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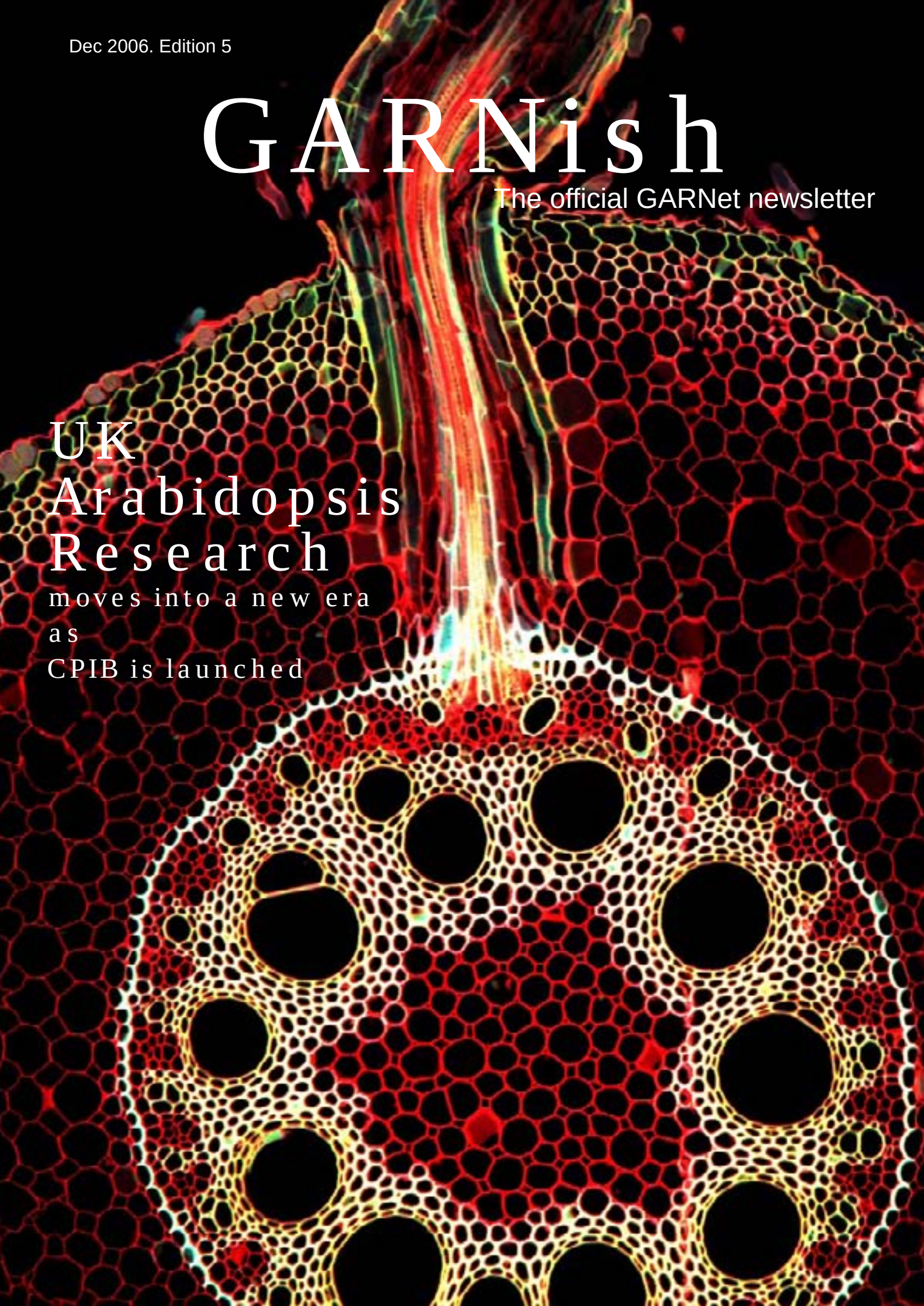
GARNish

The official GARNet newsletter



UK Arabidopsis Research

moves into a new era as CPIB is launched

Editorial

2006 has been another event packed year for GARNet. It all began back in March with an enlightening 'Interfacing systems biology with crop and ecolological modelling' workshop held in Swindon. This gathering, co-ordinated by IGER and GARNet, brought together a wide range of scientists from the systems biology, bioinformatics and agro-ecological modelling communities to exchange ideas and increase awareness of each others' fields. A meeting report is available online (http://garnet.arabidopsis.info/Modellers_Meeting_Report_final_v2.pdf) The Swindon gathering was the first of many system based events this year; in April the University of Nottingham was awarded funding by the BBSRC and EPSRC to establish a centre for plant integrative biology, for more information regarding the centre see overleaf. In June, GARNet submitted its final report on Plant Systems Biology to the BBSRC, ahead of the launch of the SABR (Systems Approaches to Biological Research) call. This BBSRC and EPSRC initiative aims to work in partnership with relevant UK universities and research institutes to establish a range of systems biology research projects. To ensure plant and crop scientists are well placed to apply for this funding, GARNet and CPIB held a discussion meeting in September to outline the remit of the call, facilitate collaborations and discuss potential applications. Good luck to all of those that have submitted expressions of interest.
The University of Bristol kindly hosted this years' annual GARNet meeting on plant networks and data integration (see below). Many thanks to all that attended and supported the meeting.
Finally, GARNet has continued to spread its wings and interact with other plant communities. For example; in collaboration with Graham King (RRes) and the SEB, GARNet held a one day meeting 'Plant Science to Crop Products' that focused on developing green products to deliver benefits for diet and health, renewable products and ameliorating the impacts of climate change. From personal experience I know that it is not easy to be self sufficient and green, but discussions at this meeting convinced me plants have a pivotal role to play in providing some of the answers to current ecological and environmental problems. Wishing you a Merry Christmas and a successful New Year.
Ruth

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Front cover image kindly suppiled by Jim Haseloff University of Cambridge

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

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

bbsrc
biotechnology and biological sciences research council

GARNet 2006 Meeting

Was it really a year ago that I said "Here's to the next one!" enthusiastically in these pages? Well my zeal was well-founded, the spirit and enthusiasm evident at last year's meeting was here again and had been built upon. This year the emphasis at the annual GARNet meeting was upon plant networks and integrating data. This is a pertinent topic, at a time when systems-based approaches and integrative biology are at the fore-front of many researchers' minds. The focus of last year's meeting, crop science, was again resonant this year and well timed given the direction of research council funding, in the UK at least. In this regard, I found the meeting really useful in terms of being steered towards many vital resources, both computer-based and "real" (I believe this is termed "wet"?) that are now available. Also there were a lot of really excellent presentations from labs which had gone some way forwards in these areas, and as case studies they were really useful and interesting.
The **Integrative Biology** session of the meeting had three presentations from Wilhelm Gruissem (ETH, Switzerland), Anna Amtmann (Glasgow, UK) and Amanda Lloyd (Aberystwyth, UK) on metabolomics and ion nutrition. These talks illustrated how predictive approaches to plant sciences are informing our current view of biology. The **Tools and Resources** session had a presentation by Heiko Schoof (Max Planck, Koeln, Germany) who explained how different web/computer based resources for handling bioinformatic data could be linked together to allow easier high-throughput analysis. Nick Provart (Toronto, Canada) described resources available from the Botany Array Resource in Toronto and Geoff Scopes (Affymetrix, UK) described the improvements made to the new generation of Affy chips, most especially the recently launched Arabidopsis whole genome tiling array. The session on **Genome Biology** had two presentations, one from Oliver Ratcliffe (Mendel Biotech, USA) describing high throughput genomic screens for useful traits in Arabidopsis and how these might be transferred to crops. In this talk it was explained that of 88 transcription factors isolated on the basis of drought tolerance, 75% were able to convey tolerance in transgenics. It was speculated that all acted through different pathways, which was good news for the patent business. The speaker also demonstrated how overexpression of *AtERF1* could convey broad range resistance to pathogens. The second talk in this session was from Helen Ougham (IGER, UK) describing novel mapping techniques for genes from large-genome monocots. The session on **Plant Networks** described three case histories from labs heavily involved in determining and modelling different plant networks, namely, root hair development (Claire Grierson, Bristol, UK), cellular networks in development (Jim Haseloff, Cambridge, UK) and the circadian clock of Arabidopsis (Laszlo Kozma-Bognar, Edinburgh, UK). These talks exemplified what is feasible in this field, and also highlighted the fact that a lot more work needs to be done if these approaches are to be widely adopted. The session on **Environmental Interactions** had a bias towards networks with Kazuko Yamaguchi-Shinozaki describing work on cold/drought stress signalling networks, yours truly describing work on calcium signalling networks and interaction between light and temperature, and Alex Webb on rhythmic regulation of calcium-signalling networks. The meeting closed with the **Bioinformatics** session, which contained presentation about two interesting web resources; FlyMine (Gos Micklem, Cambridge, UK) which allowed us to see what would be possible with Arabidopsis and ONDEX (Jacob Koehler, Rothamsted, UK). Sean May (NASC, UK) updated us on the resources/plans for NASC at the present time and in the future. Finally Jane Ward described handling of metabolomic data obtained via 1H-NMR. The poster session was lively and well-attended with some excellent work on display. The first prize went to Helen Rushton, an excellent PhD student from an excellent lab (!!!), and second prize to Mathew Lewsey, from Cambridge. Well done to both of them. Well I very much hope to be at the next GARNet meeting, and am looking forward to it. I will be there as a "civvy" having rotated off the GARNet committee, so I can just sit back and relax and enjoy the science!

Marc Knight - University of Durham

Arabidopsis Resources

Centre for Plant Integrative Biology (CPIB)

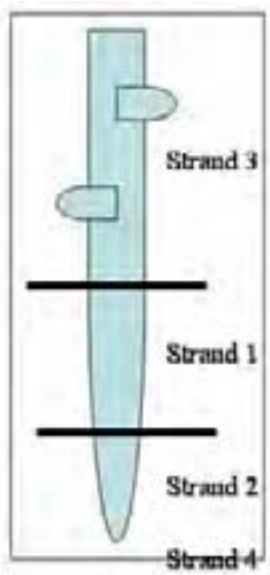
http://cpib.info

written by Malcolm Bennett, University of Nottingham.

The Centre for Plant Integrative Biology (CPIB) aims to create a *virtual root* which will serve as an exemplar for using Integrative Systems Biology (ISB) to model multi-cellular systems. CPIB is jointly funded by the BBSRC and EPSRC as part of their Systems Biology Initiative to establish a number of Centres for Integrative Systems Biology. CPIB can be differentiated from the other BBSRC/EPSRC Centres for ISB in being multi-cellular (different tissue types being studied simultaneously), multi-scale (models incorporate the levels from the molecular to entire roots) and multi-physics (including fluid mechanics of metabolite/hormone transport, thermo-dynamics of cell-wall and other macromolecular synthesis, and structural mechanics of cell wall deformation).
CPIB brings together biologists, engineers, mathematicians and computer scientists to generate new data, biological resources and virtual models of plant roots that will aid understanding of how they grow and develop. The Nottingham Centre will integrate advanced experimental and imaging approaches with innovative mathematical, engineering and computer science research in collaboration with Rothamsted Research and several international groups. CPIB liaises closely with the *Computable Plant* (US/Russia) and *AGRON-OMICS* (EU) projects to ensure our respective modelling work will migrate towards a compatible "whole seedling" system that integrates virtual root, shoot and leaf development.

Specific objectives of CPIB include:

- Generating models that probe the mechanisms regulating growth in the expansion zone (Strand 1).
- Developing predictive models of cell division and differentiation that describe the emergent heterogeneity of the root meristem (Strand 2).
- Extending the virtual cells and tissues developed in Strands 1 and 2 to encapsulate the mechanisms leading to the formation of a new lateral root organ (Strand 3).
- Developing integrative models that describe the response of the whole root system to environmental cues (Strand 4).
- Disseminate ISB-based approaches and tools through outreach and training.
- Release all experimental materials, datasets and models through NASC.



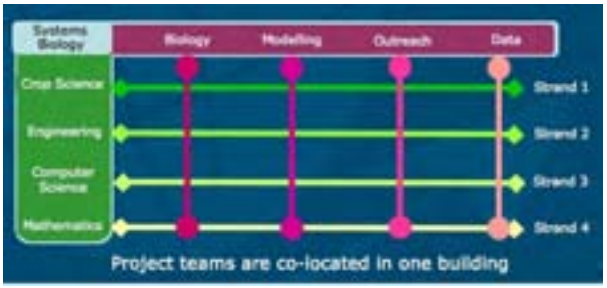
Novel experimental materials generated by CPIB will include up to 500 polyclonal antibodies raised against *Arabidopsis* proteins involved in root growth and development; datasets being created include a protein localisation atlas that will be complimentary to existing transcriptomic databases (e.g. the *Arabidopsis* gene expression database at http://affy.arabidopsis.info); and examples of modelling at different physical scales.

CPIB has plans for a series of outreach activities that will include:

- Summer schools for researchers at any level to gain in-depth experience in specific modelling and computational techniques.
- Short courses for researchers at any level to learn about defined areas of modelling, plant science (for non-biologists) and the use of CPIB's computational and physical resources, etc.
- Sandpits (aka study groups) to bring together a range of life and theoretical scientists, for a week, to focus on a small number of defined biological research problems and develop multidisciplinary research proposals.
- Conferences to bring a large number of scientists together to hear and discuss leading-edge systems biology from around the world.
- Seminars/lectures in other universities and institutes as time and opportunities permit.

