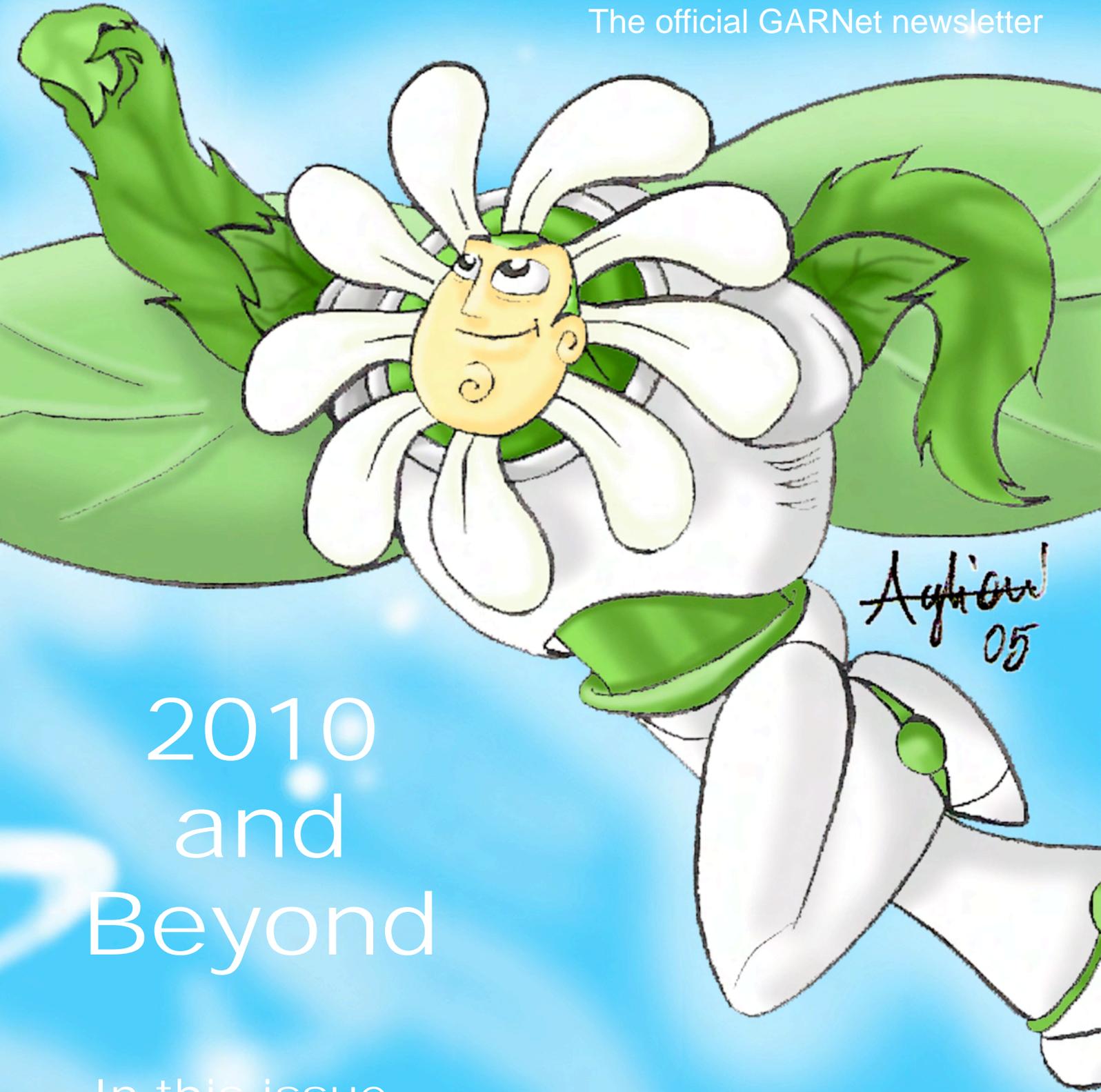


July 2005. Edition 3

GARNish

The official GARNet newsletter



2010 and Beyond

In this issue

MapMan and ProtLocDB
Spotlight on York
Plant GEMs 4



GARNet Grant Success

Welcome, to this, the 3rd issue of GARNish. We hope you have enjoyed the previous two issues and are happy to announce that GARNish will be appearing on your desk or desktop twice a year for the foreseeable future as a result of renewed BBSRC funding until 2010.

