

GARNish

The official GARNet newsletter



GARNet 2006 Plant Networks

In this issue

ACT, eFP Browser, EPSO Updates and Data Sharing
Spotlight on Sheffield, Southampton, St.Andrews and Sussex

2006 so far

Welcome, to this, the 5th issue of GARNish. So far 2006 has been an event packed and productive year for GARNet. At the start of 2006 we welcomed 3 newly elected members to the committee; Brendan Davies (University of Leeds), Paul Dupree (University of Cambridge) and Zoe Wilson (University of Nottingham). However, this sadly meant we had to say goodbye, with many thanks for all their efforts to two long standing members; Phil Gilmartin and Keith Lindsey.

January saw the submission of GARNet's interim report on UK Arabidopsis Systems Biology to the BBSRC's Integrative Systems Biology Panel (http://garnet.arabidopsis.info/interim_psb_report.pdf). This outlined GARNet's recommendations for strengthening the Arabidopsis research base in order to make the best progress in this area. To ensure the community were able to contribute to this report, GARNet held two town hall meetings, open to all, during the New Phytologist Meeting in London in January and the SEB Canterbury Meeting in March. Thanks to all of you that contributed at these gatherings.

After the success of last year's 'Succeeding in Plant Systems Biology' workshop we were encouraged to hold a follow up meeting to help facilitate interactions between mathematicians, modellers, plant researchers and crop scientists. So in collaboration with Sid Thomas, Helen Ougham and Alan Gay of IGER, GARNet hosted an 'Interfacing Systems Biology with Crop and Ecosystem Modelling' workshop in Swindon in March. A report on this workshop will soon be available on the download section of the GARNet website.

The second half of 2006 looks like it will as jam packed as the first, with the GARNet annual meeting in September and a plant and crop science interaction meeting at Rothamsted in October. Visit the website for more information and updates. <http://garnet.arabidopsis.info>

Hope you all have an enjoyable summer.
Ruth

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Many thanks to all who contributed to this issue of GARNish, especially Paul Quick, Tim Flowers, Alyson Tobin and all at Southampton who helped provide the information for the UK Plant Science articles.

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

New Centres for Integrative Systems Biology: Edinburgh, Oxford and Nottingham

Three new centres for integrative systems biology, representing an investment of £27M, were announced in April 2006 by BBSRC. This funding includes £4.8M from the Engineering and Physical Sciences Research Council (EPSRC), underlining the requirement for multidisciplinary research that brings together biologists, mathematicians and computer scientists (see GARNish 4 Dec 2006 for an outline of systems biology). The new centres will be located at the Universities of Edinburgh, Nottingham and Oxford, with additional input from collaborating institutions. Their research will focus specifically on: dynamic biological systems, such as biological clocks (Edinburgh), the nature and behaviour of plant roots (Nottingham) and signalling pathways in bacteria and yeast (Oxford). They will combine experimentation with mathematical modelling in order to process experimental results, design new experiments and to identify principles of biological organisation that are widely applicable. Each centre is expected to compete for research project funding to supplement the 5-year CISB award.

Professor Julia Goodfellow, BBSRC Chief Executive, said: "The landscape in biology is changing. It is exciting to see these three new centres joining the three we launched last year, at Imperial College, Manchester and Newcastle, as they successfully bed in. As the biological sciences become increasingly quantitative and predictive it is important that we see modern biologists as anyone tackling a biological question; be they computer scientists, mathematicians, statisticians or life scientists. These new centres, and the investment in integrative systems biology that they represent, reflect BBSRC's vision of an increasing multidisciplinary bioscience base where different university departments work together, regardless of the name above the door." Further BBSRC press releases on CISB can be found at http://www.bbsrc.ac.uk/media/pressreleases/06_04_20_sysbio.html.

Centres are becoming prominent features of the systems biology landscape in the UK. The six BBSRC-funded centres join other multidisciplinary programmes, such as the CoMPLEX at University College London and the Warwick Systems Biology Centre. UCL and Warwick, together with the Oxford, were awarded Doctoral Training Centres in Systems Biology earlier this year, from a programme led by the EPSRC Life Sciences Interface with partial funding from BBSRC. Each Centre will train around 30 PhDs.

Organisation as a Centre is intended to facilitate the constant collaboration among researchers of many different disciplines, which is a defining feature of Systems Biology. The current investment in the centres should also help to develop systems biology in other institutions, through additional research collaborations and new resources, in addition to PhD training. The Edinburgh centre, for example, will develop theoretical methods for building models of biological processes, together with a large-scale informatics system that integrates diverse data with models: these are relevant for many systems biology projects. The Nottingham centre will generate new biological resources, including polyclonal antibodies to specific plant proteins involved in hormone regulation and cell growth. Systems biology projects in the Arabidopsis community could soon look to build upon the Centre funding. The next £30M of BBSRC/EPSRC funding for systems biology will not fund additional centres, so project funding could be centre-stage.

Some centre web links:

Edinburgh: <http://csbe.bio.ed.ac.uk/>
Imperial: <http://www.doc.ic.ac.uk/bioinformatics/CISB/>
Manchester: <http://www.mib.ac.uk/>
Nottingham: <http://cpib.eu/>
Warwick: <http://www2.warwick.ac.uk/fac/sci/systemsbiology/>
UCL: <http://www.ucl.ac.uk/CoMPLEX/>



<http://cpib.eu/>

News and Views

Opportunities For Crop Science Research in the 21st Century



The genomic era was founded on the study of a limited number of model organisms that were chosen for their small genome size and experimental tractability. The use of model organisms can be powerful because a community of scientists can work collectively on a single organism, but it also encourages a reductionist approach. Intriguingly, the study of diversity and organism complexity is now gaining more prominence. The mapping of a large number of crop expressed sequence tags (ESTs), physical mapping of crop genomes, studies of synteny and studies of the organisation of sequence polymorphisms into haplotypes are major steps in elevating the biological accessibility of crops to modern scientific investigation. These developments in crop genomics vividly illustrate how model organisms provide good starting points, but their role may change as accessibility to genome technologies improves and the social and biological relevance of crop science to funding agencies and the public continues to gain prominence.

It is becoming clear that the distinction between model and crop plants is likely to become blurred as the benefits of public investment in crop genomics becomes more evident. The reality is, however, that opportunities will continue to exist at the interface between model and crop species, where perceived boundaries are rapidly disappearing. Crops offer notable advantages when compared with model organisms, including the extensive monitoring and archiving of genotypes and associated phenotype

data that has already been done and the fact that selective breeding has created unique populations adapted to various environmental conditions. These advantages will become more evident as we enter the post-genomic era. The challenge, therefore, is to synchronize and integrate basic plant science with crop-orientated research to enhance synergy and maximise opportunities for improving crop productivity. We also need to inspire young researchers to embrace the new global opportunities for crop science that are complementary to the outstanding basic plant science being conducted in the UK and elsewhere. This is based on article 'Unfashionable Crop Species Flourish in the 21st Century'. Wayne Powell and Peter Langridge, *Genome Biology* 2004,5:233.

written by Professor Wayne Powell, CEO and Director, NIAB, Huntingdon Road, Cambridge, UK CB3 0LE

Gatsby Plants

written by Celia Knight, Centre for Plant Sciences, University of Leeds

Undergraduate interest in plant science has reached a new critical low; with so few students being motivated to study plants that some Universities no longer offer a separate Plant Science degree. This raises the question "where is the next generation of British plant science researchers going to come from?"

In response to this, the Gatsby Charitable Foundation has set up Gatsby Plants to:

- Inspire 1st year undergraduates to choose plant-based courses through an annual summer school.
- Support research academics in their teaching via a web-based teaching resource.

The annual Summer School brings together 100 high-achieving 1st year undergraduates with leaders in the field of plant science research. In the relaxed setting of Bretton Hall, Wakefield, students are challenged with new ways of thinking about plants.

To find out more about this year's Summer School, you can visit the website at <http://www.gatsbyplants.leeds.ac.uk> or if you are interested in getting involved as a tutor contact Juliet Jopson on S.J.Jopson@leeds.ac.uk or 0113 343 2816.



Gatsby Plants is also involved in setting up an on-line teaching resource to help support academics in providing inspiring plant science teaching. Ultimately the resource aims to supply a mix of teaching ideas, images, movies, and practical protocols, to name but a few of the possibilities.

The project is currently in its pilot stage and is looking for people to get involved in a series of national discussion meetings to generate material for the web site and make sure that the resource works for you the lecturer. If you are interested to get involved in the discussion meetings or have ideas or teaching material you would be prepared to share, please contact Dr Aurora Levesley, a.levesley@leeds.ac.uk or 0113 343 7676.

Brassica Affymetrix Gene Chip

During 2006 Affymetrix plans to design and make available a Brassica GeneChip® under the Affymetrix GeneChip® Consortia Program (<http://www.affymetrix.com/community/research/consortia.affx>). Designs for the Consortia program are selected based on community support for creating a GeneChip array, availability of sequence information, and market demand for the finished array. Following a meeting at the Plant Animal Genome Meeting in San Diego with representatives of the Multinational Brassica Genome Project, Affymetrix released a White Paper, and are currently assessing the status of available Brassica EST sequences. More information, including the white paper, is available at <http://www.brassica.info/genechip/genechip1.htm>.



Arabidopsis Resources

Arabidopsis Co-expression Tools - analysis of a database of microarray results

www.arabidopsis.leeds.ac.uk/ACT

written by Iain Manfield, Centre for Plant Sciences, University of Leeds

There are large bodies of microarray data such as those provided by NASC, which contain information on the concerted changes in gene expression levels for thousands of genes in the Arabidopsis genome. When these data sets are used en masse they can provide the community with additional information, beyond that envisaged by the original investigator. To help users access this 'hidden' information the Arabidopsis Co-expression Tool analyses the data available from Affymetrix array experiments to produce a list of genes, ranked with respect to how closely their expression correlates with that of a gene of interest. This approach can identify groups of genes whose expression is regulated in a similar manner or whose products act in concert. The ACT set of tools may be generally useful for integration of genes into groups with coherent behaviour.

The starting point for most users will be with the Keyword Search tool which reports a list of genes likely to be of interest. This list gives the Affymetrix probe IDs for each gene which links to a pre-calculated co-expression list of the 50 genes showing the best correlation of expression with the query gene (see an example opposite). Individual specialist knowledge may reveal a theme to the annotations. Word- and GO-counting tools are being developed to provide a statistical assessment of the significance of any perceived over-representation of terms.

Although ACT gives measures of the statistical significance of the observed correlations, it is generally not clear how these numbers can be used routinely as cut-offs or thresholds of biological significance. However,

calculation of co-expression results from a user-selected set of experiments and arrays can provide corroboration of biological significance for genes highly-ranked on both the pre-calculated results (from 8K or 22K arrays) and your user-selected lists.

