetic studies of the European plant *Mercurialis annua*, which displays outstanding variation in its sexual system. Currently, research in the Pannell lab includes: studies of the population genetics of subdivided populations under different sexual systems; theoretical and empirical investigations into the evolution of inbreeding depression in subdivided and fragmented populations; the quantitative genetics of sex allocation and sexual dimorphism, where males and females have evolved different morphologies, physiologies or allocation strategies; the ecology and genetics of metapopulations in which local populations suffer recurrent stochastic extinctions and re-colonisations; and the evolution of local adaptation under contrasting climatic conditions. All this research employs both field- and lab-based approaches, as well as the development of theoretical models.

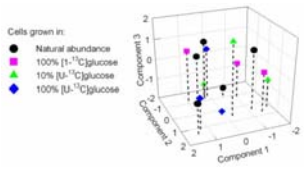


Name Gail Preston
e-mail gail.preston@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area The molecular basis of plant parasitism in *Pseudomonas*

Research Activities

Gail Preston's research addresses the molecular basis and evolution of plant pathogenesis in plant-associated bacteria, and aims to identify and understand the factors that differentiate plant pathogenic and plant growth-promoting bacteria, specifically bacteria in the genus *Pseudomonas*. Plant pathogenic *Pseudomonas* such as *Pseudomonas syringae* multiply in the intercellular spaces between plant cells during disease development, and use toxins, hormones and secreted proteins to suppress plant defences and maintain access to apoplastic nutrients. The Preston group are using analytical, molecular genetic and genomic approaches to identify which nutrients are used by *P. syringae* during apoplast colonisation, to ask whether *P. syringae* is specifically adapted for growth using apoplastic chemicals, and to investigate whether *P. syringae* manipulates plant physiology to construct a nutritionally favourable apoplastic niche. They are also collaborating with researchers within the Plant Science Department and at Rothamsted Research to investigate whether knowledge of bacterial pathogenicity mechanisms and apoplast physiology can help explain how environmental factors such as nitrogen, toxic metals and light have pronounced effects on susceptibility and disease resistance in plants. A second research area in the group is founded on the observation that many of the pathogenicity mechanisms, which have been characterised in plant pathogenic bacteria, are also present and expressed in non-pathogenic, plant colonising *Pseudomonas*. Researchers are investigating whether non-pathogenic *Pseudomonas* manipulate plant metabolism to promote bacterial growth without compromising plant health, and whether these "pathogenicity" mechanisms have alternative uses in bacterial interactions with plant-associated eukaryotes such as fungi, nematodes and amoebae.

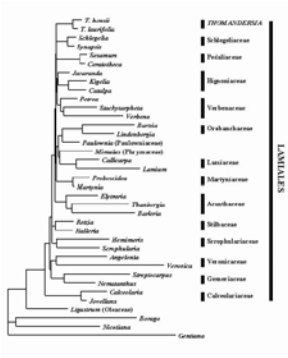
Spotlight on the University of Oxford



Name George Ratcliffe
e-mail george.ratcliffe@plants.ox.ac.uk
Website www.plants.ox.ac.uk/George_Ratcliffe
Research Area Biochemical and physiological applications of NMR spectroscopy

Research Activities

The plant NMR group uses NMR spectroscopy to test hypotheses relating to the integration and regulation of plant metabolism. Ions and metabolites in tissues and tissue extracts are analyzed using a 600 MHz NMR spectrometer with the aim of characterizing the metabolic phenotypes of wild type, mutant and transgenic plants. Collaboration is an effective vehicle for bringing the unique problem-solving capabilities of NMR to bear on worthwhile biological problems, and within the department the plant NMR group has particularly strong links with Nick Kruger and Lee Sweetlove. Currently three areas dominate these collaborations: network flux analysis, metabolomics and mitochondrial metabolism. Network flux analysis is a systems biology tool that provides a quantitative framework for assessing the effects of genetic and environmental perturbation on the metabolic phenotype. NMR contributes to this emerging field through the analysis of the redistribution of the stable isotope ^{13}C in labelling experiments. Metabolomics provides an alternative definition of the metabolic phenotype – one based on composition rather than flux – and here NMR complements mass spectrometry as a tool for generating metabolite fingerprints and profiles. Finally in the specific area of mitochondrial metabolism, continuous non-invasive NMR analysis of dilute suspensions of purified mitochondria in defined respiratory states allows direct observation of the impact caused by physiological and genetic perturbations on fluxes through mitochondrial pathways. In all three areas the versatility of NMR allows the group to generate biological insights that will ultimately contribute to the construction of predictive models of plant metabolism.