This continued funding will allow us;

1. To help researchers gain the best advantage from the current resources and facilitate the production of future services. GARNet aims to keep the Arabidopsis community up to date with functional genomic services and methods via the website, newsletter and annual meeting.
2. To promote interactions and collaborations between Arabidopsis and other UK plant communities via the ABC forum and annual meeting.
3. To aid Arabidopsis researchers make the best advantage of global opportunities by enhancing UK participation in International Research.
4. Facilitate collaborations with other plant functional genomics programmes.

GARNet is here to help and support the community. To ensure we continue to represent and meet your needs, we need to know your thoughts. Please e-mail and tell us your ideas for future services and resources.

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Front illustration by Lucio
e-mail lucioo@liberio.it

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

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

GARNet 2005 "2010 and Beyond"

This year the 6th Annual GARNet meeting 'GARNet 2005' will be held at the John Innes Centre Norwich from the 5th to the 6th September. Our overall theme, '2010 and beyond', aims to look to the future of plant research be it systems biology or greater interactions between plant communities.

With a programme that includes internationally renowned speakers such as David Baulcombe (Sainsbury Laboratory), Nam-Hai Chua (Rockefeller University), Ottoline Leyser (University of York), Wayne Powell (NIAB) and Bob Pruitt (University of Purdue) we hope that this year's meeting will be as successful as the previous five which have attracted up to 200 delegates from across the UK and Europe. In addition to the main plenary session there will be workshops to help keep you up to date with the tools and resources that are currently available, along with information on funding and co-ordination. For a full programme visit http://garnet.arabidopsis.info/garnet_meeting.htm.

In addition to our consistent and much appreciated support from the UK Brassica Community we are pleased to announce that this year's meeting will also be hosted by the UK Cereal Community, transforming the meeting into the 1st UK wide ABC (Arabidopsis, Brassica and Cereal) gathering. To ensure we capitalise on the wide range of UK plant scientists attending GARNet 2005 we are holding an ABC forum, to discuss how to improve current interactions and two-way (or more) information exchange between Arabidopsis and Crop science

Registration is now open at http://garnet.arabidopsis.info/garnet_meeting.htm.

Come to Norwich and help us make this an enjoyable and successful meeting.

A 'distributed centre' for Arabidopsis systems biology

Think of a number between 3 and 350. EPSRC and BBSRC funded three Centres for Integrative Systems Biology (CISB) earlier this year and will perhaps fund another three from the second round. Systems approaches to biology often require large-scale research projects, not just to make all the required measurements but to do so with sufficient coordination that the resulting data are comparable and can be analysed and modelled together. The UK has around 350 plant research laboratories, many of which study Arabidopsis. Can groups of these laboratories coordinate their work, in order to tackle large-scale projects in plant biology? Can we set up a *distributed* centre for systems biology, a virtual CISB?

This is the question posed to GARNet by BBSRC's panel on Integrative Systems Biology, which is also running the CISB initiative. The Streptomyces research community has been asked the same question. The notion of a UK-wide "centre" is a radical departure from the CISB awards, which are intended to concentrate all the expertise and facilities required for systems biology in a single location, even a single building. GARNet's advisory committee has been asked to report by April 2006 on the feasibility of large-scale joint research on Arabidopsis systems biology.

The collective research potential of these 350 laboratories is significant, to put it mildly, but there are some hard questions to answer before even a decent fraction of that potential could get to work on a short list of research goals. How many labs can realistically work together? How would their support mechanisms have to change? What are the best research opportunities? The GARNet advisory committee will be working on these and other questions over the next few months. The BBSRC workshop, 'Succeeding in Plant Systems Biology', in Edinburgh on July 25-26 will contribute to the process. We will be looking to all of the UK plant laboratories for your input.

Research in plant biology isn't usually organised around Grand Challenges, but some such phrase might now be appropriate. Other disciplines have Grand Challenges more often: Professor Andrew Bangham will introduce the *In Vivo-In Silico* Grand Challenge proposal at the 2005 GARNet meeting, Sept 5-6, which aims to develop a virtual bug, worm and weed (<http://www.cmp.uea.ac.uk/Research/ivis/>) in the next 12 years. A virtual weed? Just a 4-D, seed-to-seed model of Arabidopsis development, with responses to the biotic and abiotic environment and all the networks of 'omics data that prompted the establishment of GARNet, most work here will be needed in the computational aspect but for the data, will 3 labs or 350 be required?