While users can download the co-expression list for all 21 891 genes in our database, visualisation of this output is more usefully done with the Co-correlation Scatter Plot tool; plots the *r*-values for all genes against each of the two query genes (see example opposite, red squares). Empirical *r*-value cut-offs are suggested by islands of isolated symbols or by highlighting "guide genes" with known biology on these graphs. This tool can also be used to compare the expression patterns of, for example, genes encoding enzymes of a biochemical pathway (e.g. Calvin cycle, green squares) to distinguish those genes showing behaviour similar to the query or guide genes from those with differing behaviour and therefore likely to be regulated differently. In the example opposite, only some of the PGK genes show strong correlation of expression with the two light-regulated, Calvin cycle query genes and other genes of the pathway highlighted on the scatter plot.

In contrast, another tool, called Clique Finder, uses an algorithm more complex than simply employing an *r*-value cut-off to objectively identify the sets of genes which are consistently co-expressed with each other. This discriminates an ACT list into groups of genes which are likely to be regulated in different manners. Inclusion of guide genes in a cluster gives confidence in the correct inclusion of other genes, including unannotated ones.

These tools provide shortlists of genes for further analysis such as promoter motif over-representation (e.g. at TAIR or Motif Sampler) or expression analysis (e.g. using the Genevestigator Meta-Analyzer function). Observing similar properties for a set of genes can give confidence in the likely significance of any over-represented motif or expression pattern which can be followed up experimentally. ACT will therefore be valuable for function prediction for the many unannotated and poorly-characterised genes of Arabidopsis. Furthermore, by identifying sets of genes with coherent behaviour, ACT should be useful for integrating large numbers of genes into regulatory and signalling networks and systems.

YOUR QUERY GENE - e.g. RuBisCO

Affymetrix Probe IDs.

Click here for ACT list with this gene as query

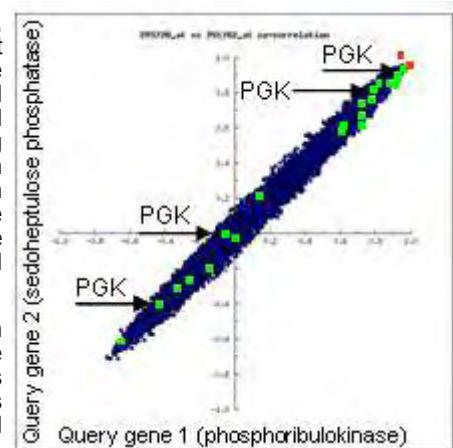
R-value correlation coefficient

Measures of statistical significance

AGI codes

Click here for information from TAIR

Genes for components of the photosynthetic apparatus are co-expressed ... with unannotated genes



Arabidopsis Resources

Arabidopsis eFP Browser

<http://bbc.botany.utoronto.ca/efp/>

written by Ben Vinegar and Nicholas Provart, University of Toronto.

The Arabidopsis electronic Fluorescent Protein, or eFP, Browser is a web-based application that permits intuitive visualization of gene expression data across approximately 22,000 genes from Arabidopsis thaliana. The user is presented with an idealized image of the Arabidopsis whereby plant tissues are coloured according to the expression level of the user's gene of interest. The tool is intended as a quick and easy means of identifying tissues of interest, and is particularly useful when exploring gene families. The eFP Browser takes AGI gene identifiers as input, and provides three basic interpretive modes – absolute, median and comparison. In the absolute mode, the expression level for a user's gene in each tissue is compared relative to the highest signal recorded for the given gene, with low levels of expression coloured yellow and high levels coloured red (see Figure 1).

The median mode colours tissues with expression levels above the median signal between yellow and red, and expression levels below the median between yellow and blue (see Figure 2). Lastly, the comparison mode takes two gene identifiers as input and compares expression levels of those two genes in every tissue, using the same colour scheme described above. This is useful for identifying tissues in which one gene is more abundantly expressed relative to another. A dynamically generated colour legend located in the bottom-left corner of the image helps users match colours to their corresponding signal values.

An optional signal threshold allows users to place an arbitrary bounds on the colour scale. Signal values at or above this threshold are coloured equally with maximum intensity. Since there are a finite number of colours available, specifying a low threshold will assign a greater number of colours to low signal values, making colour changes between them more easily distinguishable. This is useful for genes with a wide range of expression levels, where significant changes in expression between tissues might correspond to only a small change in colour.

In all three modes, each part of the “plant” is clickable, linking to the NASCArrays entry for the a given sample. Gene expression data were obtained from Schmid et al.'s Gene Expression Map of Arabidopsis Development (2005, Nature Genetics 37:501-6), and we mirror these data in the Botany Array Resource (Toufighi et al., 2005, Plant J. 43:153-63) for quicker access. Affymetrix ATH1 probe set to AGI identifier lookup is via a table provided by TAIR, called `affy25k_array_elements-2006-01-06.txt`. The information that tells the eFP Browser which part of the image corresponds to which tissue sample is stored in an XML file, while the browser itself is coded in Python. We would like to thank the Weigel Lab at the Max Planck Institute for generating the original expression data used by the browser, and also for their helpful feedback. Thanks also to Jeff Alls for his line drawings of Arabidopsis.

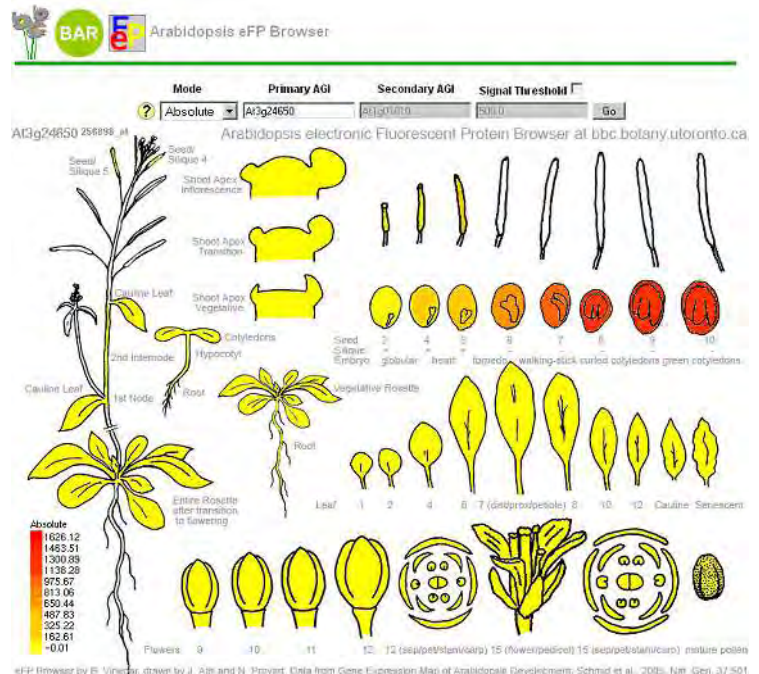


Figure 1 – Example eFP output for ABI3 (At3g24650) in the absolute mode, showing strong expression in Stage 8-10 seeds.

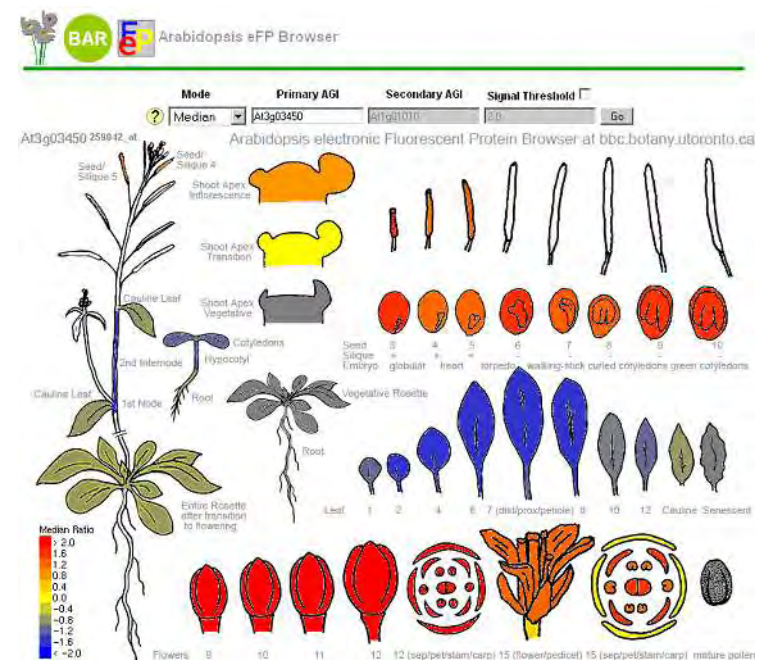


Figure 2 – RGL2 (At3g03450) median expression, showing expression levels higher than the median level of expression of RGL2 in seeds and flowers. Both areas for RGL2 expression have been described in the literature.



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, GARNish is focusing on geographic areas and institutions across the UK, bringing you a synopsis of the interests of each research group within the chosen location(s).



University of Sheffield

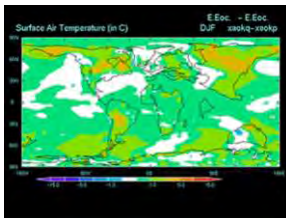
Plant Science in Sheffield comprises groups both in the Department of Animal and Plant Sciences and the Department of Molecular Biology and Biotechnology, both RAE 5* rated. Research covers a broad spectrum of topics, from molecular and genomic approaches in Arabidopsis, through studies of plant evolution, ecology, biochemistry, development, physiology and pathology, up to global scale analysis of carbon balance. Further details can be found at:

<http://www.shef.ac.uk/aps/>
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 Research Area Palaeobiology

Research Activities

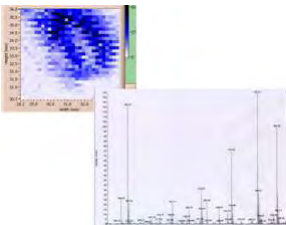
Research in the Beerling group focuses on: biogeochemical interactions between the terrestrial biosphere, atmosphere and climate across abrupt palaeoclimatic boundaries. Special emphasis is placed on global events at the Triassic-Jurassic (205 Myr ago), Cretaceous-Tertiary (65 Myr ago), and Palaeocene-Eocene (55 Myr ago) boundaries and during the Permo-Carboniferous (300 Myr ago) glaciation. Other subject areas under investigation include: experimental quantification of the effects of CO₂-rich atmosphere on the physiology and carbon balance of ancient polar forests. Development of 'Earth systems' approach to quantify the interaction between trace gas fluxes, particularly atmospheric CH₄ from terrestrial ecosystems and the chemistry of the palaeoatmosphere during ice ages and during the 'greenhouse' world of the Mesozoic. In addition the group is working towards gaining a better understanding of the controls on leaf habit of polar forests, through analyses of fossil woods, and Earth system modelling of the feedback of polar forests on climate during the Mesozoic 'greenhouse' world.