For further details about CPIB and its activities, visit www.cpib.info

CPIB Members



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Strand Managers

Strand 1: Mike Holdsworth
Strand 2: Geoff Tansley
Strand 3: Jon Garibaldi
Strand 4: Oliver Jensen

Systems Biology in the UK

Over the past two years the BBSRC in collaboration with EPSRC has invested £46.3M to establish six university-based Centres for Integrative Systems Biology. The aim of this initiative is to generate a critical mass of systems biology in the UK, capable of undertaking cutting edge systems research, and acting as a reservoir of knowledge and expertise for others. With the creation of these centres and the recent launch of the SABR initiative, GARNet thought it would be timely to provide the community with an overview (not exhaustive) of system biology research occurring in the UK; to bring you up to date and provide you with possible contacts for future collaboration.

BBSRC/EPSRC Funded Centres

CISBAN (Centre for Integrative Systems Biology of Ageing and Nutrition)
http://www.cisban.ac.uk/
CISBAN's aim is to advance understanding of the complex mechanisms underpinning the ageing process and how these are affected by nutrition.

CISBIC (Centre for Integrative Systems Biology at Imperial College)
http://www3.imperial.ac.uk/cisbic
This centre will use state-of-the-art technologies to look at the interactions of a disease causing organisms (such as *Mycobacterium, Campylobacter* and *Salmonella*) with their hosts at the level of molecules and individual cells.

CPIB (Centre for Plant Integrative Biology)
http://www.cpib.info/
The Centre for Plant Integrative Biology (CPIB) is based at the University of Nottingham and aims to create a *virtual root* which will serve as an exemplar for using Integrative Systems Biology (ISB) to model multi-cellular systems.

CSBE (Centre for Systems Biology at Edinburgh)
http://csbe.bio.ed.ac.uk/
CSBE's goal is to develop broadly-applicable methods and large-scale informatics infrastructure for modelling the temporal aspects of biological phenomena. Pilot projects will address mRNA and rRNA metabolism in yeast, interferon signalling in macrophages and the plant circadian clock.

MCISB (Manchester Centre for Integrative Systems Biology)
http://www.mcisb.org
The Manchester centre is focused on elucidating the complete systems biology of *Saccharomyces cerevisiae*. The tools and technologies developed by the centre will be useful to a wide range of organisms.

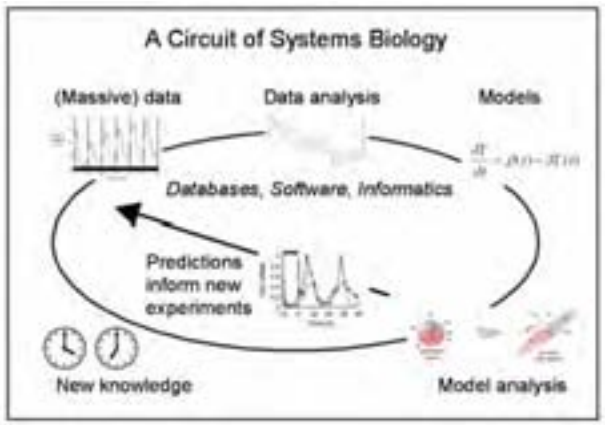
OCISB (Oxford Centre for Integrative Systems Biology)
www.sysbio.ox.ac.uk
OCISB will tackle a range of biological problems concerning network pathways. The aim of the project is to develop robust predictive models of these highly complex processes. Studies will include chemotaxis in *E.coli* and *R.sphaeroides*, eukaryote flagellum and hypoxia.

Other Centres

COMPLEX (UCL Centre of Interdisciplinary Science)
http://www.ucl.ac.uk/CoMPLEX/

WSBC (Warwick Systems Biology Centre)
http://www2.warwick.ac.uk/fac/sci/systemsbiology/

Cambridge Systems Biology Centre
http://www.bio.cam.ac.uk/news/current/csbc.html



EPSRC Post-doctoral Training Centres

Bio-nanotechnology, medical imaging and bioinformatics
University of Oxford – http://www.lsi.ox.ac.uk/

Chemical biology
Imperial College London – http://www.chemicalbiology.ac.uk/

Maths and physics in the life sciences and experimental biology
University College London – http://www.ucl.ac.uk/CoMPLEX/index.htm

Medical devices and related materials
University of Strathclyde – http://www.strath.ac.uk/dtc/

Molecular organisation and assembly in cells
University of Warwick – http://www2.warwick.ac.uk/fac/sci/moac/

Neuroinformatics
University of Edinburgh – http://www.anc.inf.ed.ac.uk/neuroinformatics/

Physical methods and life sciences
Universities of Leeds and Sheffield - http://www.physics.leeds.ac.uk/pages/WhiteRoseDoctoralTrainingCentre

Proteomic Technologies
Glasgow, Edinburgh and Dundee - http://www.gla.ac.uk/rasor/phd.html

Targeted therapeutics
University of Nottingham - http://www.nottingham.ac.uk/pharmacy/research/EPSRC-AZ-DTC.php

A copy of this list is also available on line at http://garnet.arabidopsis.info/systems_biology_centres.htm
If you know of any other centres that should be included on this list please e-mail the relevant information to ruth@arabidopsis.info

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 Reading

Plant Science research within The University of Reading takes place within the three schools of:- Biological Sciences, Agriculture Policy and Development and Chemistry, Food Biosciences and Pharmacy. Research ranges from fundamental investigations of gene function and protein structure to applied studies in agriculture and horticulture.

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Research Area Wood anatomy

Research Activities

John's research focuses on the process of secondary xylem formation from the vascular cambium of woody plants and on how the plant varies this process to enable it to cope with environmental pressures. The differentiation of secondary xylem is responsible for wood properties and of fundamental importance to the timber industry. Of particular interest is the formation of reaction wood in trees, which, by careful control, enables the tree to maintain a vertical main stem, and appropriate branch angles to ensure maximum exposure of leaves to light. Modification of this process, or its control, by genetic modification or selective breeding offers the possibility of improving productivity of trees and the quality of the timber they produce. This is complicated by the fact that the survival strategy of the tree itself produces many of the 'so-called' defects in timber, including reaction wood and juvenile wood.

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Research Area Plant developmental biology

Research Activities

The link between phenotypic divergence and mechanisms that regulate plant development is a fundamental question that impinges on the fields of plant evolution, development and ecology. Addressing this question establishes the mechanisms by which plants perceive and respond to the environment and the impact the responses have on plant development. To achieve this, individuals consistently lacking or displaying the phenotype are subjected to molecular and ecological analysis. Such an approach is being used in Nick's lab to understand: (a) the ecological, evolutionary and developmental aspects of pseudovivipary in grasses, (b) the role of *flowering locus T* (*FT*) in floral meristem commitment and reversion in *Impatiens* and *Arabidopsis* and (c) the role of *seasonal flowering locus* (*SFL*) and *FT* in the control of the life history strategy adopted by *Fragaria* species. Recent research has also been focused on monocarpic/polycarpic life strategies in wild relatives of *Arabidopsis* and the regulation of flowering and vegetative growth within these.

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Research Area Biodiversity informatics

Research Activities

Despite the plethora of publicly available biodiversity information available on the internet many researchers experience difficulties in locating the correct information and comparing this with data from other sources. To help organise this mass of information, Frank has been involved in setting up a wide range of species diversity and taxonomic information systems and networks. Once such example is the Species 2000 project, which aims to "create a validated checklist of all the world's species (plants, animals, fungi and microbes)". This is being achieved by bringing together an array of global species databases covering each of the major groups of organisms. Each database covers all known species in the group, using a consistent taxonomic system. In addition to his informatics based work, Frank is also investigating the taxonomy of the legume family in particular gorses and brooms (*Genisteae*) and vetches and peas (*Vicieae*).

Spotlight on Reading

Name Peter Caligari
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Research Area Plant breeding

Research Activities

Peter's main research activities focus on aspects underpinning plant breeding methods and strategies. The work is divided in two to areas, the first involving aspects of traditional breeding methodologies and exploring ways of improving efficiency of selection, reducing cycle times and developing new breeding strategies. The other investigates the potential of integrating new technologies in tissue culture, biotechnology and molecular biology into current/future plant breeding activities. The work involves a range of species among which are: potatoes, barley, lupins, cashew, cedar, cocoa, coffee, oil palms, peppers, sugar beet, sugar cane and wheat.

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Research Area Horticulture

Research Activities

As a member of the horticulture group within the environmental biology section, Ross's interests are applied but nevertheless wide-ranging. They include: plant propagation and establishment, plant adaptation to abiotic stress, landscape and habitat management, and therapeutic landscapes. Current projects being undertaken in the lab include: market development of composts derived from different organic waste streams, water use and plant establishment in the landscape, vegetative propagation of cashew (*Anacardium occidentale)* and establishing and perpetuating cornfield annuals.

Name Alastair Culham
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Research Area Plant taxonomy and systematics

Research Activities

Alistair's research lies at the intersection of traditional plant taxonomy and biosystematics with modern techniques of molecular biology, phytogeography and cladistics. This interest has led to research in three related areas;

(1) Evolutionary studies
   a) At the species level and above, multidisciplinary approaches to taxonomy are being used to critically examine classifications and construct evolutionary hypotheses for rapidly speciating plant groups.
   b) At the level of the individual evolutionary hypotheses are being used to study the nature and patterns of change in plant morphology and the underlying genetic mechanisms.

2) Conservation
   Studies include the use of molecular markers to analyse variation in plant population variation and investigation of the role of ex-situ plant collections in conservation.

3) Horticultural Taxonomy
   The taxonomic revision of genera of horticultural interest.

Name Jim Dunwell
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Research Area Protein evolution, gene expression and plant breeding

Research Activities

The cupin family of proteins is probably the most functionally diverse of any described to date; it includes members ranging from single-domain bacterial enzymes such as isomerases, to seed storage proteins (globulins). All family members contain a conserved beta-barrel fold ('cupa' is the Latin term for a small barrel), which Jim first discovered in germin and germin-like proteins from higher plants. Current investigations of the cupin fold and family include a study of the conservation of the active site residues within these proteins during their evolution from thermophilic prokaryotic ancestors. The group has an additional interest in the application of Serial Analysis of Gene Expression (SAGE) technology to the study of gene expression in plants, in particular in the cereals rice and wheat. Research is also being carried out in to the development and application of transgenic plants. This includes novel techniques for DNA introduction into plant cells, and the use of new methods for regeneration from single somatic cells.

Spotlight on Reading

Name Richard Ellis
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Research Area Crop production, seed, anhydrous and reproductive biology

Research Activities

In the broadest sense, Richard's work covers reproductive plant biology and its effects on seed viability and crop production. Research in to seed and anhydrous biology, includes the effect of the environment on seed, spore, and pollen survival with regard to seed quality development, development of desiccation tolerance and potential longevity. The aim of this work is to assist seed banks with the long-term storage of plant germplasm, whilst the fungal spore survival research targets new biological control methods.
Phenology based work in the lab is concerned with local and global crop adaptation in current and future climates. Climate change impacts on crops include the combined effects of increase in temperature and CO_2 on crop production and crop quality. Current studies in this area include the effects of environment and genotype on crop development and the effect of *maturity* genes on the sensitivity of phenological development to environment.
Agronomics topics under investigations by the group include seed quality and crop establishment, effect of seed quality and rate on plant population density and subsequent yield (including aspects of precision farming), and effects on crop quality.

Name Roland Fox
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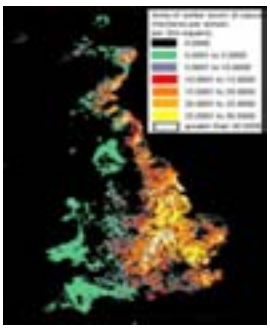
Research Area Plant pathology

Research Activities

Plants are constantly exposed to attack by a diverse range of pathogens that cause infection and disease, resulting in losses to crop yield. The classical treatment for such plant pathogens has been the use of chemical pesticides, but with increasing environmental concerns and examples of fungicide resistance, alternative and more sustainable methods of crop protection are being sought. Ronald works therefore focuses on understanding plant pathology and crop protection for the improvement of plant health and quality via ecological sensitive methods. His approach uses innovative evidence based research to apply integrated agrochemical and biological methods of disease control.



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Research Area Weed science

Research Activities

Weeds are a major problem in any cropping system, impacting on yield, quality and harvesting of the crop. As the number of truly effective herbicides decreases and the pressure for more environmentally sustainable solutions increases, there is a greater need for research into improved targeting of available herbicides and the generation of alternative (i.e. non-chemically based) methods of weed control. Added to this is the challenge that weeds are considered beneficial for the surrounding field ecology. Bob's research is focused on understanding weed populations and dynamics, crop-weed interactions and weed seed biology. The aim is to provide growers with an integrated weed and field margin management programme that optimizes the balance between the desire for high yields and high on-farm biodiversity. The group is also interested in Mediterranean agriculture and ecological genetics.