Andrew Millar, GARNet Co-ordinator

News and Views

Growth and Development Ontology Released

The first controlled vocabulary of terms describing whole plant growth stages in a generic flowering plant was released in April this year. This ontology can be used for Arabidopsis, soya bean, maize, rice and the Triticaceae, providing a useful framework for cross species queries such as which mutations affect inflorescence development in Arabidopsis and maize. A further set of descriptions for plant organ development is currently being undertaken and should be available soon. For more information see www.plantontology.com.

NASC is also currently in the process of introducing plant ontology terms into the annotation of germplasm lines to aid users when browsing and searching for data, for more information see <http://arabidopsis.info/>

Plant Tool Box

At the SEB Plant Science Frontier Meeting in March this year GARNet held a brain storming session to generate suggestions from the community for potential new services. Ideas put forward included; networks and training in systems biology, comparative mapping tools and easier access to previously generated lines/vectors. The latter led to the idea that GARNet should help to co-ordinate a publicly-accessible Plant Tool Box that would contain:-

- a) Generic vectors such as pGreen and entry vectors.
- b) Useful promoters in convenient vectors.
- c) Cellular markers.
- d) Lineage Markers.
- e) Selectable Markers.

Before GARNet undertakes such a task we would like to assess its feasibility by asking you the following:-

1. Would you use such a resource as the Plant Tool Box?
2. Do you have suggestions for items you would like to see included in the Tool Box?
3. Do you have resources in the lab, which have been thoroughly tested/ peer reviewed, that you would be happy to donate to the Tool Box?

Please e-mail all comments to ruth@arabidopsis.info

ERA-PG Update

written by Sophie Laurie BBSRC

BBSRC's early willingness to earmark funds for the ERA PG has been a driving force and many of the other partners have now also come on board for the common call. Funds in the region of €18M per year have been pledged, dependant on the successful outcome of the planning stages of the ERA Net. A report from the first workpackage is in its final draft stages and will soon be posted on the ERA PG internet site, with access from the public pages (www.erapg.org). This will present findings of a combined survey of plant genomic programmes and administrative procedures around Europe, with a view also on the main players around the world in this scientific arena.

The report will feed in to a workshop at the John Innes Centre on the 29th and 30th June 2005. The workshop programme can be viewed on the ERA PG website and will have guest speakers from academia, industry and the Technology Platform 'Plants for the Future' on the first day. The second day will be devoted to concurrent workshops aiming to build a framework for the first common call, expected late in 2005 or early in 2006. Participants have been invited with the aim of covering the spectrum of interested communities in each country, bearing in mind a strict limit on numbers. Comments are welcome on the content of the report however and further information on the programme can be obtained from Sophie Laurie at the BBSRC (sophie.laurie@bbsrc.ac.uk).



New Techniques Journal

Plant Methods is a new open access, online journal that will soon be available via BioMed Central. Plant Methods central aim is to stimulate the development and adoption of new and improved techniques/tools in plant biology. This will be achieved by providing plant biologists with rapid publication of peer-reviewed articles focusing on technological innovation in the plant sciences.

All articles published by Plant Methods will be freely available online and permanently archived in PubMed Central. There will be no page limits or restrictions on large data sets, no colour charges or limits on numbers of figures and publication will be immediate upon acceptance. There will be no publication charges at all for the first 6 months after launch. After that, authors who belong to institutions that subscribe to BioMed Central (e.g. all UK universities), won't have to pay the £410 publication charge either.

Help improve the community's access to technical innovation in plant science and support Plant Methods.

Plant Methods

Editor-in-Chief: Brian G. Forde

Deputy Editor: Mike R. Roberts

Editorial Board: Anna Amtmann, Tobias Baskin, Ton Bisseling, Oliver Fiehn, Wolf Frommer, David Galbraith, Stanton Gelvin, Simon Gilroy, Ian Graham, Claire Grierson, Thomas Guilfoyle, Jeff Harper, Andrzej Jerzmanowski, Julia Kehr, Marc Knight, Peter Langridge, Paul Lazerri, Roger Leigh, Jaideep Mathur, Harvey Millar, Scott Peck, Julian Schroeder, Motoaki Seki, Ramon Serrano, Sidney Shaw, Mark Stitt, Richard Thompson and Peter Waterhouse.