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 Research Area Carbohydrate metabolism

Research Activities

The main focus of Mike's research is to understand the control of carbohydrate metabolism in non photosynthetic storage organs such as tubers and seeds, in particular the synthesis of starch. Starch is one of the most important plant products used by man. It provides a large proportion of his calorific intake, it is important as a feedstock for farm animals and has diverse uses in industry such as food processing, papermaking and paints. Therefore both the quality (type and uniformity) and quantity of starch are important. The Burrell laboratory have produced a number of transgenic plants to investigate these traits and recently Mike has begun to use very sensitive Mass Spectrometry techniques to study the metabolism of these plants.



Name Terry Callaghan
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 Research Area Arctic environment

Research Activities

Research in the Callaghan group focuses on relationships between the arctic environment and the ecology of arctic plants and animals including ecosystem processes. The research has two components: (1) Understanding mechanisms of survival and adaptation to arctic environments, (2) Assessing the responses of organisms and ecosystems to changing environmental conditions such as climate, UV-B radiation and atmospheric CO₂ concentrations.



Name Andrew Fleming
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 Research Area Regulation of plant morphogenesis

Research Activities

Andrew's research is focussed on understanding the mechanism of plant morphogenesis. In particular, the group are interested in understanding the interplay of cell growth and division and how these parameters are integrated into the developmental program controlling leaf size and shape. Using techniques of cell and molecular biology, the group are testing hypotheses on the regulation of organogenesis. At the same time, these approaches provide functional data on gene products implicated in basic aspects of the plant cell cycle and the plant cell wall.



Focus on Sheffield



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 Research Area Signal transduction

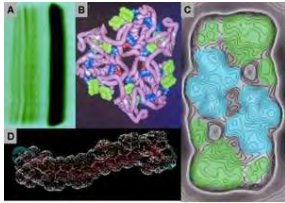
Research Activities

Julie's laboratory is focused on the use of molecular genetic techniques to investigate signal transduction pathways in plant cells. The group are particularly interested in pathways controlling stomatal aperture and development, NAD signalling and chloroplast cyclophilins.

Name Peter Horton
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 Research Area Photosynthesis in higher plants

Research Activities

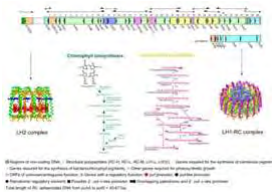
The central focus of research in the Horton lab is to understand the regulation of photosynthesis in higher plants. Photosynthesis is essential for the life of the plant and requires close regulation to prevent disruption by a number of factors including: large fluctuations in external environmental conditions, the differing states of development of the whole plant, optimum performance in terms of resource capture and avoidance of stress. Principally, the group are concerned with how plants respond to different light levels, particularly excess light. Research is multidisciplinary and aims to understand not only the molecular mechanisms involved but also how these are integrated into the growth and development of the whole plant. By gaining an understanding of these basic biological processes the group hope to apply this knowledge in the field to improve agricultural yield.



Name Neil Hunter
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 Research Area Biogenesis and function of photosynthetic membrane proteins

Research Activities

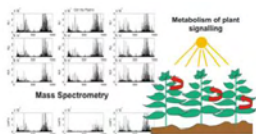
The Hunter laboratory studies the biogenesis and function of photosynthetic membrane proteins, including the biosynthesis of chlorophyll and carotenoid pigments, the assembly of the apoproteins, and the correlation of structural information with spectroscopic properties through the use of protein engineering.



Name Janice Lake
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 Research Area Plant ecophysiology

Research Activities

The main thrust of Janice's research is plant ecophysiology, focusing on physiological changes brought about by increasing carbon-dioxide levels, a topic of much political concern. Specifically looking at changes in stomatal numbers, due to increasing CO₂, Janice's research has led her to investigate biochemical signal transduction pathways in response to several major environmental variables; CO₂, light, mechanical wounding and pathogen attack. Recently, Janice has begun to use metabolomics approaches, such as mass spectrometry fingerprinting, to further investigate signal pathways in plants, and help bridge the gap between classical physiological measurements and genetic analyses of environmental responses. Research is also being undertaken to investigate differences between responses of the annual model plant *Arabidopsis thaliana* with that of perennial species *Carex caryophylla* to probe the functional significance of genetic diversity within populations using metabolomics and how life history impacts on responses to environment.



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 Research Area Carbon and nutrient cycling

Research Activities

Research in the Leake laboratory is centred on carbon and nutrient cycling processes in ecosystems and agro-ecosystems with particular emphasis on the role played by mycorrhizas (root-infecting symbiotic fungi). Jonathan's interests include the way in which carbon energy flow through mycorrhizal mycelium affects major ecosystem processes and nutrient cycles through weathering of rocks, pedogenesis and impacts on soil organisms including plants, fungi and animals. The research group has a particular interest in orchids and other myco-heterotrophs (plants which obtain their carbon from fungi). This has led to the study of phosphorus, organic and inorganic nitrogen utilisation by both mycorrhizas and root modifications lacking mycorrhizas, such as dauciform roots in the cyperaceae.



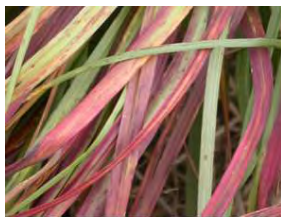
Focus on Sheffield



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 Research Area Regulation of photosynthetic carbon and nitrogen metabolism in C₃ and C₄ plants

Research Activities

Richard's research is largely concerned with the regulation and control of photosynthetic carbon and nitrogen metabolism in C₃ and C₄ plants. Work in the laboratory is focused on phosphoenolpyruvate carboxykinase, an enzyme of primary metabolism. Studies of this enzyme include; investigation of its regulation by phosphorylation, its multifarious functions in germinating seeds, its role in nitrogen metabolism in developing seeds (such as pea) and in the phloem, its role in defence tissues, such as trichomes (in *Arabidopsis*), and its function in the CO₂-concentrating mechanisms of C₄ plants and in diatoms (*Thalassiosira* spp.). Knock-outs are being utilised to study its functions in *Arabidopsis*.



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 Research Area Plant atmosphere interactions

Research Activities

Research in the Osborne Laboratory aims to better understand how plants interact with the atmosphere, and how this relationship has evolved over geological time. Current work falls into three main areas: evolution of C₄ grasses, plant-atmosphere interactions in the geological past and modern plant-climate relationships.



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 Research Area Impact of environmental change on vegetation and ecosystem processes

Research Activities

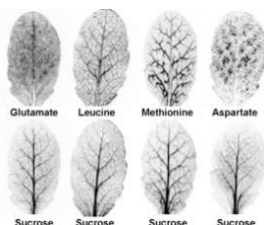
Gareth's research focuses on the impacts of environmental change on vegetation and ecosystem processes (particularly nutrient cycling and fluxes) and on how these ecosystem processes are affected by plant community structure. Current key questions include: (1) Effects of pollutant nitrogen (N) deposition on nutrient fluxes and cycling within grassland ecosystems, N deposition impacts on plant biodiversity and nutrient acquisition. (2) Effects of vegetation (plant diversity and traits, parasitic plants) on ecosystem nutrient cycling and budgets. (3) Effects of environmental change on sub-Arctic vegetation and biogeochemical cycling.



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 Research Area Parasitic plants and hosts interactions

Research Activities

Research in the Press laboratory focuses on several areas; (1) Ecological, physiological and metabolic interactions between parasitic plants and their hosts with special reference to plants in the semi-arid tropics and sub-arctic/alpine ecosystems. (2) Regeneration ecology of tropical rain forest seedlings, with emphasis on the impact of biotic (insect herbivores and mycorrhizas) and abiotic (light and nutrients) variables. (3) Impacts of global change on arctic ecosystems, particularly elevated temperatures and enhanced nutrient supply. (4) Ecophysiological responses of plants to elevated concentrations of carbon dioxide.



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 Research Area Plant carbohydrate metabolism

Research Activities

Work in Paul's group is centred on plant carbohydrate metabolism, particularly photosynthesis. To further our understanding of this area the group are investigating the biochemical and molecular basis of plant responses to their environment (e.g. CO₂, light, nutrients), how these are signalled and the subsequent effects on both cellular metabolism and plant development. In addition researchers have recently employed new technologies (such as microarray and mass spectrometry) to help broaden our knowledge of the regulation of plant processes.

Focus on Sheffield



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 Research Area Plant fungal interactions

Research Activities

David's research interests include; plant physiological ecology, plant microbial-interactions, plant-nutrient and water relations, mobilisation of soil organic matter, microbial ecology and pollution biology. The laboratory is investigating the role of plant-fungus symbioses of roots (mycorrhizas) with particular reference to their importance at the plant community and ecosystem levels.

Name Mark Rees
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 Research Area Plant population biology

Research Activities

Many plants delay reproduction for several years before flowering, understanding why they do this from an evolutionary and physiological perspective is one of the main areas of research within the Rees laboratory. Recently the group have started to explore the simultaneous evolution of delayed reproduction and seed dormancy. This work combines modelling, using integral projection models, with long-term field data to derive predictions about what plants should do in the field. Researchers are also exploring the physiological basis and life history consequences of growth-survival trade-offs. In addition to this work Mark has interests in more applied problems looking at modelling management strategies, including biological control for weed populations and the population biology of invasive plants. In addition to the group are employing other theoretical approaches including extending the integral projection modelling approach to allow for complex demographic transitions, based on size and age, and variation in the environment.

Name Stephen Rolfe
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 Research Area Plant responses to abiotic and biotic stresses

Research Activities

The Rolfe group studies the response of plants to abiotic and biotic stresses using chlorophyll fluorescence imaging and analysis of gene expression and function. Imaging techniques are also utilised in the laboratory to study microbial community structure and function in polluted groundwater. The group are exploring the exchange of nutrients between plant and fungal partners in mycorrhizal symbioses, with particular emphasis on hexose, sucrose and phosphate transporters.

Name Julie Scholes
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 Research Area Molecular basis of plant - symbiont interactions

Research Activities

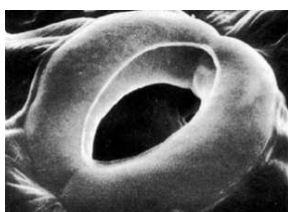
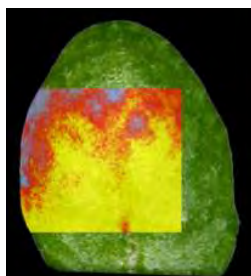
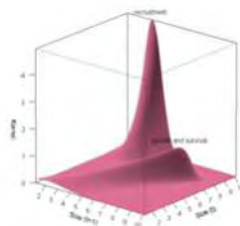
Julie's research is focused on understanding the molecular basis of plant- symbiont interactions (fungal pathogens, angiosperm parasites and mycorrhizas). Current projects include: an investigation of the molecular genetic basis of resistance in rice to the root parasite *Striga hermonthica*; an investigation of non host resistance in *Arabidopsis* to *Striga* species; elucidating the metabolic costs of resistance and susceptibility in barley to powdery mildew; understanding the role of sugar signalling pathways in susceptibility of crops to biotrophic fungi and an investigation of the role of flavohaemoglobins in fungal pathogenicity.