Name Robert Scotland
e-mail robert.scotland@plants.ox.ac.uk
Website http://herbaria.plants.ox.ac.uk/
Research Area Phylogeny, biodiversity and taxonomy

Research Activities

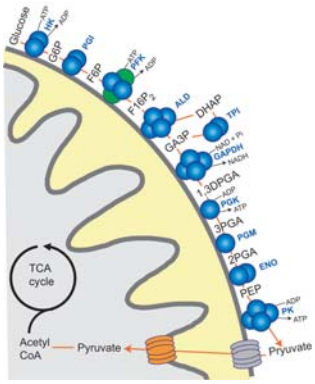
A taxonomic monograph of *Strobilanthes* (Acanthaceae) has provided an empirical platform to address a range of contemporary issues in relation to biodiversity and phylogeny. These include the study of hollow curves of diversity and what they tell us if anything about evolution; species discovery curves and what they tell us about the completeness of the global inventory of organisms; the dynamics of the species discovery process in relation to geographic range and use; monographic synonymy rates for seed plants and their implication for how many seed plants there are. Another theme derived from the monograph has been the paradox of why most of our knowledge of phylogeny stems from morphology but nevertheless DNA sequence data is now the preferred data for building phylogenies.

Name Andrew Smith
e-mail andrew.smith@plants.ox.ac.uk
Website http://www.plants.ox.ac.uk/Andrew_Smith
Research Area Metal homeostasis and hyperaccumulation

Research Activities

Plants that hyperaccumulate metals show an exceptional degree of metal tolerance, being capable of concentrating transition metals to over 1% of tissue dry biomass. Andrew Smith's laboratory is investigating what these plants can reveal about fundamental mechanisms of trace elemental acquisition, complexation, transport and sequestration in plants. Many of the naturally occurring hyperaccumulator plants are members of the *Brassicaceae*, which allows the application of certain molecular and genomic tools developed in model species such as *Arabidopsis*. The group have a particular interest in comparative studies of nickel hyperaccumulation in genera such as *Alyssum*, in which there are large numbers of both hyperaccumulator and non-accumulator species. Current work is focused on studies of the transcriptome of hyperaccumulator plants, mechanisms of metal-ion transport, and investigation into the evolutionary origins of the hyperaccumulation trait and its adaptive significance.

Spotlight on the University of Oxford



Name Lee Sweetlove
e-mail lee.sweetlove@plants.ox.ac.uk
Website www.plants.ox.ac.uk/Lee_Sweetlove
Research Area Regulation of plant metabolic networks

Research Activities

Metabolism is the ultimate driver of plant growth and development and represents one of the best characterised of all molecular interaction networks in biology. Traditional enzymology combined with more recent genomic information has provided a sound basis for a consensus view on the structure of the metabolic network in *Arabidopsis* and the regulatory mechanisms that operate within it. However, despite this wealth of information, our ability to predict the effect of genetic intervention on metabolic flux remains rudimentary. Such predictive ability is a pre-requisite to manipulating plant metabolism with a view to (a) improving plant performance in the field (minimising the negative impact of stress), (b) improving the nutritional composition of crops and (c) improving the efficiency of carbon fixation and allocation (bioenergy). Using the response of *Arabidopsis* to oxidative stress and the accumulation of metabolites during tomato fruit ripening as experimental systems, Lee's lab is attempting to build a systematic view of metabolic regulation and control. A combination of genetics and molecular profiling is being used to define different levels of regulation (transcriptional or post-translational) and investigate metabolic signalling pathways, while network analysis is being applied to encapsulate the experimental data in computational models of the entire metabolic network. The ultimate goal is to develop truly predictive metabolic models of plant metabolic networks that will facilitate precise, targeted engineering of metabolic activity.