Name Paul Hadley
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Research Area Horticultural physiology and production

Research Activities

Research in Paul's group has two main components
(1) Understanding the effect of climate/environment on crops.
Topics of interest include, environmental regulation of growth, development and yield of crop plants; effects of temperature and light on the growth and development of field grown and protected horticultural crops; development of quantitative models to predict flowering of crop plants in relation to temperature and light; prediction of maturity and yield of field and protected crops in relation to climate and collaborative research on crop growth and development in relation to global climate change.
(2) Research on cocoa (*Theobroma cacao*).
This work is linked to projects in Malaysia, Brazil & Trinidad and aims to provide cocoa germplasm for genetic improvement programmes, worldwide. To achieve this researchers are involved in the development of the international cocoa germplasm database.
The group is also involved in collaborative projects assessing the growth of crops in response to greenhouse energy saving techniques and research into the development of novel cladding materials for greenhouses.

Spotlight on Reading

Name Tom Harwood
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Research Area Spatial ecological/genetic modelling

Research Activities

Tom is currently investigating the spread of *Phytophthera ramorum* (a destructive fungus that causes the disease, sudden oak death) through the British nursery trade network and the natural environment. Using a novel linked network model and data from geographical information systems as a framework, the group are developing an epidemiological model for this fungus. The lab is also analyzing the flow of genes from commercially grown oilseed rape into its wild relative bargeman's cabbage, using spatially explicit individual and population scale models, that capture the dynamics of the seedbank. This research represents a key step towards the establishment of a model to predict the likely movement of transgenes from GM crops to wild relatives on a national scale. The group is also involved with the measurement of plant characters from digital images, (leaf samples, pot plants, strawberries) for genetic screening and horticultural scheduling.

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Research Area Ecology and plant protection

Research Activities

Plants encounter numerous pests and pathogens in the natural environment. In response to such attacks plants either become infected and die or mount an appropriate defense response, leading to tolerance or resistance mechanisms that enable the plant to survive. Many studies of resistance concentrate on signaling pathways that enable plants to recognize and respond to attack, and measure the downstream effect in either biochemical or molecular terms. But what about the response at the whole plant level?
Paul is interested in the fitness costs of attack not only for the plant but also over a range of trophic levels. The main focus of this work is the interactions between phytophagous insects, plant pathogenic fungi and their weed host-plants. Using *Rumex obustifolius* as a model system, the group is investigating these interactions in weed population dynamics and monitoring the effect of environmental variables such as nitrogen fertilization and cutting on these biotic interactions. These investigations raise important questions for the biological control of weeds; for example, will the effect of an introduced insect be enhanced or reduced by endemic fungal pathogens of the weed?
In collaboration with Drs Glenda Tinney, Nigel Paul and Jane Taylor of Lancaster University Paul is investigating interactions and possible cross-talk between the different resistance pathways induced by insect damage and fungus infection of Rumex. The aim of this project is to identify molecular markers that will enable researchers to investigate the activity of resistance pathways of Rumex in the field,
Other research interests of the Hatcher group include determining the 'hidden' costs of plant resistance (for example, are plants that are resistant to fungal attack more or less palatable to insects, or vice versa?), weed control in nature conservation and amenity areas, grass endophyte - mycorrhiza interactions, and the conservation of the endangered moth *Eustroma reticulatum* and its food plant *Impatiens noli-tangere*.

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Research Area Plant systematics

Research Activities

The main focus of Julie's research is the application of comparative DNA sequence analysis to pure and applied questions in plant biology. The Hawkins group has a number of active projects that exploit reconstruction of plant phylogeny to address important questions in plant evolutionary biology. For example, her group is using phylogenetic analysis to determine the history of the species rich flora of the Cape region of South Africa. Another project uses molecular phylogeny to reconstruct the historical distribution of an invasive species; this project will guide the development of biological control strategies. DNA sequence data are also applied to questions relating to the identity, parentage and provenance of economically important plant species. Currently Julie is developing a DNA-based certification scheme for traded cacti that will be used to distinguish legally-propagated plants from illegally-collected ones.

Spotlight on Reading

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Research Area Taxonomy and systematics

Research Activities

Throughout the centuries man has used and exploited plants for a variety of purposes, ranging from food to fuel. In recent years there has been a considerable interest in plants for medicinal purposes driven both by the commercial pharmaceutical industry looking for new drugs and those wishing to live a more sustainable or chemical free lifestyle. However, in meeting this demand one cannot assume that wild plant resources will be available on a continuing basis. Prof. Heywood is involved in a number of projects that aim to ensure the survival of useful and potentially useful wild plants. These include conservation and sustainable use of medicinal and aromatic plants, conservation of wild relatives of crops (UNEP/GEF) Euro+Med PlantBase and in situ conservation of wild species used by humans (UNEP/GEF).

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Website http://www.spindigo.net/ http://www.relu.rdg.ac.uk/
Research Area Plant biochemistry and physiology

Research Activities

Research in the John laboratory focuses on several areas:-
(1) Plant biochemistry and physiology, particularly in relation to the biochemistry of crop plants and post-harvest physiology.
(2) Indigo production from crops and the bacterial reduction of indigo for dyeing.
(3) Nutritional quality of soft fruits in relation to cultivation conditions.

Name Stephen Jury
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Website http://www.biosci.rdg.ac.uk/Staff/academic/Dr%20Stephen%20Jury.htm
Research Area Biodiversity and systematics

Research Activities

Understanding the natural distribution of plants is central to conserving biodiversity and managing ecosystems for long-term viability and sustainability. Stephen studies the ecological and geographic distribution of European and Mediterranean plants, with particular emphasis being placed on the floras of Spain and Morocco. The group is also interested in the taxonomy and nomenclature of European, Mediterranean and horticultural plant groups, with special reference to Umbelliferae, Labiatae, petaloid monocotyledon and aromatic species.

Name Michael Keith-Lucas
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Research Area Ecology

Research Activities

Michael work is centered on two main areas.
(1) Woodland studies, topics include:- woodland/tropical rainforest ecology and woodland history, especially prehistoric clearance.
(2) Pollen analysis, areas of interest include pollen studies:- on archaeological sites; in plant taxonomy; in forensic sciences and allergic reactions.

Name Alistair Murdoch
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Research Area Seed Biology

Research Activities

To ensure their survival, plants time the emergence of the next generation to coincide with favorable environmental conditions, such as that found in spring for temperate species. This is often achieved by dormancy, which stalls seed germination until the appropriate growing season arrives. The timing of germination is of great importance in weed/crop interactions. To help growers formulate a seed husbandry that favors the emergence of the crop at expense of the weed, the Murdoch group are utilising ecology, physiology and mathematical modelling to understand the processes involved in weed and crop seed dormancy and germination. Recent research in this area has focussed on germination and dormancy of parasitic plants of agricultural significance, namely *Orobanche* species (broomrapes) and *Striga* species (witchweeds).

Spotlight on Reading

Name Chris Payne
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Research Area Plant/insect interactions

Research Activities

Successful pest management is often hindered by the inherent complexity of interactions of a pest with its environment. To try and circumvent this problem the Payne group is using genetically characterised *Arabidopsis thaliana* lines to limit the number of variables during investigation into chosen pest-plant interactions.
For example the group has shown that *A.thaliana* is a suitable host for the development of the diamondback moth, *Plutella xylostella*, and its parasitoid, *Cotesia plutellae*. By exploiting the genetic diversity available in *A.thaliana* researchers have been able to show that trichomes (present in Col-0 but absent from Col-5) extend the development time of *P.xylostella* and reduced the rates of parasitism. This discovery can now be applied in the field.

Name Barbara Pickersgill
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Website http://www.biosci.rdg.ac.uk/Staff/academic/Dr%20Barbara%20Pickersgill.htm
Research Area Biodiversity and systematics

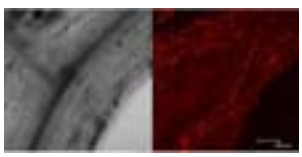
Research Activities

Barbara's work is focused on the taxonomy and evolution of cultivated plants and the conservation of crop genetic resources. Current projects include:- the evolutionary biology of Capsicum, including molecular systematics and exploitation of wild species in improvement of domesticated chile peppers; studies of crop plant domestication, using common bean (*Phaseolus vulgaris*) as a case study; genetic diversity, conservation and improvement of tropical species, particularly quinoa (*Chenopodium quinoa*) and East African Highland bananas (Musa).

Name Ian Rowland
e-mail Not assigned yet
Website http://www.food.rdg.ac.uk/
Research Area Anti-cancer activities of plant components

Research Activities

The main interest of the Rowland group is diet and cancer with a focus on phytochemicals as protective agents in colon, breast and prostate cancer. Researchers are investigating a wide range of sources of phytochemicals including soya, watercress, berries, germinating plants and olive oil. The efficacy of these foods/componds are being tested via a number of approaches including:- *in vitro,* mechanistic cellular and molecular studies, using either crude plant extracts or specific phytochemicals, animal models, and human intervention trials involving feeding whole plants or their components. Dietary components currently being studied by the group include isoflavones, lignans, glucosinolates, olive oil, polyphenols, fructans and probiotics.



Name Michael Shaw
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Research Area Plant pathology

Research Activities

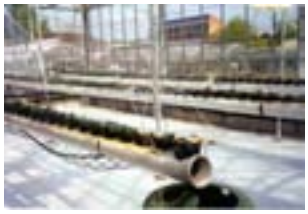
The spread and development of fungal pathogens in agri-ecosystems is determined both by genetic interactions and environmental conditions. Effectively combating of these fungal infections requires the ability to forecast changes in pathogen populations in relation to these variables. To assist growers in this process Mike's work is centered on the epidemiology and ecology of plant disease. The Shaw laboratory is particularly interested in understanding the host-pathogen adaptation and ecology of the fungal pathogens *Mycosphaerella graminicola* and *Botrytis cinerea*. Using both modeling and experiment, researchers are able to forecast foliar disease dynamics in natural agricultural ecosystems and are studying the spatial pattern and dispersal of plant pathogens. The group is also investigating the development of fungicide resistance.

Name Carol Wagstaff
e-mail Not assigned yet
Website http://www.food.rdg.ac.uk
Research Area Post-harvest nutritional quality of fresh produce

Research Activities

Carol's work is centered on maintaining and improving the levels of key phytonutrients during the shelf life of salad crops in order to provide the consumer with a healthier product. Work in the laboratory uses a variety of genetic and genomic approaches, combined with physiological and organoleptic studies to answer the following questions: a) which phytonutrients are present in the plant pre-harvest, b) what happens to them postharvest and during the consumer shelf life, c) which ones can be utilised by humans, and d) if the genetics of the plant or its growing conditions are altered to elevate chosen phytonutrients are the sensory attributes acceptable to the human palate?

Spotlight on Reading



Name Alexandra Wagstaffe
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Website http://www.plantsci.rdg.ac.uk/projects/softfruit/main.htm
Research Area Crop physiology

Research Activities

The central focus of Alex's research within the Soft Fruit Technology Group is the crop physiology of strawberry, raspberry and other 'soft fruit crops' of horticultural importance. Of particular interest is the impact of heat stress on flower initiation, emergence and abortion in strawberry, which tends to result in a lack of cropping ('thermodormancy'). Research is interdisciplinary and has, for example, included the School of Chemistry to develop polythene cladding materials for tunnels, which reduce extremes of temperature. Other work has studied the effects of red:far-red ratio of light source for raspberry cultivation. Crop growth and chill unit models have been developed for several crops, and the effects of winter chilling and plant nutrient status has been investigated on subsequent bud burst, flowering and fruiting. Current work focuses on the health beneficial properties of soft fruit crops, and methods of modifying these with spectral filters. Close collaboration with the UK soft fruit industry supports the development and application of new and sustainable technologies.

Name Andy Wetten
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Research Area Plant biochemistry and physiology

Research Activities

Research in the Wetten laboratory focuses on several areas:-
(1)Plant genetic transformation: Novel applications for Agrobacterium and biolistic-mediated gene insertion into plants are being developed along side studies of gene expression and introgression in transgenic and somatic hybrid plants. This work is being used to uncover the regulation of flower development in the model *Impatiens balsaminal*, the control of floral initiation and fruit production in perennial plants such as *Fragaria vesca*, and the effects of alien chromosome elimination in Solanum interspecific somatic hybrids.
(2)Plant cryopreservation: The goal of this work is to preserve both crop germplasm collections and species of conservation interest. Current projects include; developing protocols for the cryopreservation of cocoa germplasm in somatic embryos and fundamental studies of cryo-injury and dehydration tolerance.
(3) Somaclonal variation: This phenomenon can undermine the genetic fidelity of tissue culture-maintained germplasm collections. The group is using a range of molecular tools to assess the nature and frequency of novel mutations affecting somatic embryo derived cocoa.

Name Tim Wheeler
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Research Area Impacts of climate variability and change on crops

Research Activities

Tim is head of the crop and climate group at the University of Reading. This interdisciplinary team of crop scientists, physicists and climate scientists assess the impacts of weather, climate variability and climate change on crops. Seasonal to decadal predictions of the impacts of climate on food supplies require crop models that capture the effects of climate change and climate variability. By integrating plant experiments from controlled environments and the field, with crop simulation modeling and meteorological expertise the group have developed a new combined weather and crop forecasting methodology. This approach simulates biological and physical processes on a common spatial scale, allowing researchers to capture the effects of daily to multi-decadal variations in the weather on crops. Using this technique the group now has the ability to generate country- and region wide forecasts of the impacts of climate variability/change. The crop and climate group works closely with staff from the Hadley Centre for Climate Prediction and Research of the UK Met Office, and from the European Centre for Medium-range Weather Forecasts.