A second major research interest of the group is bioimaging and involves the development of imaging systems/techniques to non-destructively and quantitatively analyse plant and fungal metabolic processes and gene expression. Current projects in this area include the use of microbial biosensors to visualise the biodegradation of pollutants in groundwater. The group is also interested in tropical ecophysiology; in particular the role of biotic (mycorrhizas, fungal pathogens and insects) and abiotic (light and nutrients) factors in the survival and regeneration of tropical rainforest tree seedlings.

Name Ian Woodward
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 Research Area Vegetation modelling and stomatal development

Research Activities

Research in Ian's laboratory is centred on two main areas: (1) Modelling the impacts of environmental changes on vegetation at the global scale. (2) Investigating the mechanisms controlling stomatal development, with particular emphasis on identifying the network of environmental responses.



Focus on Southampton

University of Southampton



Plant Biology is one of the key research themes in the School of Biological Sciences at the University of Southampton. The overall emphasis is to use genetic and molecular techniques to answer both fundamental and applied questions relating to plant function and development, and to the response of plants to biotic and abiotic stress in the context of a changing environment. This approach involves functional genomics supported by a strong background in the biochemical, physiological and ecophysiological analysis of plant tissues. Researchers at Southampton mainly work on the model plant species *Arabidopsis* and Poplar, although applied research includes links with both the horticultural and forest industries. Key areas of research are: the functioning of plants in relation to the environment, particularly changes in light, CO₂, heavy metals, ozone and plant pathogens; membrane transport proteins that are involved in the acquisition and distribution of essential nutrients; defences against disease-causing organisms; control of chloroplast development; the regulation of tetrapyrrole synthesis; the use of trees as sources of renewable, carbon neutral energy.

Name Mark Barber
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 Research Area Lignin biosynthesis



Research Activities

Lignin is the term given to a group of complex phenolic polymers that provide strengthening and waterproofing properties to plant cell walls. Lignin also plays roles in mechanical support, solute conductance and disease resistance in plants. Lignin is derived from the spontaneous polymerization of free radicals derived from the oxidation of three hydroxycinnamyl alcohols: p-coumaryl, coniferyl and sinapyl alcohols. Mark's laboratory is focussed on two enzymes of the lignin branch pathway, cinnamoyl-CoA reductase and cinnamyl alcohol dehydrogenase as specific target sites for lignin manipulation in plants.

Name Mark Dixon
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 Research Area Plant molecular genetics/ plant-pathogen interactions

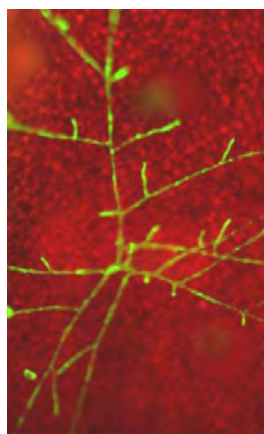


Research Activities

Plants have evolved many mechanisms to protect themselves from pathogens. Some of these are passive, such as the production of preformed antimicrobial compounds, whereas others involve the induction of defence mechanisms when a specific pathogen is recognised. Dominant resistance (R) genes in plants encode molecular receptors for pathogen-derived factors, which are the direct or indirect products of pathogen avirulence (Avr) genes. Mark's group study the interaction between tomato leaf mould (*Cladosporium fulvum*) and its host tomato. Researchers are currently investigating the fundamental nature of the recognition process and the signalling mechanisms involved to activate plant defences.

Studies in the Dixon laboratory have recently also extended to include studies on plant resistance to sap-feeding aphids, (in particular, drawing parallels with plant-pathogen interactions) and the analysis of non-tradition traits in leafy salad crops such as nutritional components and post-harvest traits. These studies are aimed at enhancing conventional crops though modern marker assisted breeding of beneficial traits from wild relatives of crop plants.

Name John Hall
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 Research Area Membrane transport and plant-pathogen interactions



Research Activities

Powdery mildews are widespread and destructive pathogens that cause major losses in crop yield. They are biotrophs that are usually restricted to the shoot epidermis where they form haustoria and acquire essential nutrients from the living host cells over a long period. The pathogen competes with host sinks for nutrients and this can cause considerable changes in carbon partitioning within the plant. John is interested in the transporters, both host and pathogen, that are involved in this process, and works mainly on the *Arabidopsis*-*Erysiphe cichoracearum* interaction. Studies have shown that infection by *Erysiphe cichoracearum* induces a number of responses in the host tissue including enhancement of glucose uptake, that coincides with the induction of the monosaccharide sugar transporter, AtSTP4. Pathogen solute uptake is thought to be driven by the pathogen transporter EcPMA1. The laboratory is currently investigating the coordination of transporter activities and aims to identify other host transporter genes that may be involved in this interaction via microarray analysis.

Focus on Southampton

Name Guy Poppy
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 Research Area GM risk assessment and insect/plant Interactions

Research Activities

The use of GM plants in agriculture is seen by many as the second green revolution. However, their introduction has caused considerable anxiety amongst society, politicians and some scientists. Work in the Poppy laboratory has focussed on quantifying the environmental risk of GM crops. New frameworks have been developed to assess non-target effects and the consequences of gene-flow to wild relatives. Scientists from many different backgrounds are researching the risks of GM and recent research is aimed at maximising the benefits of GM whilst reducing the risks. The group is also involved in advising governments and regulators throughout the world on the risk assessment and risk management of GM crops. Currently Guy's lab is developing an endpoint system for risk assessment studies that should make risk assessment a more objective science. The Poppy laboratory also study insect/plant interactions from the genetic level through to community scale interactions. The group combines proximate studies addressing the precise mechanisms of induced and constitutive plant defence through to ecological adaptive studies determining how such systems evolved. By combining molecular, chemical and ecological studies, a holistic understanding is obtained. This has led to many applied applications combining a range of plant defence strategies against insects, thus minimising the reliance on synthetic insecticides. Currently Guy is utilising Arabidopsis as a tool for developing new GM traits as well as expanding the use of Arabidopsis tools for the study of wild crucifer systems.



Name Matthew Terry
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 Research Area Photomorphogenesis

Research Activities

Plants are able to monitor the surrounding light environment and modulate their growth and development accordingly. This ability is crucial in order to maximise light capture for photosynthesis and therefore increase their chances of survival in a competitive world. Plants use a number of different photoreceptors including the blue light-absorbing cryptochromes and the phytochromes, which absorb red and far-red light. The phytochromes are important in the regulation of a wide range of developmental responses in plants including germination, growth, development of a functional photosynthetic apparatus, synthesis of protective pigments and flowering. Work in the Terry laboratory is primarily focused on how phytochrome regulates chloroplast development and in particular the tetrapyrrole biosynthesis pathway leading to the synthesis of chlorophyll, heme and phytychromobilin, the chromophore of phytochrome. This signalling is not one way and understanding how signals from the chloroplasts (plastid signals) and metabolism (sucrose) are integrated is an important part of ongoing research. Other projects in Matthew's laboratory concern the roles of membrane proteins in mediating photomorphogenic responses and light responses of marine cyanobacteria (together with members of the National Oceanographic Centre in Southampton).



Name Gail Taylor
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 Research Area Plant-environment interactions

Research Activities

The research in Gail's group aims to understand the functioning of plants in relation to the environment. The environment is changing in a number of ways, largely as a result of anthropogenic influences, and these changes will have important consequences for plants in agriculture, forestry and semi-natural plant systems. Much of the research is focussed on poplar as a model tree, on using poplar as a source or renewable energy and in employing the tools of functional genomics to answer large-scale ecological questions as well as smaller-scale questions such as what determines the size and shape of a leaf. Currents projects are focussed on understanding adaptations to global change, particularly increased atmospheric carbon dioxide and ozone, but also drought, at the level of the gene and identification of potential candidate genes involved in evolutionary adaptation. To do this researchers use a combination of transcriptome and molecular genetic (QTL) approaches – 'genetical genomics'. This has identified a number of important targets for future research. Studies on bioenergy trees have uncovered areas of the poplar genome that control traits for high yield and the group are now examining these further using a large natural population of *P. nigra* and association mapping techniques. Complementary investigations of environmental sustainable bioenergy cropping systems are also being undertaken. Southampton is also home to the Vitacress Research Unit, initiated in 2002 to investigate and improve baby leaf salads, in collaboration with Vitacress UK. This collaboration with industry will take forward a molecular breeding project that utilizes our data on salad leaf quality directly for the improvement of baby leaf salads. Gail is collaborating with a Californian seed company to take this commercialisation forward.



Focus on Southampton/St.Andrews

Name	Lorraine Williams
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Research Area	Membrane transport processes in plants



Research Activities

The transport of essential nutrients is a key process in plant growth and development. Many of the essential micronutrients required by plants are transition/heavy metals (eg. copper, zinc and manganese) that have a wide and varied function. When these metals are in short supply, a range of deficiency symptoms appear and growth is reduced. In excess, these, and non-essential metals such as cadmium and lead can become extremely toxic. Therefore, strict control is necessary so that plants are able to absorb sufficient transition metal micronutrients for normal growth and development but at the same time limit their toxicity when present in excess. Various mechanisms are employed to regulate the amounts of metals in the plant and membrane transport proteins play an important role. Transporters are crucial for the initial absorption of metals, their movement around the plant, their delivery to cells, and in controlling the levels within cells. P1B-ATPases have emerged as central players with physiological roles in metal nutrition, detoxification and delivery of metals to target proteins. Lorraine's group is studying these transporters in *Arabidopsis* and more recently in barley. Other research in the group focuses on the role of Ca²⁺-ATPases in calcium homeostasis and signalling. Ca²⁺-ATPases catalyse the active efflux of calcium into the extracellular space or into internal stores such as the vacuole, ER or Golgi, thereby maintaining low cytosolic calcium levels and allowing calcium to function as a signalling molecule. Lorraine's group has cloned several of these transporters from *Arabidopsis*, studied their tissue and membrane localisation, and determined their physiological role using knockout mutants. In addition to this research projects are being undertaken to investigate membrane transporters involved in host/fungal pathogen interactions, sugar and amino acid distribution, and light-regulated development of *Arabidopsis*.

University of St.Andrews

Plant Science in Scotland's oldest university takes place in the RAE5 rated School of Biology. Research covers a wide variety of topics and encompasses researchers from several academic areas and research groups. Areas of study range from single cell analysis to whole organism evolution as detailed below.