Name Miltos Tsiantis
e-mail miltos.tsiantis@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Comparative plant development

Research Activities

Miltos' lab is interested in understanding the genetic basis underlying a generation of different organismal forms. Leaves of seed plants offer an attractive opportunity to study morphological evolution as they demonstrate an enormous degree of phenotypic diversity. To study this problem the lab employs molecular genetic and comparative development approaches in plants with divergent leaf forms. Research within the laboratory has two main goals, firstly to build a concrete picture of the genetic networks that function to sculpt angiosperm shoot form, and secondly to understand how these networks are modified through evolution to result in the multitude of distinct leaf forms apparent in nature. To understand the basic framework of leaf development the simple leafed model organism *Arabidopsis thaliana* is used as an experimental system. For comparative development projects the Tsiantis has group developed *Cardamine hirsuta,* a small crucifer related to *A.thaliana,* into a model system for studying the evolution of form. In contrast to *A.thaliana* that has simple, undivided leaves, *C.hirsuta* has dissected leaves that are divided into leaflets. As *C.hirsuta* is amenable to both forward and reverse genetic approaches, comparative studies between these two species should provide substantial novel information on the molecular basis underlying diversification of form during evolution.

Name Sarah Watkinson
e-mail sarah.watkinson@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/
Research Area Mycology

Research Activities

Sarah Watkinson is a mycologist, working on the physiological adaptations of wood decay basidiomycete fungi. The cells of filamentous fungi (hyphae), being non-motile, forage by locating and invading spatially discrete carbon/energy and nitrogen resources on the forest floor. Nitrogen and carbon translocation occurs through extensive fungal mycelia, probably serving the function of nutrient homeostasis within the mycelial organism. The resulting spatial redistribution of nitrogen can have important effects on ecosystem carbon conversions, such as wood decay. In the boreal and temperate forests where most of the Earth's terrestrial carbon is sequestered, basidiomycetes constitute the principal component of the soil microbiota, being the only organisms that can completely decompose dead logs. During the process of wood decomposition, basidiomycetes opportunistically accumulate available nitrogen. In nitrogen-limited natural and semi-natural woodland soils this can result in fungi monopolising the available nitrogen supply. Soil mycelial networks therefore play a pivotal role in nutrient and energy cycles. However, long distance translocation of nitrogen and carbon compounds within mycelia is poorly understood. The Watkinson group (funded by NERC and BBSRC) is therefore investigating various aspects of this process, from cell to ecosystem scale, in collaboration with Warwick-HRI and Cardiff Universities. Studies of nitrogen transport in basidiomycetes are relevant not only to natural ecosystem function, but also have application for the control of wood decay fungi such as the dry rot fungus. Nitrogen translocation to conserve limiting nitrogen within a mycelial system underlies the pernicious spread of dry rot caused by the basidiomycete *Serpula lacrymans* in buildings. Feeding the fungus with high concentrations of non-metabolisable amino acid subverts its nitrogen conservation system, and so stops dry rot spreading. Sarah advises on dry rot control through Oxford University Consulting, and recently led a successful international bid to have the genome of this destructive organism sequenced.

Spotlight on the University of Oxford

Name Jane Landgdale
e-mail jane.langdale@plants.ox.ac.uk
Website http://dps.plants.ox.ac.uk/external/langdale
Research Area Genetics and evolution of leaf development

Research Activities

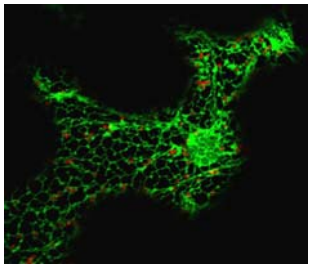
Research in Jane's group is focussed on understanding the evolution and development of shoot apical meristems and leaves. Research is split into two broad areas. In the first project, meristem function and leaf development are being investigated in non-seed plants, namely bryophytes, lycophytes and monilophytes. This work aims to elucidate the mechanistic basis of shoot development in these groups and to provide insight into how shoot form and function evolved within land plants. The second project is focussed on how functional chloroplasts develop. This work was initiated in the C_4 plant maize but was expanded into Arabidopsis and *Physcomitrella patens* to investigate the extent to which nuclear regulation of chloroplast development is conserved across land plants. The genetic distinction between C_3 and C_4 leaf development remains an area of interest that is currently being investigated in the context of programs aimed at introducing components of the C_4 machinery into C_3 crops.