Name Mike Wilkinson
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Research Area Genetics and plant breeding, agri-environmental research and applied ecology

Research Activities

Current research in the Wilkinson laboratory focuses on the application of multidisciplinary approaches to develop a more predictive understanding of the interaction between the agri-environment and natural ecosystems. The ultimate aim of this work is to develop more sustainable practices of agricultural land management. To help achieve this goal the group are building predictive models at a variety of scales ranging from the individual to the landscape, that will integrate data from molecular, genomic and epigenomic studies with information relating to life history, population genetics, species interactions and evolutionary processes. Current projects in lab include: risk assessment of genetically modified crops; genomics-led (non-GM) approaches to crop improvement (Cocoa, oil palm, Lupin, cashew); identification of genes under selection or of adaptive significance (Arabidopsis, Fragaria, Brassica); cryptic introgression of paternal DNA during parasexual hybridization (Solanum); epigenomics and plasticity (cocoa); pollen dispersal modelling, and novel approaches for genetic characterisation and utilisation of wild germplasm.

ERA-PG - first call success

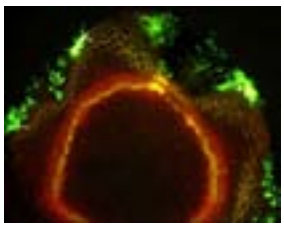
written by Sophie Laurie BBSRC

The Programme Board meeting for the first call of ERA-PG was held in Venice at the beginning of October. Both Sub Calls (A= basic science orientated, B= public private partnership) were considered by the Board, and recommendations were made to Sub Call specific moderating panels and the funding organisations involved. The consortia have received preliminary indications as to the status of their applications and the decisions will be finalised depending on some administrative procedures required by the national funding organisations. It is expected that in Sub Call A there will be funds to support 15 out of the 44 projects submitted to the second stage (from an original assessment of 70 outline proposals). The UK is participating in 13 out of these 15 and leading 5 of the first 7 selected. There was limited UK participation in Sub Call B, with only one eligible project assessed. This project was ranked highly and has also been recommended for funding.

Overall the BBSRC is very happy with the call development and management so far. The UK plant science community responded well to the initiative and this resulted in some very high quality applications being received. The new consortia are expected to bring considerable added value to this research area at the national and European level. Planning is now underway for the second ERA-PG call, expected to be announced at the end of 2007. The structure and focus of the call may change to reflect changing priorities of the funders involved. It is hoped that there will be more opportunity for the UK to participate in the public-private partnership activities in this second phase and discussions in the UK and Europe will reflect this. Framework 7 will bring new opportunities for ERA Nets, including the possibility of a 'top-up' scheme where the EC will provide additional funds to joint calls in excess of €5M equivalent to 30% of the total earmarked funding. This top up is likely to be dependant on agreement with FP7 thematic priorities and ERA-PG is waiting for further clarification. See www.erapg.org. for updates or contact Sophie Laurie at sophie.laurie@bbsrc.ac.uk.

Spotlight on Rothamsted Research

Rothamsted Research is the longest established agricultural research centre in the world and the largest in the UK, with an enviable international reputation as a centre of excellence for multidisciplinary research. The institute seeks to integrate mathematics, physics, chemistry, ecology and crop sciences (including: genetics, pathology, invertebrate biology and soil science) to contribute predictive understanding and scientifically-sound options for the maintenance of economically and environmentally sustainable systems of arable land utilisation. The work of the Institute exemplifies integrative biology by incorporating work from the genomic and molecular levels of biology and chemistry to whole cells, tissues, organisms and populations, together with soil processes and investigations at the ecosystem and landscape scale. Rothamsted has an excellent and unique combination of research facilities including 480 ha of farmland over a range of soil types, more than 1000m2 of glasshouses, state of the art controlled environment facilities for plants and insect rearing, an extensive analytical capability including bioimaging and metabolomics, and long-term experiments, soil and plant archives and datasets, supported by an increasing emphasis on bioinformatics and mathematical modelling.
http://www.rothamsted.bbsrc.ac.uk/



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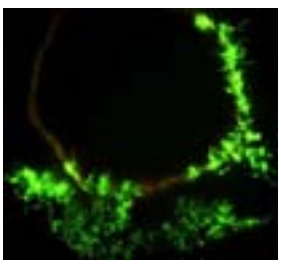
Research Area Epidemiology and host-pathogen-environment interactions

Research Activities

Research in Bruce's group focuses on the effects that environmental factors such as temperature and leaf wetness have on genetic interactions between crop plants and fungal pathogens. This is carried out in collaboration with Graham King and INRA (France). The model crop/pathogen systems used are oilseed rape (*Brassica napus*) and the ascomycetes causing phoma stem canker (*Leptosphaeria maculans/L. biglobosa*) and light leaf spot (*Pyrenopeziza brassicae*). The symptomless stages of disease development are studied using isolates of *Leptosphaeria* transformed with GFP and DsRed, and quantitative species-specific PCR. Bruce's group have recently shown that *Rlm6* the major gene resistance to *L. maculans* operating in *B. napus* leaves is temperature-sensitive. At 15°C the phenotype in leaves of lines with *Rlm6* is 'resistant' whereas at 25°C it is 'susceptible'. Using GFP-transformed isolates, they have demonstrated that where the phenotype was 'resistant', *L. maculans* was unable to spread from leaves to colonise the stems and produce phoma stem cankers. The group are also starting to examine resistance to *L. maculans* operating during the symptomless phase of the disease as it grows down leaf petioles and starts to colonise stem tissues. Researchers have demonstrated that pre-inoculation of *B. napus* leaves with ascospores of *L. biglobosa* can induce resistance to *L. maculans.* For this monocyclic disease, pre-inoculation at the start of the growing season in September to induce resistance can decrease severity of phoma stem canker at harvest 10 months later. A new project is starting to examine the operation of other gene resistance to *P. brassicae* in *B. napus.*



Spotlight on Rothamsted Research

Name Christine Foyer
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Research Area Plant stress metabolism and redox regulation

Research Activities

Environmental variability impacts significantly on agricultural yield and profitability in Europe, and these effects will rise substantially with temperature increases associated with global warming. African farmers currently face regular crop losses due to poor yield and drought and predictability of yield will become even more unreliable because of climate change. Work in the Foyer lab is focussed on obtaining a fundamental understanding of how the metabolism of model (Arabidopsis, tobacco) and crop (maize, soybean) plants is modified in response to environmental stress, particularly drought and chilling. Focussing on plant redox biology and carbon/nitrogen interactions, the lab seeks to understand how changes in primary metabolites can alter growth and defence responses when plants are exposed to environmental stress. Christine's group studies the impact of redox signals arising from primary energy exchange processes (photosynthesis and respiration) on carbon/nitrogen interactions and signalling, particularly related to the interface with plant development. They have used a range of mutants and transgenic approaches to analyse the roles of ascorbate and glutathione metabolism in redox signalling. A combination of biochemical (metabolite analysis, enzyme activity and protein contents), genetic (mutants) and genomics (micro-array and transcriptomics) approaches are being used to determine how the mitotic cell cycle is limited by environmental stress through modulation of these antioxidants in Arabidopsis and tobacco. The role of redox regulation on plant development is being studied in maize (leaves) and soybean (leaves and nodules) to identify new stress-induced senescence markers and reveal new routes to develop crops that perform well and more predictability in extreme environmental conditions.

Name Dimah Habash
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Research Area Wheat physiology and adaptation to abiotic stress

Research Activities

Abiotic stresses are major determinants of crop productivity worldwide. Dimah's research targets the understanding of nitrogen assimilation and partitioning in response to environmental constraints in wheat. The aim is to dissect the physiological, molecular and genetic factors defining complex traits such as nitrogen utilisation efficiency. In particular the group focuses on the study of gene expression and function of glutamine synthetase and its contribution to the remobilisation of assimilate to grain. Genetic linkage analysis is being utilised to deconstruct various metabolic and physiological aspects of nitrogen assimilation and assimilate partitioning. Work in the lab has illustrated the importance of linking metabolism with organ morphology and development. Several major loci have been identified which will enable future development of molecular markers and the search for candidate genes which explain the genetic variation present in wheat germplasm. Recently, the group have applied integrated approaches to study water use in *durum* wheat (EUFVI project 'Tritimed'). This research combines quantitative genetics, crop physiology, plant metabolism and genomic tools to identify loci controlling wheat responses and growth under drought conditions. These studies will also provide large datasets which will be used to inform new mechanistic systems-based models of wheat function.

Name Nigel Halford
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Website http://www.rothamsted.bbsrc.ac.uk/cpi/mers/nhd.html
Research Area Metabolic signalling and regulation

Research Activities

Nigel Halford's team studies signal transduction pathways mediating metabolic regulation of gene expression and enzyme activities. The aim is to dissect the mechanisms involved in carbon metabolite and amino acid sensing and signalling, and to establish the role of these mechanisms in the control of assimilate partitioning. The team was the first to clone and characterize a plant protein kinase, SNF1-related protein kinase-1 (SnRK1), and study it from the molecular level through to the identification of substrates and downstream effects on sucrose synthase, alpha amylase, sucrose phosphate synthase and ADP-glucose pyrophosphorylase. These studies placed SnRK1 firmly in the sugar sensing signal transduction pathway and at the heart of the control of carbon partitioning. The SnRK1 system has been manipulated to affect starch and glucose levels in potato tubers and phytosterol levels in oilseeds.
More recently the group has begun to investigate another plant protein kinase with homologues in animal and fungal systems, including the general control non-reversible (GCN2) protein kinase of yeast.
Understanding metabolic regulation underpins efforts to mitigate the risk of acrylamide formation during processing of foods derived from cereals and potato. The team is therefore applying its knowledge and materials to this key strategic area of research, in collaboration with Prof. Don Mottram's group at Reading University.

Spotlight on Rothamsted Research

Name Kim Hammond-Kosack
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Website http://www.rothamsted.bbsrc.ac.uk/ppi/wptop.html
Research Area Functional evaluation of plant defence signalling against Fusarium ear blight disease in Arabidopsis

Research Activities

Fusarium ear blight (FEB) infections of cereal crops cause considerable losses to grain quality and safety (http://www.scabusa.org/). The two main causative agents of this disease on UK wheat crops are the hemibiotrophic pathogens *F. culmorum* (*Fc*) and *F. graminearum* (*Fg*). Floral infections by *Fc* and *Fg* also cause the developing cereal grains to become contaminated with various fungal mycotoxins, including the highly toxic trichothecene mycotoxin deoxynivalenol (DON). The molecular basis of resistance to FEB in cereal species is poorly understood but it is QTL based and Fusarium species non-specific.

The Hammond-Kosack Lab has previously demonstrated that *Fc* and *Fg* conidia can infect the floral tissues of Arabidopsis to cause disease symptoms on flowers, siliques and upper stem tissue. DON mycotoxin production is detected in infected flowers. This novel Arabidopsis floral model provides a tractable system for elucidating fundamental aspects of this globally important cereal-fungal interaction.

Kim's group is undertaking a detailed forward and reverse genetics analysis of the FEB infection phenotype in Arabidopsis floral tissue. Data is being generated on the effects of gene mutations previously characterised in several pathosystems and those thought to be causally involved in basal and race-specific defence signalling in other plant tissues.

To quantitatitively and qualitatively explore the details of the FEB-Arabidopsis floral pathosystem, various transgenic fusarium strains are being used, including strains with constitutive expression of GFP or GUS. For example *TRI5* promoter mediated GUS expression marks the onset of DON mycotoxin production as well as *Fg* strains compromised in disease causing ability in wheat ears.

Name Malcolm Hawkesford
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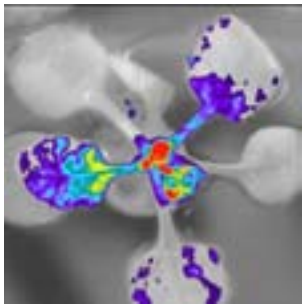
Website http://www.rothamsted.bbsrc.ac.uk/cpi/men/mh.html
Research Area Plant nutritional genomics

Research Activities

The plant nutrition research in Malcolm's group not only focuses on enhancing crop production but also on minimising inputs. Molecular mechanisms co-ordinating nutrient availability, particularly for nitrogen, potassium, phosphorus and sulphur, are targets for optimising plant nutrient use. Arabidopsis is utilised as an important genetic tool, with wheat and Brassica begin used as strategic models for examining many nutrient processes in the context of crop production. Malcolm has investigated gene families of ion transporters, with emphasis on redundancy and specialization of isoforms: individual isoforms have been shown to be responsible for uptake and distribution, storage and remobilization of ions, all of which involve transport steps in and out of the cell and between subcellular compartments. In addition, responses to nutrient status are being examined at the level of the transcriptome and metabolome to identify novel genes and processes contributing to nutrient use efficiency. Broadbalk (pictured), the oldest long-term experiment at Rothamsted, has a range of plots with contrasting nutrient inputs, and is a unique resource for these studies enabling examination of influence of form and quantity of nitrogen inputs as well as effects of specific deficiencies.