Name	Richard Abbott
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Research Area	Plant speciation

Research Activities

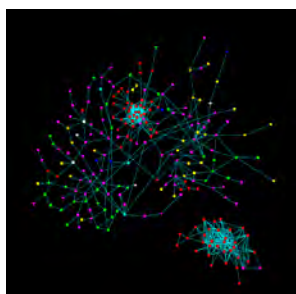
The different ways in which species originate are of central importance to an understanding of organismic evolution, yet we remain ignorant of most details of the speciation process. Significant advances to an understanding of speciation can be gained by studying the process as it occurs. This is not easy as rarely do we encounter examples of speciation in action. However, at least four new plant species have originated in the British Isles during the last 200 years which provide models for a detailed analysis of the speciation process. In the Abbott lab, these models are being used to examine the process of hybrid plant speciation at diploid and polyploid levels. Comparative genome mapping has been used to determine alterations to genome structure during hybrid speciation, and to locate genes controlling traits that are modified during this process. In collaboration with Dr. S. Hiscock and Prof. K. Edwards (Bristol University), gene expression changes during speciation have been studied along with their causes and consequences. A study of the new polyploid hybrid species *Senecio cambrensis*, which originated in Wales approximately 80 years ago, has shown large-scale alterations to gene expression between parents and their triploid hybrid that is ameliorated by chromosome doubling.



Name	Daniel Barker
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Research Area	Bioinformatics and computational phylogeny

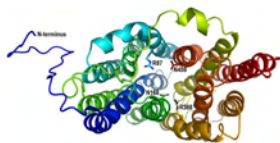
Research Activities

Daniel's research is centred in bioinformatics and computational biology. He is currently pursuing two approaches to predict protein function. (1) Use of known gene function to predict the function of unknown orthologues in other species. (2) Across species correlation; functionally linked proteins tend to show a common pattern (membership of the same pathway or structural complex) of presence or absence across a range of genomes. Development of the latter approach has focused on baker's yeast, allowing the use of many existing experimental results to validate the bioinformatic technique and now this approach is being applied to fungi and flowering plants.



Focus on St. Andrews

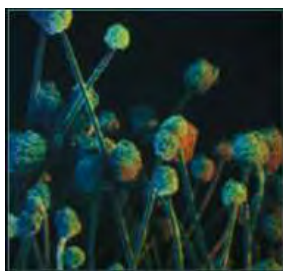
Name	Jim Kinghorn
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Research Area	Nitrite utilisation



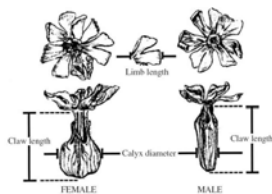
Research Activities

Chemicals that are necessary for life must be recycled. This includes nitrogen that is present in all proteins and nucleic acids and in many other biological molecules. One of the major intermediates of the nitrogen cycle in terrestrial, freshwater and marine environments is the anion nitrite. When oxygen is present, nitrite is liberated by a community of closely related bacteria that carry out the oxidation of ammonium as part of the process of nitrification. Available nitrite can be taken up by cells of other groups of organisms, using protein catalysts (transporters) located in the cell membrane. Once inside the cell, nitrite can be converted into organic forms of nitrogen such as amino acids for cell growth and multiplication.

As there is little information regarding the mechanisms involved in nitrite uptake, the overall objective of John's research is to obtain detailed information regarding the structure and function of NitA, a membrane protein that is responsible for nitrite transport. This permease has 6 membrane spanning domains, within which are highly conserved motifs likely to be of functional and/or structural significance. The laboratory uses the eukaryotic fungus *Aspergillus nidulans*, which can use nitrite as its sole nitrogen source. Using site-directed mutagenesis, biochemical analyses (including the newly developed tracer ^{13}N -nitrite), and intragenic genetic reversion, the group aims to obtain detailed functional information on the amino acid residues and motifs required for nitrite transport in NitA. The knowledge gained from this research will be of interest to both plant and microbial environmentalists as nitrite is an environmentally and agriculturally (via the rhizosphere) important nitrogen source. Increasing our understanding of how nitrogen is taken into cells will also benefit researchers in the areas of plant nutrition and soil science.



Name	Thomas Meagher
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Research Area	Plant evolution, evolutionary genomics, biodiversity & conservation biology



Research Activities

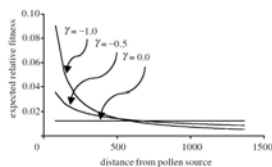
There is growing realization that the future of science will require interdisciplinary integration of approaches to tackle complex problems. An ethos that is reflected in Thomas's work, which spans ecological field work, quantitative genetics, molecular biology and conservation biology. Current research in the Meagher laboratory falls into three general areas. (1) Genealogy reconstruction and pedigree analysis in natural populations. (2) The relationship between genome organization and phenotypic evolution. (3) Integration of population biology into biodiversity indicators for local and global conservation efforts.

Work on genealogical reconstruction centres on the use of genetic information to study the ecological properties of natural populations. For example the group have developed and applied genetic marker-based paternity analysis to *Chamaelirium luteum*, *Silene latifolia*, *Solanum carolinense*, and *Agrostis palustris*. More recent work has focused on development of statistical methods to integrate paternity analysis and ML quantitative genetic analysis.

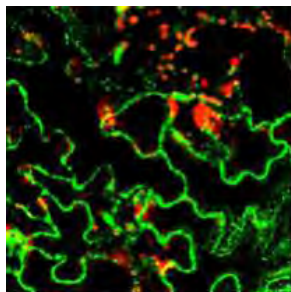
The group is also investigating the evolution of sexual dimorphism. Previous studies in this area have included in-depth field analysis of life history differences between male and female *Chamaelirium luteum* plants and the use of *Silene latifolia* as a research tool to study the evolutionary dynamics of sexual dimorphism in flower size, addressing quantitative genetic bases and potential for evolutionary change. Current investigations at the genomic level have illustrated a negative correlation between nuclear DNA content and flower size.

In a developing collaboration with Professor Sir Peter Crane and Dr. Eimear Nic Lughadha at the Royal Botanical Gardens, Kew, Thomas hopes to explore connections between population dynamics of individual plant species and biodiversity both generally and more specifically in connection with proposed biodiversity indicators being developed for the UN Convention on Biological Diversity for global assessment of plant biodiversity. The goal is to better understand causal bases underlying large-scale trends in biodiversity change.

Finally, Thomas has contributed to application of evolutionary biology to areas of social concern including co-chairing the US Evolution, Science & Society initiative to explore scientific contributions of evolutionary biology and contribution to the UK GM debate through the Royal Society-London, the Royal Society-Edinburgh, and the BBSRC and he is currently a member of DEFRA Science Advisory Council.



Focus on St. Andrews

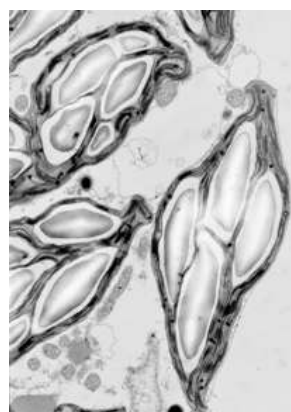


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 Research Area Plant cell physiology

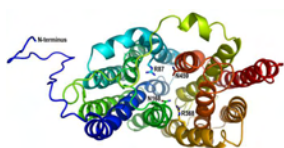
Research Activities

Alyson's research is focused on the function of plant cell organelles, particularly mitochondria and plastids. How metabolism is compartmentalised both within and between cells is of particular interest to Alyson's group. The laboratory has been exploring the metabolic potential of plastids and mitochondria in relation to leaf cell development and differentiation. Researchers have used in situ labelling methods and, more recently, proteomics-based analysis of isolated plastids, in order to determine cellular differences in photosynthesis, nitrogen and carbon metabolism. In a BBSRC-funded collaboration with Dr. Caroline Bowsher (Manchester University) researchers have succeeded in isolating novel forms of plastids from leaf epidermal cells. These show unique properties at both the morphological and biochemical level, and work is now being carried out to understand how these properties impact on metabolism and leaf physiology. This research builds on earlier observations of the compartmentation of nitrogen and carbon metabolism pathways, and of component isoenzymes, in C3 leaves. In collaboration with Prof. Tomoyuki Yamaya (Tohoku University, Japan) models of the partitioning of carbon and nitrogen metabolism within roots and leaves of cereals have been produced and highlight distinct and differing roles for glutamine synthetase and glutamate synthase isoforms within and between cells. These investigations are providing us with a better understanding of how nitrogen is used and mobilised during crop growth. As part of a current collaboration with Dr. David Leader and Dr. Robbie Waugh (SCRI, Dundee) researchers are taking a TILLING-based approach to isolate glutamine synthetase mutants in barley to further our understanding of how the individual isoforms affect partitioning of nitrogen and carbon.

Early studies in the Tobin laboratory on leaf mitochondria showed that there are distinct and differing zones of division and metabolic specialisation during cell development and differentiation. This finding is now being taken forward with Dr. David Logan (University of St. Andrews) who has isolated several mutants with altered mitochondrial shape/size/distribution in Arabidopsis leaves, with the aim of identifying the genetic control of mitochondrial division and biogenesis. The Tobin lab also has a further research interest in the impact of ultraviolet B radiation on plants. This specifically relates to DNA damage and repair processes but also includes the wider influence on plant growth and development in environments with high UV-B exposure. The latter has been facilitated through collaborations with Dr. Sharon Robinson (Wollongong) and scientists at the British Antarctic Survey, Cambridge.



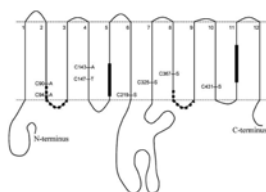
Name Shiela Unkles
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 Research Area Structure/function of nitrate transporters



Research Activities

Global nitrogen fertiliser use is currently at record levels per annum. However, as much as 50% of this may be lost from the soil into ground waters, rivers and oceans as inorganic nitrate. This inefficient nitrogen use is economically wasteful, but perhaps more importantly, it contributes to environmental damage by fuelling explosive growth of harmful algae that can cause shell fish toxicity and kill fish. As world populations continue to grow, demands for increasing crop yield and corresponding fertiliser requirements will exacerbate both aspects of this problem. To help address this problem Shiela's research group is investigating how microbial and plant cells take up nitrate from the environment.

Cell membranes form a lipid barrier to most compounds, but within the membrane there are protein transporters that facilitate movement of nitrate into the cell. Such transporters are part of a large family of proteins, the amino acid sequences of which have certain features in common. They characteristically have 12 domains of around 21 amino acids in length that traverse the cell membrane in a zigzag fashion. Within these transmembrane domains there are a number of amino acid residues which are conserved in all nitrate transporters, from bacteria to plants. By creating mutations in these highly conserved residues in the fungus *A. nidulans* and carrying out kinetic analysis of the resulting mutant strains, the group are beginning to build a three dimensional picture of the transporter and the role of such conserved residues. By understanding the mechanism of nitrate transport Shiela aims to manipulate the process and facilitate a more efficient management of nitrate in the environment.



Focus on Sussex

University of Sussex

Research in Plant Science at the University of Sussex takes place within two departments of the RAE-5-rated School of Life Sciences; the Departments of Biochemistry and Biology and Environmental Science. The basis of most of the research is the interaction of plants with their environment with a particular focus on responses to stress, both biotic and abiotic. Details of the various projects being undertaken is provided below.