Spotlight on Oxford Brookes University

OXFORD BROOKES UNIVERSITY
School of Life Sciences

Oxford Brookes University's School of Life Sciences has research groups that specialise in plant cell biology and systems biology. Several groups utilise imaging technology to study cellular function. Fluorescent protein marking of cellular components for study of living-cell processes was embraced early on at Brookes to complement their transmission electron microscopy-based cell biology research. Current research includes cell biology of the endomembrane system (ER, Golgi bodies, and other membrane bounded compartments), nuclear envelope, plasma membrane and cytoskeleton, and a project to develop a metabolic profile of Arabidopsis.

Name Chris Hawes
e-mail chawes@brookes.ac.uk
Website http://www.brookes.ac.uk/lifesci/plant_bio.html!
Research Area Cell secretory pathway

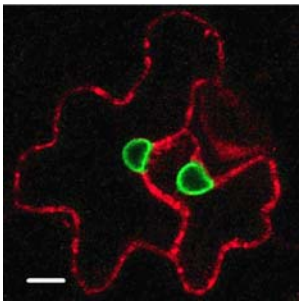


Research Activities

Chris is the Director of the Research School of Life Sciences. His group's research is primarily focused on the study of membrane flow and transport of proteins within the endomembrane system in living plant cells, looking both at the exocytotic (secretion) and endocytic (internalisation) pathways. Organelles that play a role in these processes include the endoplasmic reticulum and Golgi bodies which he has studied extensively during the last 10 years. Recently, Chris has broadened his study of secretory pathway function in conjunction with Dr. Imogen Sparkes who is investigating peroxisome biogenesis and actin cytoskeleton control of organelle dynamics. The group also plays a role in the PharmaPlanta consortium (http://www.pharma-planta.org/):- Dr. Sarah Irons is investigating production, folding and secretion of medically important antibodies in plant cells.

One of the major strengths of the group is in the application and development of fluorescent protein technology for in vivo imaging of plant cells by confocal microscopy. Oxford Brookes School of Life Sciences also possess high pressure freezing/freeze substitution technology which allows members of Chris' group including Barry Martin and Dr. Eric Hummel to preserve cellular structure and protein antigenicity in a manner that is superior to conventional fixation and embedding for structural and immunocytochemical studies by TEM.

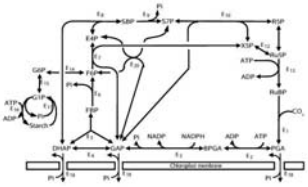
Spotlight on Oxford Brookes University



Name	David Evans
e-mail	deevans@brookes.ac.uk
Website	http://www.brookes.ac.uk/lifesci/plant_membrane.html!
Research Area	Membrane biology

Research Activities

David is a Reader in Plant Cell Biology, Deputy Post-graduate Tutor and University Research Training Co-ordinator. From a background of research into plant membrane transporters, especially plant calcium ATPases, work in David's group has progressed to in-depth study of the plant nuclear envelope. This interest developed following the observation that a homologue of the mammalian SR/ER Ca^{++} pump localises to the nuclear envelope. Shortly after, in pursuit of markers, they discovered that a GFP-tagged truncated probe based on the mammalian lamin B receptor authentically localised to the inner nuclear envelope. In the absence of lamin homologues - and indeed of the lamin B receptor - David's group have investigated the mechanisms underlying the targeting of this probe and are gaining useful information on the processes involved in delivering and retaining proteins in the nuclear envelope in plants. Currently, Katja Graumann in David's lab is using fluorescent protein constructs to study the behaviour of homologues of the mammalian SUN1 and SUN2 inner nuclear envelope proteins in plants and investigate their roles. The group works extensively with the other members of the Plant Cell Biology Group at Oxford Brookes, including Chris Hawes, John Runions and Sarah Irons (a former PhD student who pioneered the work on the lamin B receptor in plants) and collaborates with Iris Meier (Ohio State) and Federica Brandizzi (MSU DOE). For those interested in nuclear envelopes, David is co-organising a Society for Experimental Biology 'Satellite' meeting in Marseille (July 10th 2008); all participants and contributors are welcome to attend.