CAMBIA release alternative to Agrobacterium

In February this year CAMBIA (the non-profit Australia-based Centre for the Application of Molecular Biology to International Agriculture) reported in Nature that bacteria other than *Agrobacterium* can be used for gene transfer. Using a modified Ti plasmid introduced into *Rhizobium*, *Sinorhizobium* and *Mesorhizobium*, CAMBIA researchers showed that it was possible to introduce a GUSPlus (™) marker into Arabidopsis, rice and tobacco. This is an exciting breakthrough, it not only provides an alternative method for gene transfer, but also presents the community with a tool that is easily accessible to researchers across the globe as a result of CAMBIA's 'open source' agreement which has no commercial restrictions. CAMBIA hope that this will equip researchers in developing countries with transformation technology which has previously been inaccessible as a result of the patenting of *Agrobacterium*-based methods.

For more information on CAMBIA see <http://www.cambia.org/>

Arabidopsis Resources

ProtLocDB

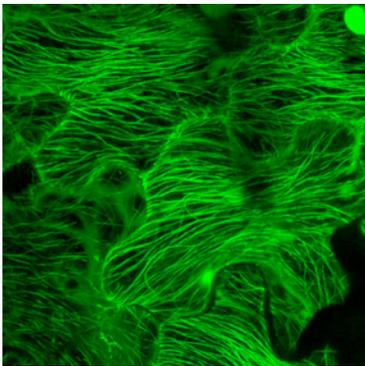
<http://bioinf.scri.sari.ac.uk/protlocdb.html>
written by Kenny Bell, SCRl

PROTLOCDB

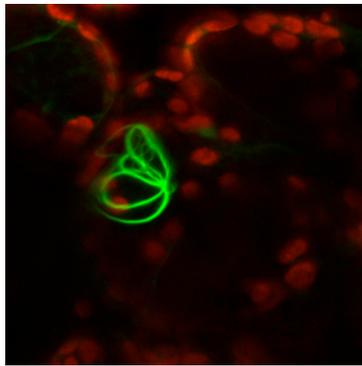
ProtlocDB (<http://bioinf.scri.sari.ac.uk/protlocdb.html>) is a new web resource for the plant science community, showing high quality images of subcellular protein targeting generated using green fluorescent protein (GFP) tagging and viral expression. The images have been created as part of a Scottish Crop Research Institute project on functional genomics of plant cell organelles, funded by the Gatsby Foundation. The project runs within the Cell to Cell Communications programme with assistance from the Computational Biology group.

The basis of the project is cloning, *en masse*, of CAP-dependant cDNA libraries (i.e. with 5' cDNA ends intact) into a tobacco mosaic virus GFP vector. When the viral libraries are inoculated onto *Nicotiana* leaves, the cloned cDNAs are expressed with GFP fused to the C-terminus. Since each infection locus expresses a single cDNA-GFP fusion, subcellular targeting of individual fusion proteins can then be determined by confocal microscopy. The sequence of the cDNA responsible for a particular phenotype is then retrieved by excision of the lesion, RNA extraction, RT-PCR and sequencing.

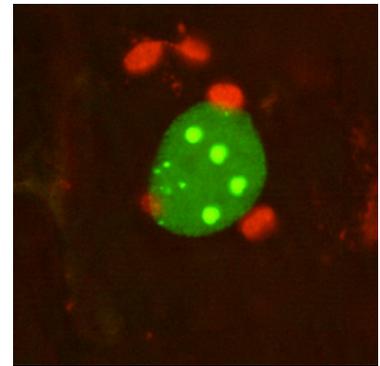
Libraries have been created from *Nicotiana* root tissue and from *Arabidopsis* aerial tissue and cell culture material. For *Arabidopsis* cDNAs, the corresponding gene can readily be identified from the complete genome sequence. Proteins that localize to numerous locations have been observed and the fidelity of localization of characterized *Arabidopsis* proteins is generally conserved when produced in *Nicotiana* hosts. The localization of unknown proteins has provided clues as to their function, while in some cases putative localizations tally with those observed *in planta*. Sometimes entire organelles are labelled but we have also observed more specific labelling within organelles, plasmodesmata, cytoskeleton and unknown cytosolic bodies. Sequencing and screening for more novel proteins is ongoing.