Name Tim Flowers
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 Research Area Effects of salinity on plants

Research Activities

Naturally occurring salt-affected soils, which are mostly in coastal salt marshes or inland deserts, cover about a billion hectares, an area roughly the size of Canada. These natural salt-affected soils are not, unfortunately, the only ones suffering from salt: human activity has caused farmland to become salinised through irrigation and forest clearance; perhaps half of all irrigation schemes have some salt-affected soil, generally associated with a high water table. In Australia, dryland salinity is also linked to rising water tables, but brought about by increased deep drainage of rainfall following land clearance.

Current work in the Salinity Laboratory at Sussex is focussed on two contrasting species, the halophyte *Suaeda maritima*, an annual that grows rapidly at high salinity, and the salt-sensitive crop *Oryza sativa*. The group have evidence for two distinct low-affinity Na⁺ uptake pathways in *S. maritima*: one might be mediated by an HKT-type transporter and the other by an AKT1-type channel. Researchers in Sussex are currently investigating interactions between salinity and waterlogging (two 'stresses' that commonly occur together) and their effects on growth and ion transport. Using rice, the group are continuing to study the pathway by which sodium bypasses symplastic control in its passage from roots to shoots, using the spittlebug *Philaenus spumarius* to sample xylem sap. Recent evidence demonstrates a correlation between deposits of silicon in rhizodermis and exodermis and a decrease in bypass flow.

Research is also about to start for the herb industry, on the selection of new varieties of coriander and their optimal growing conditions.



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 Research Area Plant population biology

Research Activities

Mike's research centres on population and plant community ecology and all topics of interest have both basic and applied aspects to them. Areas currently under investigation include: (1) the conservation of rare and endangered species, including members of the family Orchidaceae, (2) studies of restoration and regeneration of species-rich plant communities on ex-arable land, (3) ways of maximising plant production through manipulation of spatial and temporal pattern of resource supply, (4) the foraging behaviour of plants, plant plasticity and physiological integration, (5) the ecology of clonal species, and (6) the responses of individual plants, their populations and their communities to spatial and temporal heterogeneity in supply of essential resources.

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 Research Area Community ecology

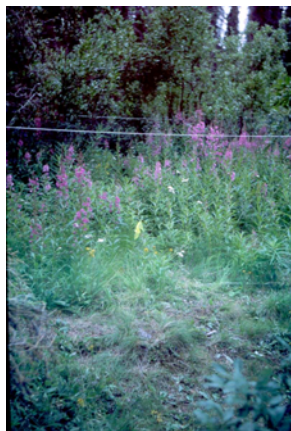
Research Activities

Sue specialises in the study of plant-herbivore interactions. Her research interests include; multi-trophic interactions: how plants modify the interactions between insect herbivores and other organisms; herbivory and plant defence: how environmental factors (e.g. climate change) alter plant allocation to defence and the consequences for insect herbivores; and herbivory and plant communities: how herbivory and resource availability interact to affect the competitive balance between plant species.

Current projects include work on grass based systems. Grasses dominate many terrestrial ecosystems and are of great ecological and economic importance, as are the grazing mammals associated with them. Although co-evolution between grasses and grazers has received a great deal of attention, the ecological mechanisms by which grasses defend themselves against herbivores remain poorly understood. Grasses contain high levels of silica, which is thought to act as an anti-herbivore defence due to the abrasive nature of silica bodies (phytoliths) found in the leaves, but evidence in support of this remains largely correlative. Increased levels of silica lead to increased abrasiveness of grasses, which deters feeding by voles and reduces the growth rates of female voles by decreasing the digestibility of grass leaves. The underlying mechanism for this is that voles feeding on grasses containing silica fail to extract as much nitrogen from their food as voles feeding on grasses with very low levels of silica. Furthermore, feeding by voles actually induces high levels of silica in grasses, suggesting a dynamic feedback response defending grasses against future herbivore damage. Herbivore-induced silica defence is a mechanism by which food quality could influence the reproductive performance and population growth of small mammalian herbivores.



Focus on Sussex

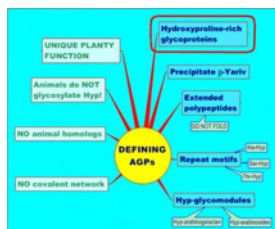


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 Website <http://www.sussex.ac.uk/biology/profile1399.html>
 Research Area Experimental plant ecology

Research Activities

Libby is an experimental plant ecologist interested in the processes affecting the structure and composition of plant communities. Areas of interest include:

1. Ecological consequences of habitat heterogeneity: the pattern in which resources are supplied to plants can have far reaching consequences for the growth of plants, plant populations and plant communities. This is explored in greenhouse and field experiments.
2. Effects of herbivores and nutrient availability on plant community structure: Field experiments have shown that the relative importance of nutrient supply and herbivore activity and their interaction is ecosystem dependent. Nutrients deposited in patches (e.g. urine from large herbivores) can have surprising consequences for plant fitness, because of the risks of being made more attractive to small herbivores.
3. Fine-scale interactions between plants: Recent work has demonstrated that the plant root system architecture is sensitive to the genetic identity of competitor roots, as well as the pattern of nutrient delivery; this is an area of current activity.



Name Derek Lamport
 e-mail d.t.a.lamport@sussex.ac.uk
 Website <http://www.sussex.ac.uk/biology/profile128272.html>
 Research Area Cell wall biochemistry

Research Activities

Derek Lamport's 'retirement projects' continue the quest for the elusive Snark, a trinity of riddle myth and enigma that describe the role of wall proteins, in particular those structural hydroxyproline-rich glycoproteins comprising the extensins (crosslinked networks), soluble arabinogalactan-proteins (AGPs) and close relatives. His most recent discovery that salt-stress dramatically upregulates AGP biosynthesis from 5 to 10-fold hints at an unexpected eco-physiological role for AGP-pectin coacervates as a major molecular contributor to the fleshy habit of coastal halophytes.

Name Tony Moore
 e-mail a.l.moore@sussex.ac.uk
 Website <http://www.sussex.ac.uk/biochemistry/profile1865.html>
 Research Area Plant mitochondrial biochemistry: the alternative oxidase



Research Activities

Work in the Moore laboratory at Sussex is focused on gaining a greater understanding of the structure and function of the cyanide- and antimycin-resistant alternative oxidase.

The alternative oxidase is present in all plants, some fungi, yeasts and trypanosomes (it is the possible cause of African sleeping sickness), but not in animals. Although the alternative oxidase plays a key role in respiration in all of these organisms its precise structure and function is still uncertain. Apart from its role in the production of heat in thermogenic plant species, a general physiological role for the oxidase has not been established conclusively. No crystallographic data for the alternative oxidase is currently available but the generally adopted view is that it comprises of a non-haem diiron centre.

The overall objective of Tony's current and future research programme is to elucidate the molecular nature of the alternative oxidase. Clearly, such fundamental knowledge is of considerable industrial relevance, as it has the potential to greatly facilitate the rational design of phytopathogenic fungicides and anti-parasitic pharmaceuticals that are targeted at mitochondrial respiration. The structural and mechanistic insights that are gained from these studies will furthermore improve our fundamental understanding of the (mitochondrial) energy metabolism of plants. Given the wasteful effect that alternative oxidase activity has on plant respiration, this enhanced understanding could also have potential future agro-biotechnological implications.

Name Mike Ramsey
 e-mail m.h.ramsey@sussex.ac.uk
 Website <http://www.sussex.ac.uk/biology/profile107899.html>
 Research Area Uncertainty in environmental contamination

Research Activities

Current research focuses on improving models of plant uptake of metals. One particularly interesting aspect is quantifying the role of the heterogeneity of the metal distribution in the soil on the uptake coefficients. Current uptake models do not consider this property of the soil. This heterogeneity can be quantified and has been shown to have a substantial effect on the uptake of cadmium by lettuce plants. Other factors that can also affect the uptake of toxic metals such as cadmium metals include the concentration and heterogeneity of other metals, soil pH and the form of the metal in the soil. It appears that the effect of the heterogeneity in the soil is related to the morphology of the root in comparison with the scale of the heterogeneity. The effects that are reported in the literature can however be limited by the quality of the field sampling and the contamination of the plant material by soil and dust. This research has implications for improved assessment of exposure to toxic metals for human health risk assessment and for phytoremediation.



Focus on Sussex

Name Steve Pearce
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 Website <http://www.sussex.ac.uk/biology/profile110655.html>
 Research Area Plant genomic evolution/retrotransposon biology

Research Activities

Plant genomes are complex and show high levels of change over short evolutionary timescales. Retrotransposons are related to retroviruses and make up large proportions of plant genomes: their activity makes them a key factor in causing mutations and driving genomic change in plant genomes.

Steve's research uses the study of retrotransposon insertions to investigate how plant genome structures have changed over evolutionary timescales. For example researchers are currently using retroelement sequences to understand the phylogenetic relationships within the tequila agaves. These plants form the basis of a billion dollar industry in Mexico. Relatively recent cultivation practices which rely on single cultivars have led to major erosion of the genetic diversity in this crop resulting in substantial losses to fungal and bacterial pathogens. By studying phylogenetic relationships within the tequila agaves the group have identified varieties which could provide plant breeders with novel sources of germplasm to improve the sustainability of this crop. Other projects in the laboratory involve the conservation of rare orchid species and the role of retrotransposons in generating somaclonal variation in clonal plants.



Name Peter Scott
 e-mail P.B.Scott@Sussex.ac.uk
 Website http://www.lifesci.sussex.ac.uk/home/Peter_Scott/Index.html
 Research Area Plant adaptations to drought stress

Research Activities

Water stress is one of the major stressors that plants encounter. It is therefore important that we understand how plants that are highly adapted to drought stress manage to survive and even thrive under such conditions.

The Scott laboratory is investigating various plant systems as models to study drought stress. One such model is *Craterostigma*, a poikilohydric plant which can survive severe water loss. Researchers at Sussex have made many advances with transgenic physiological studies on this plant. Peter has also been analyzing the physiology of UK orchids and how they are supremely adapted to drought-stressed soils by using dormancy as a means of protection.



Name John Zhou
 e-mail j.zhou.sussex.ac.uk
 Website <http://www.sussex.ac.uk/biology/profile107898.html>
 Research Area Environmental chemistry

Research Activities

Research on the impacts of air pollution on plants has previously focussed on sulphur dioxide, nitrogenous compounds and ozone. However, little is known regarding the effects of other toxic compounds, including polyaromatic hydrocarbons, and this is the focus of John's research. Polyaromatic hydrocarbons or PAHs are a group of over 100 different chemicals many of which are known to be toxic, and often carcinogenic and mutagenic. They are formed during incomplete combustion of organic material and are emitted into the atmosphere by natural processes such as volcanoes and bush fires; as well as through human activities, mainly from the burning of fossil fuels for heating and operation of motor vehicles. PAHs can exist in the atmosphere in gaseous form or attached to particles, and will eventually be deposited onto soil or water where they may persist for many years. These pollutants may accumulate in the environment and living tissues of plants or animals, and may therefore enter the human food chain. The group's research is concerned with the impacts of PAHs (both single compounds and mixtures) on the germination, growth, and photosynthesis of important plant crops (such as wheat, maize and leek) in the Transmanche regions of northern France, and south-east England. The laboratory is also interested in effects on associated mycorrhiza (with collaboration from University of Kent and Université du Littoral Côte d'Opale in France) and whether mycorrhizal infection confers resistance of the plants to pollutant exposure. Uptake of PAHs by the plant and degradation in the soil by associated soil flora is also of interest being relevant to human health and phytoremediation, respectively.