Name Peter Hedden, Andy Phillips and Steve Thomas
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Website http://www.rothamsted.bbsrc.ac.uk/cpi/tms/index.html
Research Area Gibberellin signalling and crop genetic improvement

Research Activities

Gibberellins are involved in many developmental processes and environmental responses in plants. Consequently, chemical and genetic control of gibberellin biosynthesis and signal transduction are routinely used to manipulate the development of a wide variety of arable and horticultural crops. Peter, Andy and Steve are studying the biochemical mechanisms of the gibberellin signalling system, concentrating on the later stages of GA biosynthesis, GA perception and early signalling events and linking these events to important growth processes such as root development, stem elongation and reproductive growth. Their principal experimental systems are Arabidopsis and wheat: in the crop species they have on-going projects on GA signalling in relation to stem height and to grain size and quality. In addition, the group have also developed a mutagenised population of bread wheat, which they are screening for mutations in specific genes using TILLING. This technology is now offered as a service for the wheat research and plant breeding communities for candidate gene validation and crop improvement.

Spotlight on Rothamsted Research

Name Huw Jones
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Website http://www.rothamsted.bbsrc.ac.uk/cpi/wdi/hj.html
Research Area Transgenic approaches to investigate gene function in cereals

Research Activities

Genetic transformation is a powerful research tool to study many aspects of plant gene function and Huw's transformation group occupies a leading position in the ability to routinely transform commercial varieties of wheat. Building on a robust transformation platform based increasingly on Agrobacterium co-cultivation, Huw is developing technologies to refine transgenic experimental approaches in wheat (and in the near future, Brachypodium) including clean-gene systems; robust RNAi silencing, the use of matrix attachment region sequences and tissue-specific or inducible promoters to give predictable transgene expression, incorporation of targeting sequences and epitope tags to direct and track proteins to subcellular compartments and approaches for the generation of tagged and knockout lines in hexaploid wheat using Ac/Ds-mediated transposition. To facilitate model-to-crop research, Huw has recently calculated the full economic costs of producing >20 transgenic wheat lines per gene construct and can offer this transformation service to UK scientists via the BBSRC MONOGRAM programme.

Name Angela Karp
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Website http://www.rothamsted.ac.uk/pie/PlantBiodiversityAndPopulationGenetics.html
Research Area Bioenergy crops – genetic improvement and land-use impacts

Research Activities

Angela leads research on Bioenergy Crops at Rothamsted Reserach. Her research activities include, genetic improvement of short rotation coppice (SRC) willow, studies on pests and diseases of SRC, characterisation of the National Willow Collection (held at Rothamsted Research), energy grass (Miscanthus, switchgrass and reed canary grass) improvement and the impacts of land-use change from arable to perennial energy crops. Anglea is the overall coordinator of the UK DEFRA Genetic Improvement Network on SRC willow (BEGIN; biomass4energy.org), which involves willow breeding underpinned by trait mapping and genomics. She also coordinates a project (http://www.relu-biomass.org.uk/) on the social, environmental and economic implications of increasing rural land use for energy crops, funded by the UK RELU (Rural Economy and Land Use) programme and is a partner in a TSEC (Towards a Sustainable Energy Economy) consortium (http://www.serc-wales.org.uk/tsec.html). The group has additional interests in translating knowledge of development from models such as Arabidopsis to help understand growth, architecture and other traits of relevance to biomass yield in willows. For example high yielding willows can have few, thick stems or many, thin stems and this may have an influence on lignocellulosic composition. To understand this further Angela is collaborating with Prof. Ottoline Leyser to investigate how Arabidopsis genes influence stem number and thickness.

Name Brian Kerry and Penny Hirsch
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Website http://www.rothamsted.bbsrc.ac.uk/ppi/rhizo/
Research Area Rhizosphere biology

Research Activities

Biological interactions in the rhizosphere are studied at the molecular, whole organism and population scale with especial emphasis on plant parasitic nematodes and the microbial community. The research programme within the lab targets sustainable management of nematodes, the role of the rhizosphere microbial community in plant nutrition and disease suppression, and the impact of environmental changes on the microbial community structure and function. Genes and proteins involved in nematode recognition of plant roots are being studied by the group with particular reference to secretions from the nematode sense cells. In collaboration with North Carolina State University, the genome of the bacterial hyperparasite of nematodes, *Pasteuria penetrans*, is being sequenced. Researchers are also investigating interactions between isolates of the fungus, *Pochonia chlamydosporia* and the signalling systems that control the trophic phases of this facultative pathogen to determine their importance in the regulation of nematode populations. This research has delivered new management options for potato growers in the UK and a biological control agent for use against root-knot nematodes in tropical vegetable production. A suite of molecular tools have also been developed by the group and are being used to diagnose and quantify specific fungal and bacterial isolates in soils, for example researchers have demonstrated that GM plants with anti-microbial resistance have limited impact on the rhizosphere microbial community structure and function.

Spotlight on Rothamsted Research

Name Graham King
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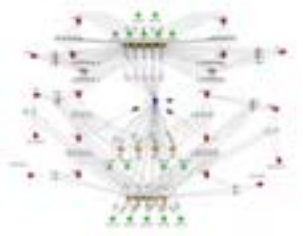
Website http://www.rothamsted.bbsrc.ac.uk/cpi/wdi/gk.html
Research Area Brassica genetics and genomics underpinning crop improvement

Research Activities

Oilseed rape is the primary source of vegetable oil in Northern Europe, and an important component of UK arable rotations. It also has the potential to provide new nutritional and non-food products, including renewable energy. However, it is a crop that was introduced relatively recently, and there is still much scope for genetic enhancement of yield. The *Brassica* improvement programme exploits the relatedness of *Brassica* rapeseed and the reference species *Arabidopsis thaliana*. Fundamental research in Graham's group is focused on understanding the role of genome structure and organisation in regulating gene expression. This may have particular relevance for understanding the basis of interactions between genetic, developmental and environmental factors contributing to harvestable product quality. Variation at DNA sequence and chromatin level mediates epigenetic regulation, and so sequence-dependent constraints on nucleosome positioning are first being characterised in Arabidopsis, and the distribution of methylated DNA in *Brassica* genomes is being established in the context of the ongoing international *B. rapa* sequencing programme (www.brassica.info). Graham's group contributes to the Multinational *Brassica* Genome Project, and has a particular interest in genetic and genomic data integration in the context of crop trait loci.



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Research Area Bioinformatics – Plant molecular systems biology

Research Activities

Jacob and Chris are using a number of different mathematical and computer modelling techniques to represent the quantitative dynamic changes in biochemical and signalling pathways in plants. These projects are collaborations with plant scientists at Rothamsted and elsewhere and include aspects of plant physiology such as Gibberellin biosynthesis, nutrient transporter systems in the root and the interactions between C and N metabolism. They use a number of different modelling methods but have particular interest in hybrid Petri-nets and ordinary differential equation models. Their long term aim is to link models of plant molecular processes at the gene level to dynamic models of plant growth and development so that they can simulate the phenotypic effect of processes such as gene knockout experiments, and in the longer term more general genotype-phenotype relationships.

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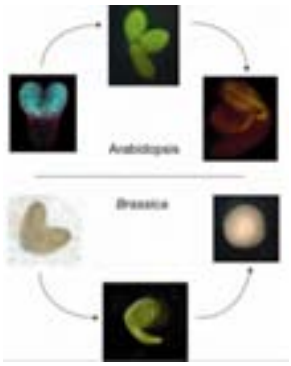
Research Area Bioinformatics – Data integration

Research Activities

Integrating data from the many databases and internet sources utilised by plant molecular geneticists to analyse and interpret their results is a recognised challenge in bioinformatics. Jacob and Chris have therefore developed a generic data integration framework called ONDEX, which can be used in a number of important application areas such as transcriptome analysis, protein interaction analysis, gene annotation, data mining and text mining. Data may be imported to ONDEX through a number of 'parsers' of public-domain and other databases such as TRANSFAC, TRANSPATH, BRENDA, GO, KEGG, Drastic, ENZYME, Pathway Tools Pathway Genomes (PGDBs), Cell Ontology, and Medical Subject Headings Vocabulary (MeSH) together with associated sequence data where available. The imported data may be utilised with the data mining features and specific applications or extensions of the ONDEX framework. The ONDEX user interface is an example of an ONDEX application package and this displays the data as a set of linked graphs with the nodes representing a data object and the edges (or links between the nodes) representing a relationship between the two nodes. 'Filters' are provided to assist the user to focus on the interactions that are most important. In addition, a powerful filter is available to import microarray expression level data and globally analyse the relations between the different genes being expressed. ONDEX is developed as an open source software project and more details can be found on the ONDEX SourceForge website http://ondex.sourceforge.net/

Spotlight on Rothamsted Research



Name Smita Kurup
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Research Area Comparative Developmental biology in Brassicaceae

Research Activities

Smita's research focuses on the comparative developmental biology between Arabidopsis and *Brassica*, specifically with regard to seed development. To underpin knowledge-based improvement of oilseed rape, requires a better understanding of the interplay between genetic and developmental mechanisms that control the biochemical pathways associated with seed oil profile and quality. The embryo in *Brassica* is the site of rapeseed oil production. As well as playing a key role in the yield, quality and profitability of oilseed rape, embryo development affects the early stages of crop establishment through its contribution to seedling vigour. The components traits associated with embryo development, such as cotyledon size, seed size, and the ratio between the cotyledon and other embryo organs are likely to be important components of oilseed harvestable yield. However, at present relatively little is known about their relative contribution and the effects of developmental, environmental or genetic variation on oil yield and quality. A comparative genomics approach, exploiting the well characterized Arabidopsis embryo, is being used to identify and define the key stages of rapeseed embryo development, and provide a developmental framework for understanding the co-ordination of the biochemical oil synthesis and modification pathways with respect to seed development.

Name John Lucas
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Research Area Pathogen population biology and disease management

Research Activities

Disease epidemics occur due to dynamic changes in pathogen populations in space and time. John's research aims to integrate fundamental understanding of the population biology of plant pathogens with improved methods of disease detection and diagnosis to devise more precise and sustainable strategies for disease control. Factors underlying epidemic development, such as inoculum production and dispersal, as well as interactions determining infection of the plant, host resistance and susceptibility are included in this work. The group are using biological, genetic and molecular approaches to study evolutionary changes in pathogen populations, exemplified by the emergence of new pathotypes, and the development of fungicide resistance. The major foliar fungal pathogens of arable crops including *Mycosphaerella graminicola* and *Rhynchosporium secalis* on cereals, and *Leptosphaeria maculans* and *Pyrenopeziza brassicae* on oilseed rape are a main focus of the lab's research programme. In addition to this work, researchers are also involved in overseas and extension projects aimed at the diagnosis of diseases of tropical crops, especially those caused by phytoplasmas, and the development of oilseed brassicas with improved disease resistance and drought tolerance for rain-fed and irrigated agriculture in Asia. Practical outputs from the programme include germplasm with improved resistance to disease, models of disease dynamics and epidemic risk, strategies for the management of fungicide resistance, and decision support systems to optimise disease control.

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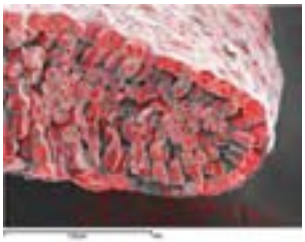
Research Area Contaminants and micronutrients in plants



Research Activities

Steve's lab is researching the uptake and sequestration of contaminants by plants, in particular heavy metals and metalloids. The group are specifically interested in how uptake and sequestration is influenced by the chemical forms of pollutants in soils and the environment. One focus is the ability of some plant species to hyperaccumulate Zn, Cd and As which could have applications in phytoremediation of contaminated sites. Researchers are investigating the physiology and molecular mechanisms of uptake and transport, followed by the method of sequestration in the plants. In contrast, essential micronutrients are deficient for humans and animals in many parts of the developing world, and even in developed areas such as Northern Europe, where for example Se is limited. The group are therefore investigating variation in uptake, transport and speciation of micronutrients in plants, and how these change over time in the long-term Rothamsted field experiments in order to develop methods to enrich these at the base of the food chain and provide a healthier diet.

Spotlight on Rothamsted Research

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Research Area Plant membrane transporters and nutrient signalling

Research Activities

Maintaining crops with optimal nutrition often requires the application of excess fertiliser, resulting in wasteful and damaging losses to the environment. Furthermore, adequate nutrition is important, not only for maintaining growth and yield, but also for plant resistance to other stresses including diseases and pests. An ongoing goal for sustainable agriculture is to optimise yield by matching the demand of the crop to soil supply and minimise leaching. The efficient use of applied nitrogenous fertilisers depends on understanding how the plant cell senses and responds to changes in the external supply of nitrogen (N). Several different techniques are being used in the Miller group to measure the N status of plants, ranging from changes in gene expression to single cell sampling methods including ion-selective microelectrode measurements in leaves (upper image) and roots (lower image). In cereals and Arabidopsis, nitrate- and ammonium-selective microelectrodes are used to identify how cellular concentrations of these forms of N change under surplus and deficient conditions. Researchers in the lab have also adapted this sensor technology to measure nutrient availability in the rhizosphere and bulk soil, including field measurements. In addition the group are genetic manipulating the expression of transporters to identify potential strategies for improving N-use in crop plants. This research is also important for conventional breeding programmes aimed at developing more sustainable crops that maintain yield and quality but require lower fertiliser inputs. As vacuolar stored nitrate is important for osmotic balance Tony's research also has important implications for drought and salinity tolerance.