Viral expression of a kinesin motor protein-GFP fusion resulting in microtubule labeling.



Viral expression of an unknown protein (At5g41970) as a GFP fusion resulting in an unknown labeled string-like structure.



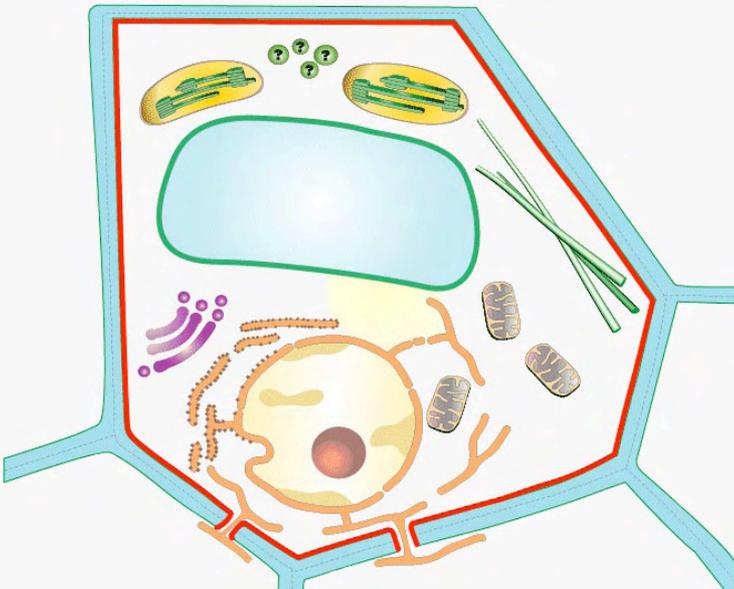
Viral expression of a zinc finger family protein (At3g12630) as a GFP fusion resulting in nuclear labeling including bodies in the nucleoplasm.

Search by location

Use the drop down list box or click on the image to retrieve images from a desired location.

This page allows you to search for images in the database that have been localised to a defined position within the cell.

Either select a location from the list box then click the "Search" button or click on the image of the plant cell at the location you are interested in.



Select images from the database which are localised to the

Nucleus

And from species

Arabidopsis thaliana

The website shows high quality images of protein targeting that may be resized by the viewer. The images are linked directly to both the sequence and BLAST information for each clone. Data can be searched and sorted by various criteria, for example by viewing images showing targeting to particular organelles or by searching the sequence descriptions for particular terms. Users may request higher resolution images and clones of special interest. This project is providing clues to the role of a growing number of proteins of unknown function and is providing information not readily obtainable by other means e.g. on "difficult" and precise subcellular localisations. We hope therefore that the website will be of value and interest to the plant science community.

Arabidopsis Resources

MapMan – Integrative display of profiling data

<http://gabi.rzpd.de/projects/MapMan/>

written by Oliver Thimm, CNAP - University of York

The technical advance of high-throughput techniques profoundly revolutionised plant biology and now provides the opportunity to generate complementary datasets that allow a detailed insight into plant systems. The publicly available MapMan software tool offers scientists a combination of biological pre-knowledge, data visualization, and bioinformatics solutions, which help to access profiling data in an intuitive and purposive way. The MapMan software functionally categorizes genomic and metabolomic profiles in order to display colour-coded data onto biochemical pathways or customized maps. This approach allows the user to investigate data assigned to certain biological processes, or in any desired combination, to represent individual research interests.