Diary Highlights

3rd EPSO Conference

Visegrad, Hungary

28 May – 1 June, 2006

<http://www.epsoweb.org/catalog/Conf2006.htm>

8th Annual Plant Sciences Institute Symposium

Iowa State University, USA

22 - 25 June, 2006

<http://www.plantsciences.iastate.edu/symposia/>

17th International Conference on Arabidopsis Research

Madison, WI, USA

27 June - 2 July 2006

<http://www.union.wisc.edu/arabidopsis/>

Federation of European Societies of Plant Biology (FESPB)

Lyon, France

17 - 21 July, 2006

<http://fespb.org/Congress.htm>

ASPB

Boston, USA

5 - 9 August, 2006

<http://www.aspb.org/meetings/pb-2006/>

FASEB - Mechanisms in Plant Development

Vermont, USA

5 - 9 August, 2006

<http://src.faseb.org/>

ISPMB 2006

8th International Congress of Plant Molecular Biology

Adelaide Convention Centre, South Australia

20 - 25 August, 2006

<http://www.sallyjayconferences.com.au/ispmb2006/>

GARNet 2006: Plant Networks- How to Integrate your data

Bristol University, UK

11 - 12 September, 2006

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

Plant GEMs 5

Venice, Italy

11 - 14 October, 2006

<http://www.plant-gems.org>

EPSO Updates

written by Mike Bevan. Vice-chair, EPSO, UK representative.
michael.bevan@bbsrc.ac.uk



The European Plant Science Organisation (EPSO) was founded over 5 years ago to address the lack of recognition of plant and agricultural science by the EC Framework Programme 6. EPSO has now grown to represent over 50 member organisations from 23 European countries and has formed working partnerships with sister organisations such as ELSF, EMBO, ASPB and the Initiative for Science in Europe (ISE). EPSO has contributed to several important initiatives in its first 5 years. In 2002 it responded to the invitation of the Spanish Presidency and the EC to develop a proposal for a "European Research Area" in plant genomics (ERA-PG). This proposal enabled national funding agencies to align relevant research

programmes and develop sustainable funding mechanisms to support plant genomics research across Europe. The first deadline for pre-proposals has just past and UK scientists have had a good opportunity to develop collaborative projects thanks to the early commitment of the BBSRC to ERA-PG.

EPSO was active in setting up a Technology Platform, "Plants for the Future" (TP). Its purpose is to establish a forward look for European plant science that involves the input of academics, industrialists, farmers and consumer groups. The TP has recently completed a wide ranging review of plant science, available at <http://www.epsoweb.org/commun/>. A national consultation was held in London on Dec 13 2005 involving over 50 scientists, and their feedback has gone back to the TP for incorporation into their findings. This and the reports of many other TPs are now being used to establish research priorities in Framework Programme 7 (see below).

As a member of the Initiative for Science in Europe, EPSO has played an important role in the creation of the European Research Council (ERC), to support high quality basic research in a bottom up approach encompassing all areas of science. ISE became one of the major forces giving rise to the inclusion of the ERC in the European Commission's FP7 proposal. EPSO is a discussion partner for policy makers on European science policy, such as the European Framework Program. For example we provided early input on FP7 via the European Commission online consultations. EPSO is also an information broker for the ongoing FP6. EPSO organised a workshop in Koln to share experience on the first call of FP6 and drawing conclusions for future submissions. EPSO also provides online information on granted projects and on upcoming calls.

Through EPSO, European plant scientists have established regular international conferences to discuss state of the art and future avenues for research, develop networks and discuss science policy. The third EPSO Conference in Visegrad, Hungary on 29 May has a top-level line-up of speakers.

EPSO members actively lobby MEPs and EC officials to ensure the relevance and importance of plant science is understood and projected. An analysis by EPSO showed that the European bio-economy (defined as the industries that produce, process or use biological resources and the plant-based non-food products sector) have an annual turnover of approximately €1500 b and employ 20m people. EPSO aims to make sure the research and development budget set by MEPs, the EC and the Council of Ministers is commensurate with this large and important sector. Currently as the budget of FP7 is set against a reduced funding envelope, EPSO and other organisations are trying to protect the budget for biotechnology.

As EPSO matures it aims to raise its profile further and initiate new activities to improve cohesion and competitiveness in European plant science. Future work through the ISE involves making sure the ERC moves onto a firm independent footing. EPSO also aims to foster stronger links between plant science groups and institutes in Europe and reaching out to new members. Current UK members include Rothamsted Research, Scottish Crop Research Institute, HRI Warwick, Univ. Lancaster and the John Innes Centre. University Depts can form clusters to share an annual "A class" membership fee of €7,500 and it is hoped more UK members can contribute to developing EPSO as it starts its second 5 years. In a couple of weeks EPSO will be requesting, on behalf of the TP, research topics from plant scientists in Europe for potential inclusion in the FP7 work programme. These topics should address the primary objectives of the Food, Agriculture and Biotechnology (FAB) Programme and be relevant to the priorities defined by the TP. It would be very useful if you digested the summary "Plants for the Future" (<http://www.epsoweb.org/Catalog/TP/docs/SRA-I.PDF>) and the current draft of the FP7 FAB Work Programme (http://garnet.arabidopsis.info/FP7_Work_Programme.pdf) in preparation for this. An explanatory guide "FP7 in a nutshell" is also available at http://garnet.arabidopsis.info/FP7_in_a_nutshell.pdf. Further details on this call for research topics will be distributed through GARNet and crop science distribution networks.

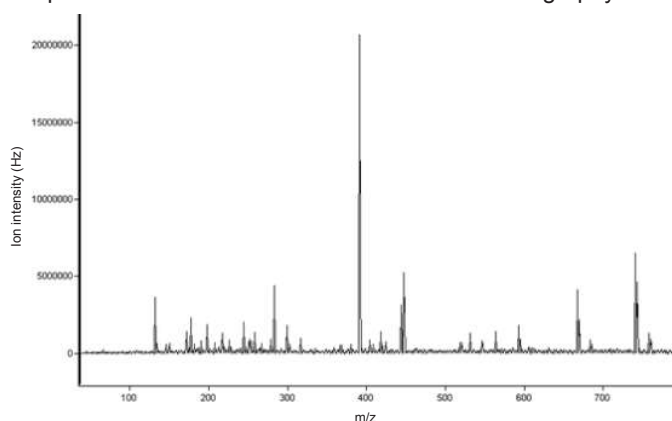
Data Standards: Enabling effective data handling

written by Helen Jenkins, Computational Biology Research Group, Department of Computer Science, University of Wales, Aberystwyth.

You have run your experiment and produced a data set. There are many things that you want to do with your data: Send it to your collaborator, submit it as supporting data for a publication, store it in a database, analyse it using statistical and/or data mining techniques. Then you find that your database expects your data to be in a particular format before you can upload it and your data analysis software expects a different format again. Meanwhile your collaborator has filled your inbox with questions about the experimental context of the data set and the journal to which you submitted it has complained that it doesn't contain standard nomenclature. What you need is a data standard.

Data standards are formal descriptions of the structure and content of datasets. They provide a common understanding of the shape of data sets which enables any experimentalist to interpret and use them. In addition this common understanding enables standard mechanisms for data handling to be developed for use by all.

Development of a data standard takes place in two stages. First, the biological domain of interest is analysed to identify the data items that are necessary (those that enable proper interpretation of a data set) and sufficient (the minimal set of necessary data items) to fully describe an experiment. For example, to properly interpret a data set that results from Gas Chromatography-Mass Spectrometry it is necessary to have access to information about the configuration of the instrument at the time of the analysis (e.g. column description, type of carrier gas), however, there will be subset of the complete set of instrument configuration parameters that is sufficient to enable an experimentalist to make reasonable judgements about the data set; the remaining parameters having little bearing on its content, (e.g. solvent delay). Getting the necessary/sufficient balance right is key to ensuring that a data standard is useful whilst maximising its chances of adoption through minimising the effort involved in data collection. Necessary data will include the data set itself, the experimental context necessary for its correct interpretation and information about sources of experimental variability that may obscure the biological variability that is of interest. The output from this stage is a written definition of the required data items that provides the basis for common understanding of the data sets that conform to it, e.g. SMRS (Standard Metabolic Reporting Structure, [1]) and MIAMET (Minimum Information about a Metabolomics Experiment, [2]) for metabolomics experiments. The second stage of development involves the construction of a formal data model. This involves structuring the data items and identifying the relationships between them. It often involves iterations with experimentalists to check understanding and in this way serves to verify the written description. The output from this stage is a formal data model that may be used as the basis for the design of automated data handling and storage tools, e.g. ArMet (Architecture for Metabolomics, [3]).



Direct injection Fourier-transform ion cyclotron (FT-IC-MS) metabolomic "fingerprint" of Arabidopsis seedlings at Dawn. S Thain, D Tomos, A Hall (unpublished).

Key to the usefulness of data standards is common vocabulary. Even if a data set conforms to a data standard it may still be misinterpreted simply because it contains non-standard terminology. Ontologies provide hierarchical formal specifications of the concepts within a domain and specify the vocabulary that may be used to refer to those concepts and, therefore, the development of ontologies is an integral part of data standardisation.

Current data standardisation initiatives for the 'omics are being organised by the MGED Society (Microarray Gene Expression Data Society, <http://www.mged.org>), PSI (the Proteomics Standards Initiative, <http://psidev.sourceforge.net/gps/index.html>) and MSI (the Metabolomics Standards Initiative, <http://www.metabolomicsociety.org/mstandards.html>). In the future it will become more common for transcriptomic, proteomic and metabolomic analyses to be combined in integrative experiments, creating a requirement for "pan-omic" data standards for experiment and sample descriptions. Recent work carried out under the FuGE (Functional Genomics Experiment, <http://fuge.sourceforge.net/index.php>) project has created a framework that enables integration of pre-existing data formats to support integrative experiments. A sister project FuGO (Functional Genomics Investigation Ontology, <http://fugo.sourceforge.net>) is aiming to produce a single ontology that will provide a source of terms for consistent annotation of functional genomics experiments.

Some of the outputs of these standards groups are already well-accepted, for the others only time will tell, but it is highly likely that their success or failure will depend, to a large extent, on their attempts to involve the community during the development process.