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Research Area Sugar beet biotechnology research

Research Activities

Sugar beet is an important spring break crop which, in the UK is grown in rotations dominated by winter cereals. The environmental benefits of sugar beet in the arable landscape are well documented and include increased biodiversity and provision of food and habitat for endangered bird species. Specific targets for UK crop improvement include drought tolerance, the control of aphid transmitted yellowing viruses, soil-borne rhizomania virus, powdery mildew, and cold-induced premature bolting and flowering. These are not priority targets for multinational breeding companies and must therefore be addressed in part, by the UK industry (growers and the processor, British Sugar Plc) which funds research through the British Beet Research Organisation (BBRO). Effie's group is engaged in transgenic research to evaluate genes of agronomic interest for all key targets and to conduct molecular genetic analysis of bolting and flowering. The group, in collaboration with Peter Hedden, Andy Phillips and Christian Jung (Plant Breeding Institute, University of Kiel, Germany), has identified and mapped a number of important bolting and flowering control genes in the photoperiod and gibberellin pathways. The role of the sugar beet biotechnology research group is to conduct the basic research that enables rapid and efficient uptake of UK targets for further development by the breeding companies. This demands clear focus and a closely integrated research strategy that provides a balanced approach to scientific, as well as the growers', breeders' and the processor's requirements.

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Research Area Lipid metabolism and signalling

Research Activities

Johnathan's research is focussed on understanding and exploiting aspects of plant lipid metabolism. His main area of research is the biosynthesis of omega-3 long chain polyunsaturated fatty acids, with the specific goal of producing these "fish oils" in transgenic plants. He is also interested in the role of sphingolipids and their metabolites in plants, as both signalling molecules and components of so-called "lipid rafts". He also collaborates with John Pickett on the orphan jasmonate cis-jasmone, which acts both as an insect semiochemical and modulator of plant gene expression.

Spotlight on Rothamsted Research

Name Eric Ober
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Research Area Drought tolerance research

Research Activities

Even in the temperate oceanic climate of England, drought stress is the biggest single cause of yield loss for the sugar beet crop, which is grown mainly in eastern counties, often on sandy soils. Eric Ober leads projects at Broom's Barn in search of drought tolerance and water use efficiency amongst diverse ranges of genotypes of sugar beet and winter wheat. His work is in close collaboration with breeders and partly funded by multinational seed companies. The group has developed expertise for growing field crops under large rain-out shelters so that drought (and accurately metered trickle irrigation) can be imposed on many genotypes simultaneously while whole-crop characteristics (e.g. canopy cover, soil water extraction) can be assessed. Phenotypic characterisation focuses on key morphological and physiological traits that confer improved performance under water limiting conditions. The emphasis is on traits that can be measured effectively on large numbers of genotypes typical of breeding trials. The development of these screening procedures for breeders will also allow the identification of molecular markers in mapping populations. This work will enable breeders to cull inferior materials in early stages of breeding programmes, and hence enhance conventional breeding for drought tolerance. The group has also developed a multi-environment variety trials approach to screening for drought tolerance.

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Research Area Crop improvement – regulation of primary metabolism

Research Activities

Research in Martin's group is directed towards the goals of sustainable production in future climates, increased biomass production and quality. His research, within a holistic context, is focused on improving the photosynthetic potential and efficiency of crop plants by understanding and modifying the molecular and biochemical controls that determine assimilation and assimilate partitioning in relation to both environment and genotype. For example through projects aimed at ameliorating effects of drought on wheat production and in determining specific adaptations of photosynthetic mechanisms in plants from arid regions. Recently the group have (i) discovered the biosynthetic pathway for the nocturnal Rubisco inhibitor, CA1P; (ii) provided the first evidence that CA1P can protect Rubisco against stress-related inactivation; (iii) established unequivocally that CA1P and a naturally-occurring daytime inhibitor of Rubisco are both chloroplastic and regulate Rubisco activity in vivo; and (iv) created a TILLING population of Durum wheat. To achieve its objectives the lab's research programme exploits a wide variety of molecular, biochemical and physiological approaches (e.g. genomics, transcriptomics, proteomics, metabolomics, plant transformation, TILLING).

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Research Area Metabolic signalling

Research Activities

Trehalose, a non-reducing disaccharide formed of two alpha- 1,1 linked glucose units, is one of the most abundant sugars in the biosphere. Its chemistry is harnessed as circulatory sugar, carbon source and stress protectant in arthropods, fungi and bacteria, but it is largely absent in plants except in a few highly specialised resurrection species. Nevertheless, the genes for the trehalose pathway have diversified in *Plantae*. We have been a key player over the last seven years or so in the discovery that trehalose 6-phosphate (T6P) is an indispensable sugar signal in plants, influencing processes such as development, metabolism, photosynthesis and nutritional and environmental stress resistance. Matthew's Lab is focused on understanding how T6P signals to regulate metabolism, leaf development and photosynthesis using biochemical, molecular and new chemical approaches to improve crops and for biotechnological application.

Spotlight on Rothamsted Research

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Research Area Activation of plant defence by biotic stress related signals

Research Activities

Plants suffering biotic stress produce small lipophilic molecular signals that, via aerial or rhizosphere transport, can activate defence in undamaged plants or prime these for greater defence when placed under stress. Such signals are identified in John's laboratory by using electrophysiological recordings from insects to "listen in" on these processes and include *cis*-jasmone which has advantages over other members of the jasmonate signalling pathway for practical use in the field by activating defence in cereals against insect pests and potentially weeds and pathogens. Defence activation can involve induced expression of genes for biosythesis of volatile repellents against pests and attractants of predators and parasitoids or antibiotic defence compounds for example the hydroxamic acids or benzoxazinoids. Certain plants, even without biotic stress, can imitate damaged plants and this is exploited in Africa for poor farmers by companion cropping against insect pests and more recently the parasitic witchweed e.g. *Striga hermonthica.*

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Research Area Manager of the long-term experiments at Rothamsted

Research Activities

There are more than 15 long-term field experiments at Rothamsted. Some were started in the mid-1800s and were designed to answer questions on soil fertility, the nutrition of important arable crops and of permanent grassland cut for hay. They have been progressively modified so that they remain relevant to modern agriculture and/or environmental concerns. With contrasting fertilizer and manure treatments and crop management and a detailed history they are an unparalleled resource upon which new research can be based. For example, ^{15}N-labelled nitrogen has been applied to microplots within the long-term wheat (Broadbalk), barley (Hoos Barley) and grassland (Park Grass) experiments to look at the efficiency with which fertilizer N is used by the crop, how much remains in the soil and how much is lost. Park Grass has also been used extensively to study how plant species diversity is affected by nutrient additions, soil pH and climate. A unique archive of plant and soil samples from the experiments is also maintained. The retrospective analysis of archived material allows researchers to look back over more than 160 years at many aspects of plant nutrition, soil fertility and atmospheric pollution. For example, samples have been analysed for poly-aromatic hydrocarbons and dioxins, which have increased in the atmosphere since the early 1900s and to show that plutonium contamination from the nuclear bomb tests carried out in the US in 1952/3 reached Northern Europe. Data from the experiments is being secured within the Electronic Rothamsted Archive (e-RA).

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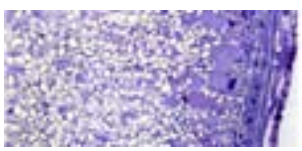
Research Area Crop Modelling

Research Activities

Crop simulation models are used increasingly in basic and applied research in the plant sciences and in natural resource management. They provide the best-known approach for integrating our understanding of complex plant processes as influenced by environment and management. Crop models are useful in guiding the direction of fundamental research by providing quantitative predictions and highlighting gaps in our knowledge. Sirius is a process-based wheat simulation model, which was developed in collaboration between Rothamsted Research and Crop & Food Research, NZ and tested against independent experiments in geographically diverse sites with different environments. The latest developments in understanding nitrogen uptake and redistribution, and wheat phenology allow us to describe and model these processes more mechanistically than in the past, making it possible to link model cultivar parameters with simple physiological traits. This creates a framework for the analysis of complex wheat traits, e.g. nitrogen use efficiency, and the design of the optimal wheat ideotype.



Name Peter Shewry
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Research Area Development, composition and end use properties of cereal grain.

Research Activities

Cereals form a major part of the diet of humans and livestock, contributing proteins, calories, fibre and micronutrients. Peter's group are studying aspects of wheat grain development in order to improve the quality for human nutrition (fibre and phenolics content) and the processing properties (protein content and properties, and grain architecture). Researchers are also exploring the use of cereals for biofuel and bioethanol production.

Spotlight on Rothamsted Research

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Research Area Sugar beet virology research

Research Activities

Sugar beet is susceptible to a number of economically important viruses such as the aphid transmitted yellowing complex and the soil-borne rhizomania disease. Virus strains that differ in characteristics such as pathogenicity and host range exist in the field and rhizomania resistance in commercial sugar beet varieties appears to be under threat of breakdown in certain countries. There are no commercial varieties available that are resistant to any of the yellowing viruses, and sources of virus resistance are being sought via conventional and transgenic approaches. Mark's research group, primarily funded by the BBRO, is engaged in developing molecular tools to characterise the viruses and to improve the understanding of disease epidemiology and, has, in collaboration with INRA-Colmar, France and USDA-Salinas, USA successfully determined the biological and molecular properties of the yellowing viruses and reclassified them within the beet polerovirus complex. A key area of basic research within the group is the study of interactions between the viruses, their vectors and plant hosts. The group has established an *Arabidopsis*-based experimental model system that enables differential analysis of beet yellowing viruses and is currently being used to investigate host/non-host interactions of *Beet mild yellowing virus* (BMYV) and the closely related *Beet chlorosis virus.* The group has also developed a full length infectious clone of BMYV tagged with GFP that is now being used to study virus-virus and vector-virus interactions.

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Research Area Lipid metabolism and signalling

Research Activities

The transport of lipids and lipid metabolites is central to metabolism, signalling and development but the molecular basis of these processes is poorly understood in plants. Freddie's research aims to identify and characterise transporter proteins involved in the movement of lipids and their metabolites across membranes and to elucidate their cellular and physiological roles. A specific goal is to understand how substrates, cosubstrates and cofactors of beta-oxidation are imported into peroxisomes and how peroxisomal metabolism is co-ordinated with that of other cellular compartments. Current research is focussed on COMATOSE, an ATP Binding Cassette (ABC) transporter which regulates peroxisomal import of substrates for beta-oxidation. A future target is the identification of novel lipid transporters.

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Research Area Epidemiology and evolutionary ecology of plant pathogens

Research Activities

The mapping of genotype/molecular-interactions to the phenotype of a plant pathogen needs to be underpinned by a definition of the plant's life history, in particular components that constitute the relevant phenotypic characteristics for its epidemiology and evolutionary ecology. For example, resistance to a plant virus can be expressed through (i) reduced acquisition, (ii) reduced virus titre, (iii) reduced symptom expression, etc. Frank's group have shown that some of these resistance phenotypes cause the virus to evolve a higher multiplication rate, whereas others do not. Epidemiology research in the lab, aims to determine the key life-history components for (i) invasion of new pathogens or new pathogen strains, (ii) the persistence of these invaders and (iii) the possible coexistence of multiple species/strains. Researchers use methods from evolutionary ecology to investigate, for example, how disease control by sanitation, pathogen vector control and in-vitro propagation affect the evolution of more aggressive strains.
Working systematically through the chain from biotic and abiotic factors that affect the pathogen life-history components, through to its epidemiology, which in turn determines its evolutionary ecology, the group are now able to define the key phenotypic aspects that need to be predicted from models of cell and molecular processes. With further research on epidemiology and evolutionary ecology researchers will be addressing the challenge of mapping from molecular processes to plant and pathogen phenotype.

Spotlight on Royal Holloway - University of London

Plant science research at Royal Holloway, University of London combines researchers from the Centre for Plant Molecular Sciences and the Centre for Ecology, Evolution and Behaviour. Research at RHUL addresses a number of fundamental aspects of plant development, reproduction and metabolism at the cellular and molecular level. This work is carried out alongside studies of plant interactions with other organisms of potential agricultural importance. Areas of strength include plant cell wall biochemistry, carotenoid biosynthesis, leaf and chloroplast development, photocontrol of gene expression, hormone perception and stress signalling networks.

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Research Area Kinase signalling in plants

Research Activities

The molecular genetic dissection of kinase signalling in plants is the main theme of Richard's work. Studies in the laboratory centre on characterising AtPDK1 a master plant kinase. AtPDK1 acts as a central regulator of key plant processes including oxidative stress and pathogen defence. In addition to this work researchers have also unravelled a number of the signalling events downstream of AtPDK1 including the mechanism by which pinoid kinase and thus auxin transport is connected to AtPDK1 signalling.

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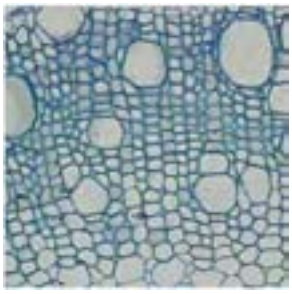
Research Area Plant molecular biology

Research Activities

In higher plants, growth is coordinated by both developmental cues and the environment. To gain a better understanding of these processes, researchers in the Bogre laboratory are investigating intracellular signalling mechanisms that regulate plant growth and cell proliferation. The main focus of the group is on MAP kinase signalling and the 40S ribosomal S6 kinase. S6K is able to integrate growth-stimulating inputs, through the TOR and PDK1 signalling pathways, into growth-promoting outputs. This signalling pathway has been associated with the preferential translation of ribosomal proteins that constitute the protein synthesis machinery of the cell and that are required for the growth response. The lab is particularly interested in the interrelationship between cell growth, proliferation and differentiation. In collaborative projects researchers are also studying how signalling pathways regulate plant cytoskeleton organisation.