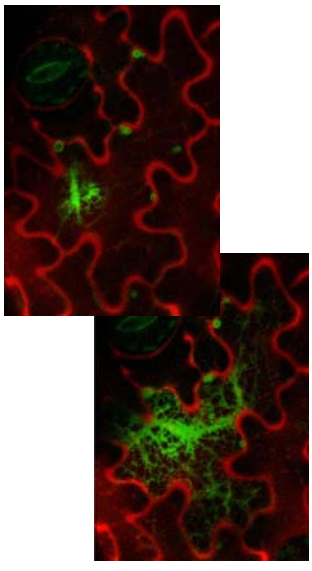
Name	David Fell
e-mail	dfell@brookes.ac.uk
Website	http://www.brookes.ac.uk/lifesci/cell_systems.html!
Research Area	Cell systems modelling

Research Activities

The unifying theme in David's research is the attempt to understand the general principles governing the organization, regulation and control of metabolism. He and Dr. Mark Poolman are involved in the development and application of suitable theoretical tools for the study of metabolism: metabolic control analysis, computer simulation and other forms of algebraic and numerical analysis. Potential applications of this research are:-

1) The rational design of changes in metabolism (metabolic engineering)
2) An improved understanding of how hormonal and environmental signals can cause large changes in specific metabolic processes yet minimally affect other processes in the cell.

The molecules that make up the cells of biological organisms do not function in isolation but do so by interacting with other molecules. Cells thus consist of a complex network of interacting molecules. Because the behaviour of an individual molecule is influenced not only by its own properties but also by those of interacting molecules, networks display emergent properties - that is the behaviour of the network as a whole cannot be simply predicted from the properties of its components in isolation. One way of getting to grips with network behaviour is to construct mathematical models that allow network parameters to be computed. Presently, in conjunction with Dr. Lee Sweetlove's group of Oxford University's department of Plant Sciences, David's group are attempting to generate a mathematical model that will provide insight into the metabolic network of *Arabidopsis thaliana*.



Name	John Runions
e-mail	jrunions@brookes.ac.uk
Website	http://www.brookes.ac.uk/lifesci/runions/HTMLpages/index.html!
Research Area	Membrane biology and bioimaging

Research Activities

John is a Research Fellow who specialises in live-cell imaging. Recently, he has been studying the organellar components of the protein secretory pathway - the endoplasmic reticulum and Golgi bodies - in conjunction with Professor Chris Hawes and his group. Whenever people see timelapse imaging of the dynamic elements of the secretory pathway, they ask a couple of seemingly innocuous questions: why does the endoplasmic reticulum move around and remodel like it does (you have to see it to believe it), and are the Golgi bodies attached in some way directly to the endoplasmic reticulum or do proteins move from one to the other via vesicular transport? John's technique du jour is the use of photoactivatable green fluorescent protein (PAGFP) which is activated with a short wavelength laser beam. Using it, his group have discovered two things, i) fluorescent protein targeted to the endoplasmic reticulum membrane as a fusion to calnexin is actively translocated in an actin-dependant manner and is also free to diffuse, and ii) that there is a strong correlation between the movement of the endoplasmic reticulum surface and the Golgi bodies, which suggests that there is an attachement between these two organelles; the ER exit site.

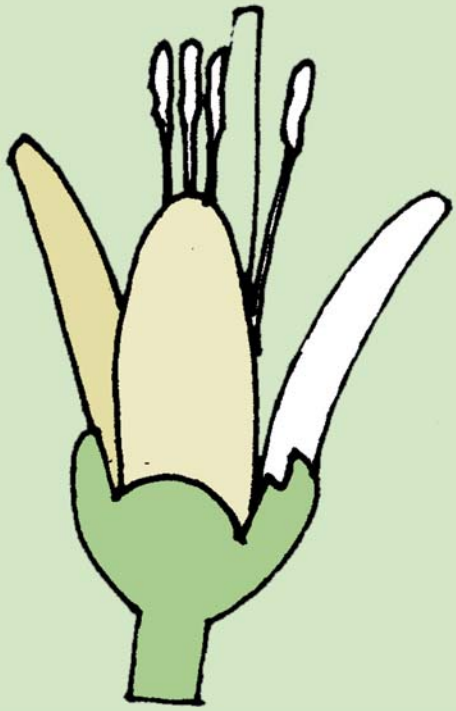
As an extension of his work with photoactivatable GFP, John has recently turned his attention to other membrane systems within the cell, the plasma membrane and the tonoplast, in an attempt to compare the movement of proteins in different membrane types.