References

1. J. C. Lindon, J. K. Nicholson, E. Holmes, H. C. Keun, A. Craig, J. T. M. Pearce, S. J. Bruce, N. Hardy, S. A. Sansone, H. Antti, P. Jonsson, C. Daykin, M. Navarange, R. D. Beger, E. R. Verheij, A. Amberg, D. Baunsgaard, G. H. Cantor, L. Lehman-McKeeman, M. Earll, S. Wold, E. Johansson, J. N. Haselden, K. Kramer, C. Thomas, J. Lindberg, I. Schuppe-Koistinen, I. D. Wilson, M. D. Reilly, D. G. Robertson, H. Senn, A. Krotzky, S. Kochhar, J. Powell, F. van der Ouderaa, R. Plumb, H. Schaefer and M. Spraul, Summary recommendations for standardization and reporting of metabolic analyses, *Nat. Biotechnol.* 23 (2005), no. 7, 833-838.
2. R. J. Bino, R. D. Hall, O. Fiehn, J. Kopka, K. Saito, J. Draper, B. J. Nikolau, P. Mendes, U. Roessner-Tunali, M. H. Beale, R. N. Trethewey, B. M. Lange, E. S. Wurtele and L. W. Sumner, Potential of metabolomics as a functional genomics tool, *Trends Plant Sci.* 9 (2004), no. 9, 418-425.
3. H. Jenkins, N. Hardy, M. Beckmann, J. Draper, A. R. Smith, J. Taylor, O. Fiehn, R. Goodacre, R. J. Bino, R. Hall, J. Kopka, G. A. Lane, B. M. Lange, J. R. Liu, P. Mendes, B. J. Nikolau, S. G. Oliver, N. W. Paton, S. Rhee, U. Roessner-Tunali, K. Saito, J. Smedsgaard, L. W. Sumner, T. Wang, S. Walsh, E. S. Wurtele and D. B. Kell, A proposed framework for the description of plant metabolomics experiments and their results, *Nat. Biotechnol.* 22 (2004), no. 12, 1601-1606.

Transcriptomics Data Exchange and Data Standards

<http://affymetrix.arabidopsis.info>

written by Sean May & Beatrice Schildknecht, Nottingham Arabidopsis Stock Centre.

Microarray experiments generate vast quantities of data, and it has become a very significant challenge to structure, manipulate and communicate these data. The terminology used to describe comparable objects in different databases can often be quite disparate and even conflicting, leading to the twin dangers of misinterpretation and loss of context. Standards, such as those described by Helen Jenkins' in this issue of GARNish (pg20), can no longer be simply viewed as optional or avoidable. NASC has proactively adopted international standards and ontologies, such as MIAME (www.mged.org/Workgroups/MIAME/miame.html) and more recently Plant Ontology (www.plantontology.org/) in order to sensibly structure, annotate and interconnect data. This article will explore those standards in the context of NASC's databases.

MIAME, (Minimum Information About a Microarray Experiment) is a set of guidelines about how to unambiguously describe a microarray experiment without dictating how this data is to be structured. MIAME was developed several years ago by the MGED (MicroarrayGene Expression Data) Society and has been taken up by NASCArrays and microarray repositories such as ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>) both of which are purposefully MIAME supportive.

MAGE-ML, Microarray Gene Expression Markup Language is a language, based on XML that is designed to describe microarray experiments, from experimental design and array manufacture to data analysis results. Microarray experiments annotated using the 'MIAME annotation' can be represented using MAGE-ML. NASC exports MAGE-ML from NASCArrays, for incorporation into ArrayExpress at the EBI.

The Plant Ontology was developed by the Plant Ontology Consortium, in order to structure and annotate phenotypic descriptions. NASCArrays uses plant ontologies for describing the part of the plant used in the experiment. This benefits plant researchers by allowing them to query the database using defined terminologies.

NASCArrays [Get access, collection, grid button, grid viewer, file name, experiment, bio source, organism, alias, stock, age, affymetrix chip, NASC home](#)

Experiment: Response to cold, soil grown plants

Experiment Description

NASCArrays Experiment Reference Number: [NASCArrays-354](#)

This experiment was annotated by TAIR (<http://arabidopsis.org>).

This experiment looks at changes in gene expression in Col-0 plants grown in soil in response to low temperature over time.

About the Experimenter	About this Experiment
Name: Daniel Zarka	Experiment Type: time_series_design
Head of Institute: Crystal Thomasbow	Number of Slides: 8

Experiment Type: time_series_design

Number of Slides: 8

Experimental Parameters:

parameter: timepoint

Slide: [A2-exp1-Hammo-P06](#) [Add to Slide Selection](#) [Get the data!](#)

BioSource 1 Information

BioSource Name: A2-exp1-Hammo-P06

Organism: Arabidopsis thaliana

Alias: Col-5

Stock Code: [N1644](#)

Age: 4 hours after nutrient removal

Tissue: Rosette leaves

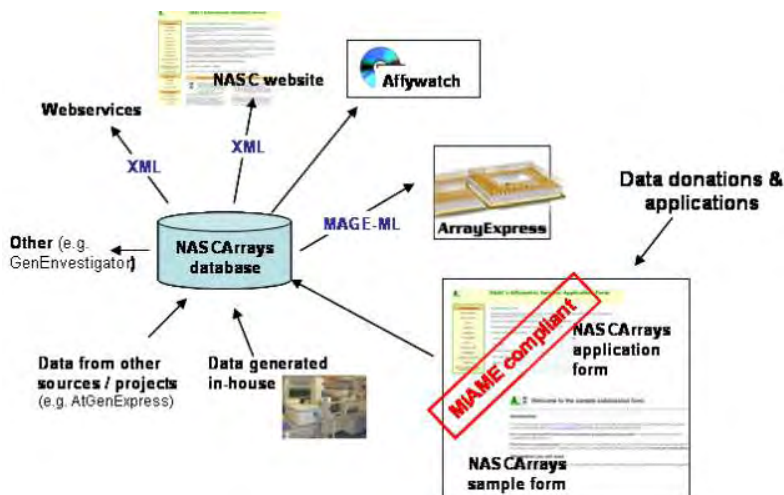
Plant Ontology terms for this tissue type:

[PO:0000014](#) rosette leaf

Tissue: Rosette leaves

Plant Ontology terms for this tissue type:

[PO:0000014](#) rosette leaf



Data Exchange

Data from microarray experiments are stored in NASC's transcriptomics database, NASCArrays. Data is either generated in house, or is donated by the research community. It is then disseminated to the community through a variety of channels, some of which are illustrated left.

However, the data generated from microarray experiments has little meaning without its context. Data standards are therefore essential to allow others to efficiently use the data and are particularly important in data exchange. Customers who use NASC's hybridisation service to perform Arabidopsis experiments automatically have their data put into NASCArrays and it is a pre-requisite that all users provide the necessary information to make their data MIAME-compliant. Those wishing to donate data to NASC also need to ensure they provide full MIAME compliant data.

Do you have array data that you would like to donate to NASC?

If so the procedure is very easy. To begin with just send an email to the Affy Team at NASC (affy@arabidopsis.info), saying that you would like to donate data. A confirmation email will then be sent back to you.

The next step is to fill in an application form (<http://affymetrix.arabidopsis.info/transcriptomics.html>), making sure to tick the checkbox stating that the form is for a data donation. If you wish for your experiment to remain confidential for a period of time (before publication, for example), please just let us know, as you will need a reference number for this.

A sample submission form (<http://affymetrix.arabidopsis.info/sampleform.html>) then needs to be filled in for every sample donated.

Lastly, the actual original .CEL files should be delivered or made accessible to us. This can be done by any method of your choice, for example, by email, CD/DVD by post, or by FTP.

It really is that simple!

Further information on how to donate data to NASCArrays can be found at: <http://affymetrix.arabidopsis.info/donating.html>.



17th International Conference on Arabidopsis Research

June 28- July 2, 2006
Madison, WI, USA

www.union.wisc.edu/arabidopsis

****THE ABSTRACT SUBMISSION DEADLINE HAS BEEN EXTENDED TO MAY 1ST****

****Online registration available until May 26th, On-site registration is available****

****To guarantee accommodations, the deadline date for registration is Friday, May 26th****

NOTE: Abstract submission is now password protected so you must enter the password (extra) prior to entering the registration number assigned after completion of online registration.

Keynote Lecture

Mark Estelle (Indiana University) *Genetic analysis of auxin signaling: A long road to a short pathway*

Special Lecture

Richard Young (M.I.T) *Connecting signal transduction and gene expression*

All Sessions are Plenary and will include over 60 talks:

- *Systems Biology (Philip Benfey, Duke Univ.)
- *Bioinformatics (Christ Town, TIGR)
- *Environment 1: Abiotic (Pill-Soon Song, Kumho Life & Environmental Science Laboratory, and Cheju National University, Korea)
- *Environment 2: Biotic (Xinnian Dong, Duke Univ.)
- *Genetic and Epigenetic Mechanisms (Judith Bender, Johns Hopkins Univ.)
- *Natural Variation and Comparative Genomics (Annie Schmitt, Brown University)
- *Development 1: Flower, Fertilization, Fruit, and Seed (Caroline Dean, John Innes Centre, U. K.)
- *Development 2: Shoot and Root (Dominique Bergman, Stanford University)
- *Metabolism (Harvey Millar, University of Western Australia, AUSTRALIA)
- *Signaling (Ute Hoecker, University of Duesseldorf, GERMANY)
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- *Cell Biology (Jiri Friml, Univ. of Tuebingen, GERMANY)
- *Energy (Steven Rothstein, University of Guelph, CANADA)
- *Arabidopsis 2010
- *NAASC choices (Rob McClung, Dartmouth University)

*Session will include presentations by invited and those chosen by session chairs from submitted poster abstracts. Session chairs are listed in parentheses.

Planned workshops

- Bioinformatics (Web Services and demonstrations)
- AT2010 (data management and submission to repositories)
- PREP (Partnership for Research and Education in Plants)
- The Arabidopsis Information Resource (TAIR)

The conference this year includes an evening of fireworks on the lake on Saturday, July 1st in advance of the July 4th Independence Day holiday.

If you have any questions, please contact the conference organizer (Nancy Kujak-Ford, nmkujak@wisc.edu) or the MASC Coordinator (jdfriesner@stanford.edu).

5 Plant GEMs

■ 11-14 October 2006, Venice, Italy

Plant Genomics European Meetings

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STEFAN JANSSON (UMEÅ, SWEDEN)
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GENE AND GENOME EVOLUTION UNDER DOMESTICATION
GENOMICS OF QUANTITATIVE TRAITS
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Speakers to include

- Willem Gruissem
- Kazuko Y-Shinozaki
- Joanna Schmitt
- Oliver Ratcliffe
- Jim Haseloff

- ETH Zurich
- Tokyo University
- Brown University
- Mendel Biotechnology
- University of Cambridge