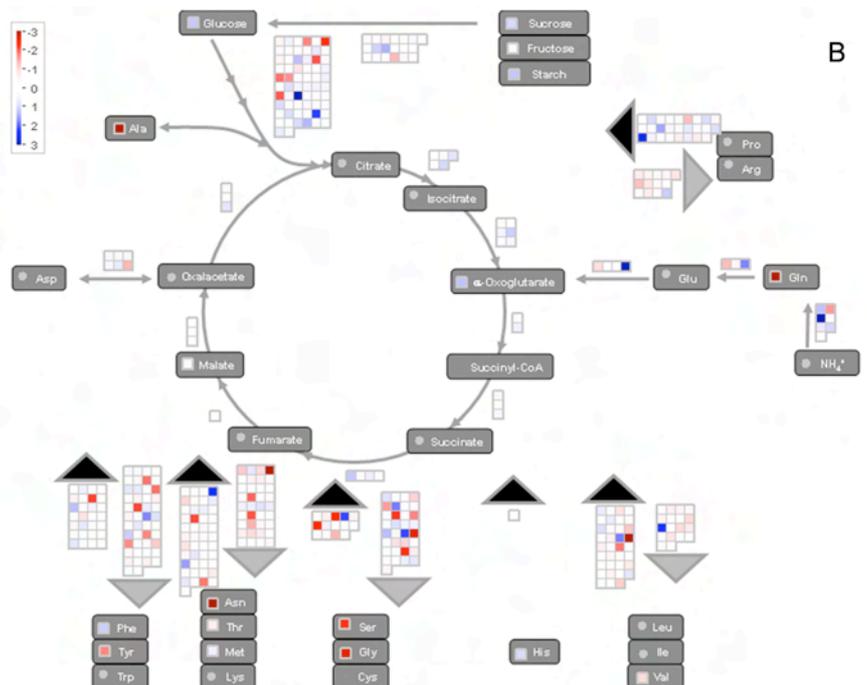
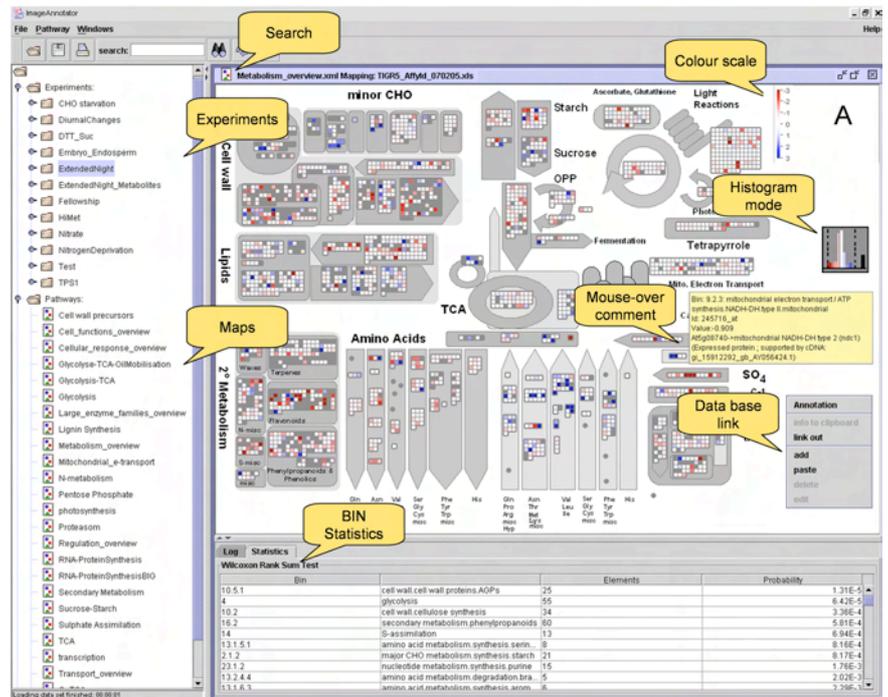
The intuitive structure of the Mapman ontology allows biologists a quick access to their area of interest. Profiling data can be inspected in overview modes e.g. central metabolism, (A) or be analysed at an enzyme/metabolite level (B) for detailed data interpretation. To ensure a high quality of functional assignments and maps, annotations are regularly updated, manually curated and improved by expert annotations.

The MapMan interface was also designed to allow an easy and intuitive handling of maps and experimental data. To display data the user simply selects a map of interest, a corresponding mapping file and the experimental data. Individual data can be identified by *mouse-over comments* or by the *search function* using regular expressions. Additional information from public data bases is provided by an integrated *link out function*. Changes at the level of functional categories (BINs) can be inspected using the *histogram mode*; a bar plot indicating the distribution of data in a particular group of genes or metabolites. *Statistical support* is provided by a built-in Wilcoxon rank sum test module. BINs are tested for response differences in comparison to all other BINs and resulting p-values are shown on demand.