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Research Area Plant biochemistry and molecular biology

Research Activities

The central focus of research in the Bolwell lab is the regulation of biosynthesis and modification of plant cell wall components during development and in response to fungal attack. Paul's group has also made key discoveries in the areas of lignin, xylan and cellulose biosynthesis and is involved in genetic manipulation to modify lignin and hemicellulose content for improved fibre extraction for industrial use and as a resource for biofuel production. In terms of plant defence, the focus has been on the apoplastic oxidative burst and data from the lab supports a peroxidase-dependent mechanism which is crucial to basal resistance. They have also collaborated with the Bramley and Fraser group on engineering flavonoid antioxidant content in tomato fruit.

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Research Area Plant biochemistry and molecular biology

Research Activities

Carotenoids are a group of major plant pigments responsible for most of the yellow to red colours of flowers, fruits and vegetables. In the diet they act as powerful antioxidants and are believed to protect the body against free radical attack and hence reduce the incidence of cataracts, heart disease and certain cancers.
To try and increase the dietary intake of these beneficial compounds, the Bramley laboratory are utilising biochemical and molecular biology techniques to dissect the carotenoid biosynthesis pathway in tomatoes. The knowledge gained by these studies will then be used to manipulate cartenoid levels in fruit and vegetables.

Spotlight on Royal Holloway - University of London

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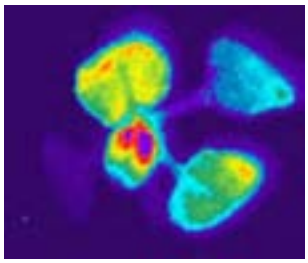
Research Area Signal perception and transduction in plants

Research Activities

Plants react to microbial infection with a broad range of defence responses aimed at restricting the growth of the pathogen and ultimately destroying it. Dewi's laboratory is interested in the mechanism by which plants perceive pathogens and the subsequent events which trigger a set of general defence reactions such as the reinforcement of the cell wall, synthesis of anti-microbial proteins and the production of phytoalexins. The Davies lab uses a model system, the treatment of suspension-cultured French bean cells with elicitor macromolecules extracted from the cell walls of the bean pathogen *Colletotrichum lindemuthianum*. They are particularly interested in the role of hydrogen peroxide and enzyme phosphorylation in response to fungal elicitors.



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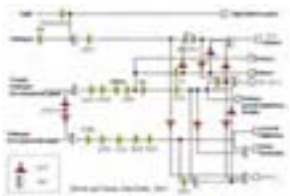
Research Area Light signalling

Research Activities

In order to modulate their growth and development plants need to perceive and respond to their surrounding light environment. One way plants sense light is via the red light-absorbing photoreceptor, phytochrome. Phytochromes play key roles throughout the lifecycle of plants, from seed germination to architecture of the mature plant and the onset of reproduction. To help us gain a better understanding of how phytochromes function, the Devlin laboratory is investigating phytochrome signalling pathways involved in two key responses in adult plants; the daily entrainment of circadian clock and the shade avoidance response. The group is also part of a collaboration carrying out a molecular analysis of plant microbe interactions on the leaf surface.



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Research Area Hormone perception and stress signalling in plants

Research Activities

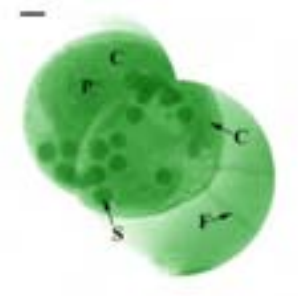
Plant growth, and therefore yield, is strongly dependent on both genetic and environmental conditions. It is frequently observed that stresses not only induce plant resistance but also affect growth rate and cell division. The external signals that predicate stress act not only on proteins that are involved in cell division, but also trigger a response in differentiated tissue, and in some way this response is then coupled to the regulation of the cell cycle. Jasmonate production can be considered as a 'switch' that, when triggered, acts to reprogram plant metabolism, growth and development.
The Devoto group aims to understand the link between jasmonate signalling and the cell cycle. By utilising genomic-wide studies such as transcriptomics and metabolomics, researchers in the lab are constructing complex high order gene regulatory networks related to plant stresses and hormones. These networks can then be used to identify/predict novel/unknown genes in the pathway. The group are also involved in engineering plants for jasmonate-mediated production of secondary products such as drugs and fragrances.

Name Paul Fraser
e-mail p.fraser@rhul.ac.uk
Website http://www.rhul.ac.uk/biological-sciences/AcademicStaff/Fraser/
Research Area Genetic engineering for crop improvement

Research Activities

Plant based research interests in the Fraser group includes biosynthesis, regulation and manipulation of health-promoting phytochemicals. Isoprenoids, especially high-value carotenoids, are of particular interest. Metabolite profiling/metabolomics, proteomics and quantitative gene expression techniques are being used to identify and characterise these nutritionally enhanced traits, generated both by GM and non-GM approaches.

Spotlight on Royal Holloway - University of London



Name Tom Ford
e-mail t.ford@rhul.ac.uk
Website http://www.rhul.ac.uk/Biological-Sciences/AcademicStaff/Ford/
Research Area Plant physiology

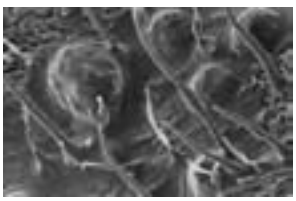
Research Activities

Current research in the Ford laboratory is concerned with physiological and biochemical studies on algae from extreme environments, especially in relation to possible survival mechanisms. Tom's work is particularly concerned with thermophilic algae. The alga *Cyanidium caldarium*, the most thermophilic, photosynthetic eukaryote, is being examined to identify the component(s) responsible for dictating the maximum temperature for growth. Their research is particularly focussed on the components of the photosynthetic electron transport chain. Researchers in the lab are also developing novel biological applications of X-ray imaging. Soft X-ray contact microscopy (SXCM) using soft X-rays in the so-called 'water window' (2.3-4.4nm) has the potential to improve upon electron microscopy in the analysis of the fine structure of algal cells by allowing whole live cell imaging. SXCM also makes possible studies on the 3D spatial organization.

Name Alan Gange
e-mail a.gange@rhul.ac.uk
Website http://www.rhul.ac.uk/biological-sciences/AcademicStaff/Gange/
Research Area Plant microbe interactions

Research Activities

Alan's studies concentrate on the interactions between mycorrhizal and endophytic fungi, plants and insects. The group is also investigating the relationship between soil microbial diversity and vascular plant diversity in natural and managed plant communities. Applications involve the conservation of rare plants and insects, and biological weed and disease control in sports turf.



Name Julia Koricheva
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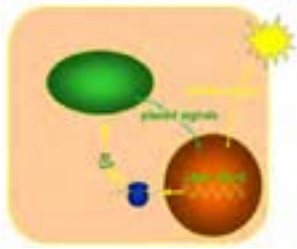
Website http://www.rhul.ac.uk/biological-sciences/AcademicStaff/Koricheva/
Research Area Plant-herbivore interactions

Research Activities

The work in Julia's group centres on plant chemical and mechanical defences against herbivores. Her work also concerns biodiversity and ecosystem functioning, particularly the effects of forest diversity on herbivores. The Koricheva lab uses meta-analysis and research synthesis and is particularly interested in publication and related biases in ecology.



Name Enrique Lopez-Juez
e-mail e.lopez@rhul.ac.uk
Website http://www.rhul.ac.uk/Biological-Sciences/AcademicStaff/Lopez-Juez/
Research Area Photosynthetic development

Research Activities

Enrique's work focuses on the molecular genetics of light control of chloroplast and leaf development in Arabidopsis thaliana, and of plastid development in tomato fruit. The Lopez-Juez lab is interested in light control of photosynthetic gene expression. They and others have shown that this light control closely relates to chloroplast-to-nucleus communication signals regulating the same genes. They have obtained some of the first evidence on the tetrapyrrole nature of one class of such 'plastid signals'. Researchers in the group are also exploiting the fact that leaf development is dependent on the 'light switch' to search for basic mechanisms of chloroplast and leaf differentiation.

Name Tony Stead
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Website http://www.rhul.ac.uk/Biological-Sciences/AcademicStaff/Stead/
Research Area Post-harvest physiology and the molecular control of senescence in plants.

Research Activities

The death of some species of flowers appears to be regulated by ethylene and, if the petals wilt prior to abscising, the process may resemble programmed cell death (PCD). Tony's lab has generated several RNAi lines in Petunia showing down regulation of genes believed to be PCD-related and is investigating the consequences of this on gene expression using their own oligo-based array comprising >5000 floral genes. In comparison, their previous studies in *Alstroemeria*, again using their own array (cDNA), have identified several genes that appear critical in the control of petal inrolling; an ethylene-insensitive process. They are now comparing gene expression in long and short-lived varieties, between those treated with or without floral preservatives and in different tissues of the same petal. Concurrently the Stead lab is improving the composition and use of floral preservatives to provide the consumer with long-lived flowers. They are also developing diagnostic tools to detect floral quality (pre- and post-harvest) and to predict potential vase-life; it is believed that these techniques could have wide applicability with leafy vegetables and fruit too.

Arabidopsis Resources

VirtualPlant:
A software platform to support Systems Biology research in the post-genomic era.

http://www.virtualplant.org

Manpreet S. Katari[1], Felipe F. Aceituno [2], Steve D. Nowicki[1], Dennis E. Shasha[3], Gloria M. Coruzzi[1] and Rodrigo A. Gutiérrez[1, 2,*].

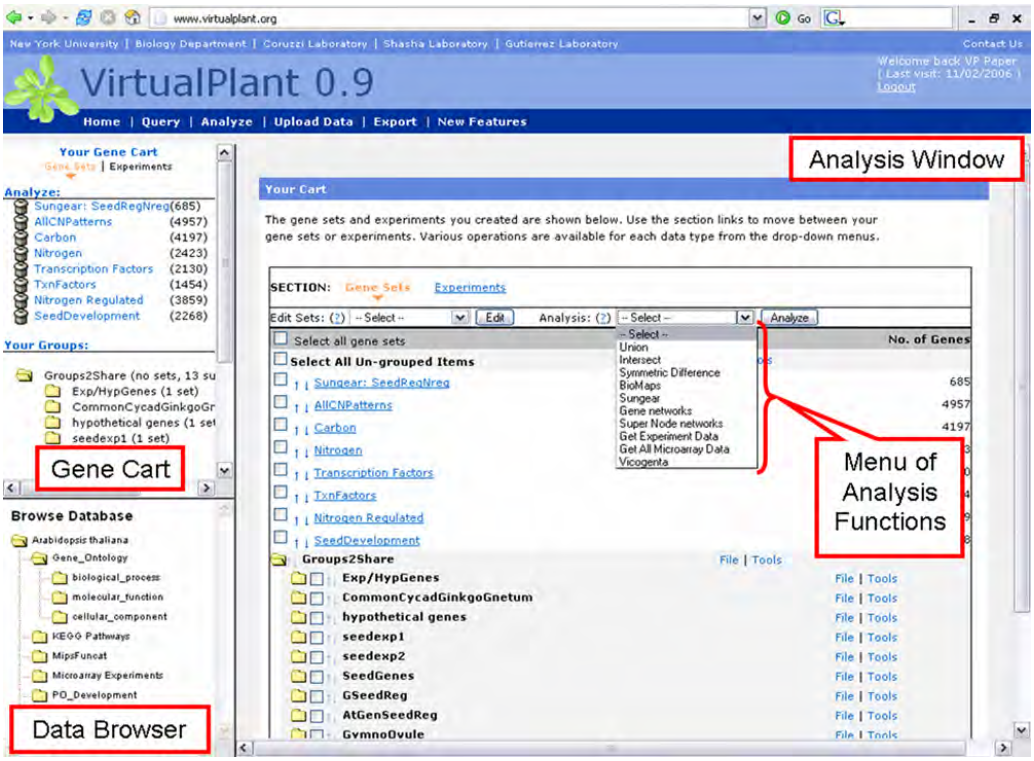
1. Department of Biology, New York University. 2. Departamento de Genética Molecular y Microbiología. P. Universidad Católica de Chile.

*3. Courant Institute of Mathematical Sciences, New York University. *To whom correspondence should be addressed: rgutierrez@bio.puc.cl*

There is a growing need for visualization and analysis tools for rapid and efficient exploration of genomic data. The goal of VirtualPlant is to provide these tools and thereby to help researchers generate biological hypotheses. To achieve this goal, we start by integrating genome-wide data concerning the known relationships among genes, proteins and molecules (extracted from public databases and/or generated with predictive algorithms), as well as experimental measurements under many different treatments. We provide mathematical and statistical methods to help summarize and quantify the data. We also provide novel visualization techniques to render the megabytes of experimental data in visual formats that facilitate inference of biological concepts. We implement and combine these approaches in a user-friendly software system we term "VirtualPlant". VirtualPlant has been designed using the familiar paradigms of an e-commerce site. By adding gene sets to a “cart”, users can perform a number of “checkout” functions. These functions are the various data analysis and visualization tools. Most checkout functions allow the user to send the results of the analysis back to the cart for further processing.