Expanding Knowledge, Focusing Ideas

GARNet 2007

John Innes Centre
Norwich

10-11 September



Speakers to include:-

Malcolm Bennett
Nottingham, UK

Mike Bevan
John Innes Centre, UK

Rodrigo Gutierrez
Santiago, Chile

Pierre Hilson
Ghent, Belgium

Ralph Panstruga
Cologne, Germany

Jan Traas
Lyon, France

Chris Town
TIGR, USA

Jian-Kang Zhu
California, USA

Workshops @ GARNet 2007

Tools and Resources
Genespring at NASC

Hands-On Tutorials
Taverna and Pathway Editor

Funding Initiatives
ERA-PG and Systems Biology

Abstract Submission Deadline 27th July 2007

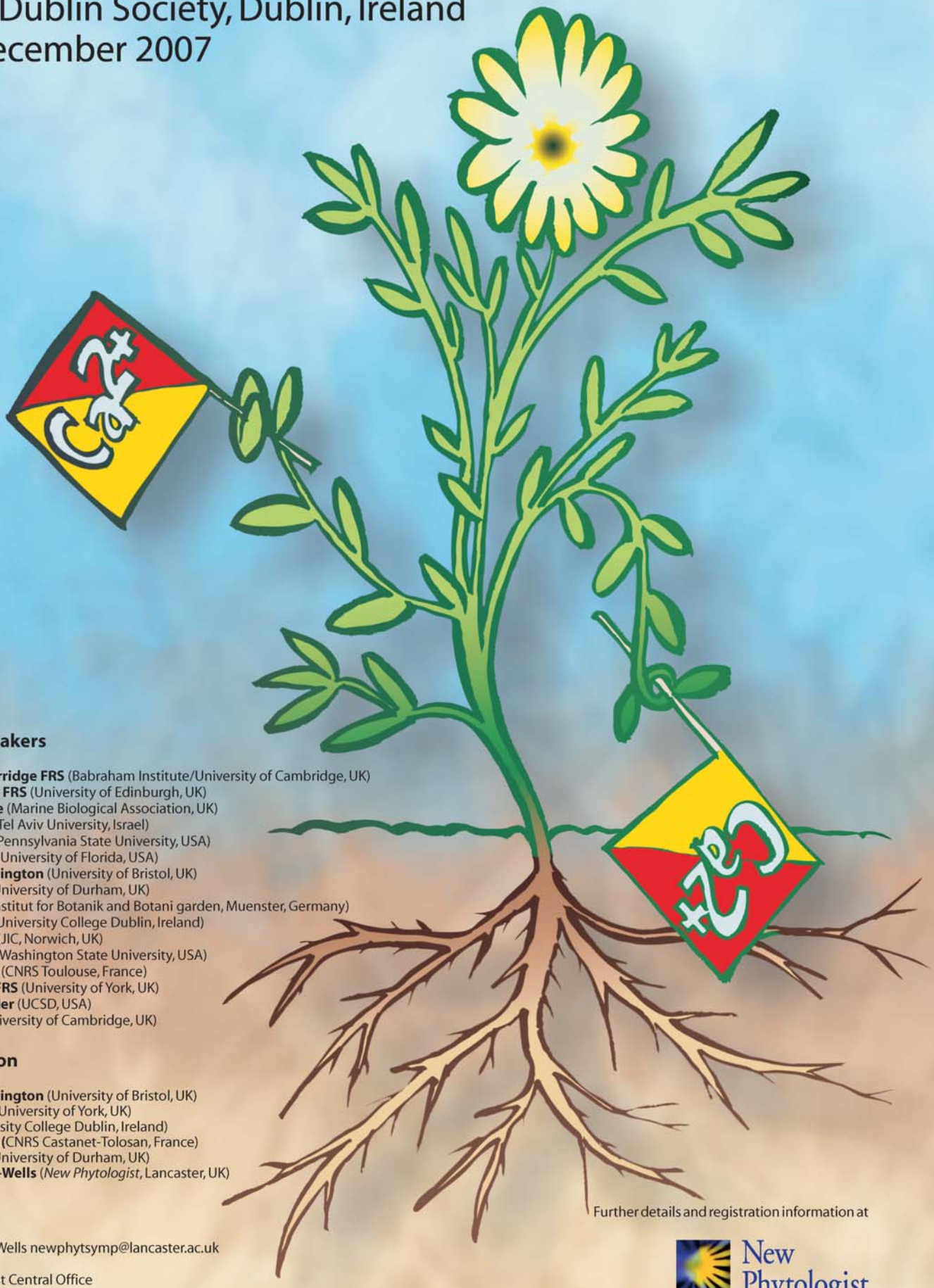
Contact Ruth Bastow - ruth@arabidopsis.info