The current version of MapMan also allows the *integrative display* of data sets from complementary approaches (e.g. transcript and metabolite profiles) on a single map (B). This new feature substantially facilitates the analysis and interpretation of different profiling data as well as the generation of hypothesis.

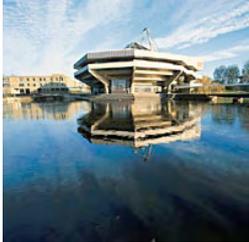
Current developments include the functional annotation of other plant genomes and the implementation of additional statistics modules.

We are grateful to many experts who helped to improve the functional gene annotation of MapMan. To simplify the exchange of knowledge we will release a new curation tool called *MapCave* that allows a transparent and interactive editing of functional gene annotations. For further information and support please contact usadel@mpimp-golm.mpg.de or nagel@rzpd.de.



Spotlight on York

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 will be focusing on geographic areas and institutions across the UK, bringing you a synopsis of the interests of each research group within the chosen location. We start our tour in York.



Department of Biology at York

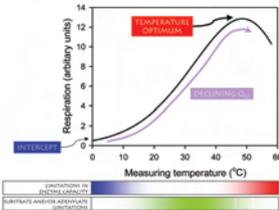
Founded in 1965, the Department of Biology at York expanded into new laboratories in 2002, funded by a £21.6 million JIF award from the BBSRC. The labs provide 10,000m² of research space for 61 research groups, the Structural Biology Laboratory from the Department of Chemistry and a Technology Facility which offers state of the art equipment to all members of the department. 18 research groups within the department carry out plant research on a wide range of topics from physiological adaptation to secondary metabolism as outlined below.

Plant Research

Name Owen Atkin
e-mail oka1@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/oka.htm>
Research Area Plant carbon metabolism and temperature.

Research Activities

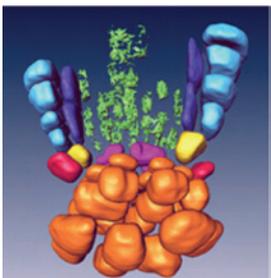
Owen's laboratory investigates the interplay between the genetic potential of plants and the environment in which they grow. Research is particularly focused on the impact of variable temperatures on plant carbon metabolism. The group is carrying out ecological studies on a wide range of plant species, characteristic of contrasting habitats, to understand how variable temperatures affect growth and carbon metabolism. The aim of this work is to establish criteria by which the temperature responses of photosynthesis and respiration can be predicted. The physiological and biochemical processes that underpin variability in the response of plant respiration to short and long term changes in temperature are also being investigated.



Name Sue Bougourd
e-mail smb12@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/smb.htm>
Research Area Coordination of cell division during plant growth and development.

Research Activities

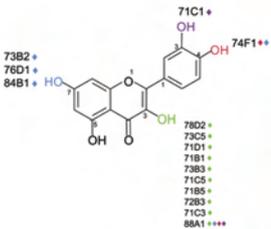
Cell division is a basic characteristic of living organisms, playing a key role in generating the cells that will subsequently expand during plant growth and development. To study this highly coordinated process, cell division is perturbed in specific cell layers of the *Arabidopsis* root meristem during embryogenesis, via targeted misexpression of cell cycle regulators. Using this approach Sue hopes to gain a better understanding of how growth and division are influenced by neighbouring cells and layers. Complementary studies of root meristem mutants displaying aberrant patterns of cell division and/or expansion are also being undertaken. In addition work is being carried out into the role of cell division and expansion during leaf growth and morphogenesis, and the role of cell division in stomatal patterning. To aid these research areas, new methods for fluorescent imaging of *Arabidopsis* embryos are being developed in collaboration with Jim Haseloff.



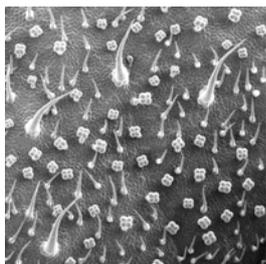
Name Dianna Bowles
e-mail djb32@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/djb.htm>
Research Area Plant glycosyltransferases: functions *in vivo*, utility *in vitro*.