The current version of the VirtualPlant database includes:

- TAIR Arabidopsis genome annotation version 6
- Gene Ontology terms and their association to Arabidopsis genes
- MIPS functional categories and their association to Arabidopsis genes.
- Affymetrix probes for Arabidopsis AG and ATH1 chips and their association to Arabidopsis genes from TAIR.
- Biochemical Pathways, including enzymes, reactions, and small molecules from the KEGG database.
- Protein interaction data from the BIND database.
- Regulatory interaction data from the AGRIS database.
- Expression data from the NASC database.



All microarray experiments were normalized in “R” using the RMA package. Normalized and pair-wise correlation values are stored in the VirtualPlant database and available to users through the “checkout” functions of the Gene Cart or in the probe detail pages.

Below is a list of some of the tools available through VirtualPlant:

- **Query**

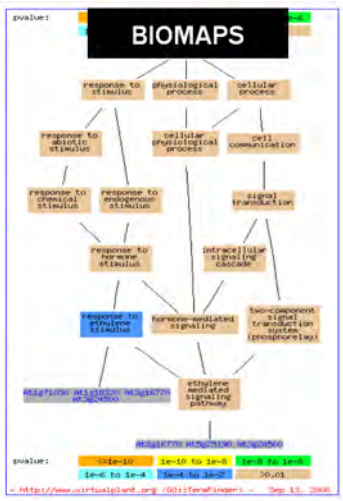
Users can search the VirtualPlant database using keywords or known identifiers (e.g. gene locus, probe id). Our search engine supports Boolean queries. The user can also restrict the search to specific data types (e.g. genes, microarray experiments, enzymes and GO terms).

- **Set Operations**

We support the set operations union, intersect, and symmetric difference. All set operations can be simultaneously performed on 2 or more sets. Sets can also be renamed, deleted, or assigned to a “group”. Groups behave like folders in the Windows operating system. Groups can hold gene sets, experiments or other Groups. Thus, Groups allow the user to organize their data sets in VirtualPlant in a personalized fashion

- **BioMaps**

BioMaps takes one or more set of genes and analyzes the functional terms (GO or MIPS functional terms) associated to the genes in each set. BioMaps determines which functional terms are statistically over-represented as compared to a background population (e.g. Arabidopsis genome). BioMaps presents a graphical output that shows over-represented GO terms as color-coded nodes in a graph, with the relevant genes attached to them. In addition, a table is provided (not pictured), listing the GO terms that are over-represented and the genes annotated to this term. These genes can be added to the gene cart. A p-value cut-off can be set to determine which GO terms are significant, and different annotations can be used (e.g. MIPS funcat, Gene Ontology). This is a very useful tool to made a quick survey of the function(s) of a set of genes of interest.



Arabidopsis Resources

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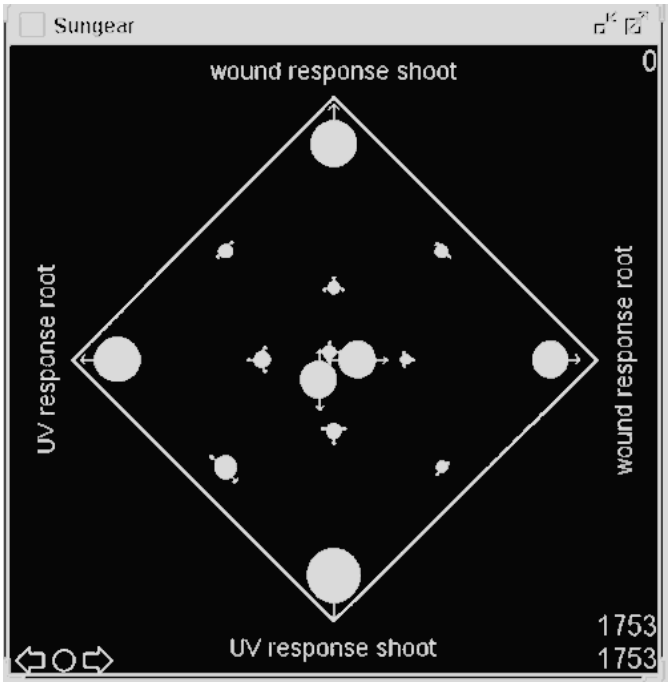
http://www.virtualplant.org

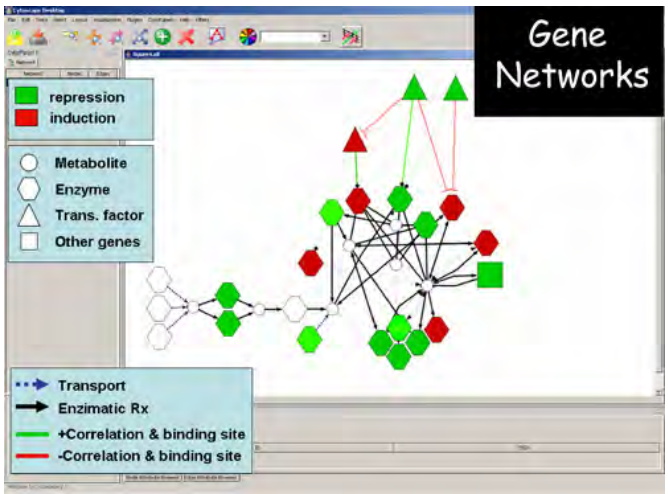
- **Sungear**

Many software tools are available to analyze genomic data and other large data sets, but no existing tool supports a rapid, visually interactive and biologist-driven exploration of standard questions on many experiments at a genomic scale. Sungear can represent an arbitrary number of experiments/lists. The experiment names are listed around the vertices of a polygon, and these names are linked to the list of genes in that experiment (e.g. regulated genes from a microarray experiment). A circle within the polygon with arrows pointing to one or more vertices indicates the number of genes associated to one or more lists. The size of a circle is proportional to the number of genes and the location of the circle vessel within the polygon is largely determined by the position of the vertices with which it is associated. As an example, the figure shows the use of Sungear to represent regulated genes from selected microarray experiments from the AtGenExpress project. The circle closest to the label "UV response shoot" corresponds to those genes that are regulated in only the "UV response shoot" experiment. Circles with two or more arrows correspond to intersections between the corresponding experiments. Simple mouse-click operations executed within the Sungear window enable the user to identify, for example, those genes whose responses are robust across a series of microarray experiments (the genes corresponding to the center circle), while linked GO annotation features (not pictured) help the user to determine which experiments influence which functionalities. Sungear can be used with other data sets, for example to compare entire genomes to uncover the patterns of conservation of gene function across the tree of life.



- **Gene Networks**

Gene Networks analysis allows the user to query one or more gene lists for known and predicted interactions between the corresponding gene products. Our current network data consists of metabolic interactions (from KEGG and AraCyc), protein interaction data from BIND, regulatory interactions from AGRIS, Transfac, and extracted from the published literature with the Geneways software (a text mining tool), and gene expression correlation across microarray experiments. We also included predicted protein-protein interaction data based on homology to proteins that interact in other organisms (Interologs) and predicted regulatory interactions based on transcription factor binding sites over-represented in the promoter regions of putative targets. The network data is displayed to the user in the *Cytoscape (www.cytoscape.org)* software.



- **Supernode Networks**

This tool groups nodes from networks generated with the "Gene Networks" tool based on function (GO or KEGG associations) and/or annotation. Each group is represented by one node in the supernode network. The interactions between the original nodes are retained and displayed as interactions between the nodes in the supernode network. Supernode networks simplify complex gene networks, often obtained when querying our network model with a long list of genes.

- **Microarray Experiments**

Users can perform basic statistical analysis to determine differentially expressed genes on publicly available microarray experiments that have been normalized using RMA. Users can also upload their own Affymetrix CEL files for analysis. Our microarray tools allow the user to rapidly create lists of genes that are stored in the gene cart and available for data analysis with other tools from the VirtualPlant system.

Final remarks

VirtualPlant allows experimental biologists to view their data in the context of selected genomic data with a few mouse clicks. We hope VirtualPlant becomes a worldwide resource, assisting researchers to build hypotheses which they can test experimentally. VirtualPlant allows for rapid and easy integration of new data analysis tools. If you would like your tool to be added to the VirtualPlant toolbox, do not hesitate to contact us.

The 18th International Conference on Arabidopsis Research

Beijing, China

June 20-23, 2007

www.Arabidopsis2007.com

The 18th International Conference will be held in Beijing, China, marking the first time the annual meeting will be held in an Asian country. In addition to presentations of significant and innovative Arabidopsis-based research, the conference will include discussions of other relevant plant systems throughout most of the sessions. This complementary approach, initially allocated one special session during the 2004 Berlin ICAR, will emphasize the importance and usefulness of Arabidopsis as the reference plant and its impact on other systems.

The meeting will be held at the Jiuhua Spa and Resort, a comprehensive deluxe resort located on the grounds of the ancient Qing and Ming dynasties on the outskirts of the lively international city of Beijing. The Resort is arranged around numerous natural hot springs and provides a variety of on-site recreation, entertainment and fitness-related activities, as well as dozens of restaurants serving a diverse assortment of Chinese regional cuisines.

Session Topics Include:

Developmental mechanisms Genomics and genetics**Plant responses to the environment
Plant responses to microbial organisms Signal transduction**Cell biology**Metabolism/Bioenergy

Preliminary Confirmed Speakers:

Klaus Apel	Bonnie Bartel	David Baulcombe	Philip Benfey	Ton Bisseling
Harro Bouwmeester	Judy Callis	James Carrington	Sudip Chattopadhyay	Joanne Chory
Gloria Coruzzi	George Coupland	Caroline Dean	Joe Ecker	David Ehrhardt
Mark Estelle	Ken Feldmann	Geoffrey Fincher	Ueli Grossniklaus	Wilhelm Gruissem
Mary Lou Guerinot	Christian Hardtke	Barbara Hohn	Roger Innes	Steve Jacobsen
Jonathan Jones	Gerd Jurgens	Tatsuo Kakimoto	Maarten Koornneef	Clark Lagarias
Bill Lucas	Rob Martienssen	Makoto Matsuoka	Elliot Meyerowitz	Todd Mockler
Hong Gil Nam	Kiyotaka Okada	Jane Parker	Ben Scheres	John Schiefelbein
Peter Shaw	Ko Shimamoto	Kazuo Shinozaki	Ken Shirasu	Neelima Sinha
Chris Somerville	Shauna Somerville	Richard Vierstra		

Important Deadlines

Early/Discounted Registration	**March 20, 2007**
Hotel Registration	**May 1, 2007**

Registration Fees

The registration fee includes one abstract submission, admission to all conference sessions and exhibitions, an invitation to the Reception Dinner, three meals for each of the three conference days, coffee breaks, an invitation to the Conference Dinner and Farewell Party, Conference bag and materials), final program and copies of the Abstract book. Publication of your abstract will be guaranteed upon receipt of your registration fee. The registration fee does not include room cost.

Important Visa information

Valid visas are required to enter China. An official invitation letter will be issued to those who have returned the final Registration Form. With this letter, you can go to the nearest Chinese Embassy or Consulate to apply for entry visa(s). To allow ample time to secure visas you should register by the early deadline.

Workshop information

As for past conferences, rooms will be provided for each of the three evenings of June 20, 21 and 22, from 8:00pm-11:00pm, for selected self-organized workshops. Those who are interested in organizing a workshop should first contact Joanna Friesner (MASC Coordinator, jdfriesner@stanford.edu or jdfriesner@ucdavis.edu) with a topic title and tentative speaker list.

For the most current Conference information, please see the conference website:
www.arabidopsis2007.com

SEB at Glasgow 2007

The Scottish Exhibition and Conference Centre, 31 March - 4 April 2007

CROSS-SECTIONAL SESSION

Aging and Oxidants - Cross Sectional Session

ANIMAL

In vitro Techniques for Invertebrate and Piscine Physiological and Ecotoxicological Studies (JOINT ANIMAL/CELL/EDUCATION)

Integrating Animal Physiology and Behaviour: towards ecological relevance and animal welfare

Drinking, Salt and Osmoregulation

It's All a Matter of Taste

Membrane Traffic at the Synapse in Health and Disease

General Biomechanics

Biomimetics and Biomechanics: smart solutions from nature

Surfaces to Biomimetics: a Tribute to Jon Barnes

Freeze Tolerance in Animals

Integrative Red Blood Cell Functions: oxygen sensing and regulation of local blood flow

Cardiac Adaptations to Temperature Change

General Animal Biology

PLANT

Symbiosis

Photomorphogenesis

Transport of Growth Regulators

Nutritional Genomics

Redox Signals and Plant Stress

Developments in Plant Biology

CELL

General Cell Biology (RMS)

Programmed Cell Death

Beneficial Acclimation: how do physiological responses to temperature contribute to fitness?

Cardiovascular Control of Cellular Regulation

General Thermobiology

EDUCATION

Identifying & Selling Your Skills

Getting Popular Science Published

European Funding Fellowships

Effective Research Presentation

Women in Science Dinner

Getting Science To The Wider Public

CV Workshop

REGISTRATION

Early registration from 06-08-2006 to 09-02-2007
Late Registration from 10-02-2007 to 16-03-2007
£50 Discount for Early Registration

ABSTRACT SUBMISSION

Online Submission Closes 12/01/07

www.sebiology.org