Register at http://garnet.arabidopsis.info/garnet_meeting.htm

18th *New Phytologist* Symposium

Calcium-based signalling systems in plants

Royal Dublin Society, Dublin, Ireland
5-7 December 2007



Invited speakers

Sir Michael Berridge FRS (Babraham Institute/University of Cambridge, UK)
Tony Trewavas FRS (University of Edinburgh, UK)
Colin Brownlee (Marine Biological Association, UK)
Hillel Fromm (Tel Aviv University, Israel)
Simon Gilroy (Pennsylvania State University, USA)
Alice Harmon (University of Florida, USA)
Alistair Hetherington (University of Bristol, UK)
Marc Knight (University of Durham, UK)
Joerg Kudla (Institut for Botanik and Botani garden, Muenster, Germany)
Paul McCabe (University College Dublin, Ireland)
Giles Oldroyd (JIC, Norwich, UK)
Joe Poovaiah (Washington State University, USA)
Raoul Ranjeva (CNRS Toulouse, France)
Dale Sanders FRS (University of York, UK)
Julian Schroeder (UCSD, USA)
Alex Webb (University of Cambridge, UK)

Organization

Alistair Hetherington (University of Bristol, UK)
Dale Sanders (University of York, UK)
Carl Ng (University College Dublin, Ireland)
Raoul Ranjeva (CNRS Castanet-Tolosan, France)
Marc Knight (University of Durham, UK)
Helen Pinfield-Wells (*New Phytologist*, Lancaster, UK)

Contact

Helen Pinfield-Wells newphytsymp@lancaster.ac.uk

New Phytologist Central Office
Bailrigg House
Lancaster University
LA1 4YE, UK.
Tel: +441524 594691
Fax: +441524 594696

Further details and registration information at

New Phytologist

www.newphytologist.org

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THE SOCIETY FOR EXPERIMENTAL BIOLOGY
ANNUAL MAIN MEETING 6TH - 10TH JULY 2008
PARC-CHANOT, MARSEILLE, FRANCE

CROSS-SECTIONAL SESSION
Systems Biology (of cell signalling)

PLANT
Ubiquitination
Green Products (Bioenergy and Pharmaceuticals)
Developments in Plant Biology

CELL
The Cytoskeleton in Plant Development
Circadian Clocks
Thermobiology
Glycosylation

ANIMAL
The Multifunctional Gut
Linking Mechanics and Energetics
General Biomechanics
Predator/Prey Interactions
Insect Physiology and Functional Genomics
General Animal Biology
Physiological Strategies to Optimise Oxygen Delivery
Sources and Consequences of Intra-Specific Diversity
The Secondary Circulation System
Neurobiology

Parc-Chanot is a modern conference and exhibition centre situated in the very centre of Marseille, which is served by the Marseille Metro.

The cosmopolitan port town of Marseille is France's oldest city. There are many sight-seeing opportunities from the Romenesque Abbaye St-Victor to the 16th century fortress-turned-prison Chateau D'If.

Restaurants abound in Marseille, serving a variety of dishes with Oriental and North African as well as traditional French influences. The city also has a dynamic music and club scene.

For more information on the city and the surrounding area please visit the Marseille Tourist Office website: www.marseille-tourisme.com.

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