Research Activities

Glycosyltransferases that recognise small molecules play a central role in cellular homeostasis, regulating flux through pathways of secondary metabolism, levels of bioactive hormones and clearance of biotic and abiotic toxins. Dianna's laboratory is studying the multigene family of these glycosyltransferases from *Arabidopsis thaliana*. They have developed a platform of 107 recombinant enzymes that can be screened for their activity and discovered those that glycosylate; (1) hormones including auxins, cytokinins, abscisic acid and salicylic acid, (2) phenylpropanoids and related monolignols and aldehydes, and (3) anti-oxidants such as quercetin which can be regiospecifically glycosylated in whole cell biocatalysis. Research into glycosyltransferases function *in planta* focuses on the involvement of these enzymes in abiotic and biotic stress responses. *In vitro* studies include development of novel combinatorial biocatalysis systems and modification of specificity and affinity via domain-swapping and additional engineering.



Spotlight on York



Name Pierre Broun
e-mail pbk22@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/pb.htm>
Research Area Regulation of epidermal wax biosynthesis and epidermal cell differentiation.

Research Activities

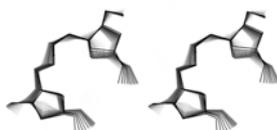
The epidermis defines the interface between plants and their environment and plays a critical role in a wide range of processes including defence and response to abiotic and biotic stress. This functional versatility of the epidermis stems from its ability to produce a wide variety of chemicals and to differentiate cellular structures that can produce and store these compounds. Pierre's laboratory focuses on the molecular mechanisms that govern the differentiation of epidermal cells into specialised cellular factories. This is achieved by; (1) investigating the ability of epidermal cells to produce and secrete protective hydrophobic waxes, in particular the lab is interested in the role played by transcription factors in controlling this metabolic process, and (2) understanding the molecular nature of signals that trigger the formation of trichomes, which in many plant species are a major site of metabolite accumulation. In addition work is being carried out to investigate how secondary metabolism is controlled in the secretory cells of trichomes.



Name Neil Bruce
e-mail ncb5@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/ncb.htm>
Research Area Engineering transgenic plants for the phytoremediation of pollutants.

Research Activities

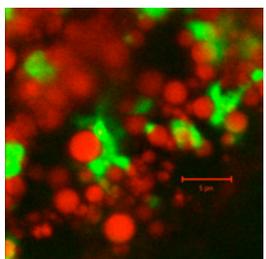
Phytoremediation offers an environmentally friendly means of removing pollutants, such as toxic explosive residues, from contaminated sites. Plants have a remarkable ability to extract, sequester and detoxify pollutants from the soil, water and air. However, the innate biodegradative abilities of plants are less than those of adapted bacteria and fungi. In addition phytoremediation of organic pollutants by plants can result in phytotoxicity and death. It is possible to overcome these limitations by using genetically engineered plants possessing bacterial genes conferring the ability for the degradation of pollutants or transformation of toxic explosives such as TNT. For example, the Bruce lab have recently shown that transgenic plants expressing a bacterial nitroreductase are able to remove more TNT from the soil than wild-type plants, work is currently underway to engineer plants for the phytoremediation of all the major classes of explosives.



Name Leo Caves
e-mail lsdc1@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/lscd.htm>
Research Area Computational Biology.

Research Activities

Computational biology has become an integral part of biological research in the post-genomic era, to assist biologists make the best possible progress in this field, research in Leo's group is focused on the following areas. Firstly the development of tools for the support of data analysis and representation, for example the development of interactive data visualisation tools for large datasets produced by transcriptomics and proteomics. Secondly, biomolecular modelling and simulation, for example by studying the sequence and structure of kinesin, in combination with simulations of its dynamics and intermolecular interactions, the group has been able to further our understanding of the anatomy and physiology of this enzyme.

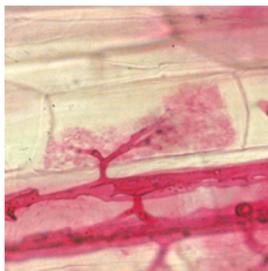


Name Peter Eastmond
e-mail pje4@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/pje.htm>
Research Area Regulation of storage oil breakdown in germinating seeds.

Research Activities

Many eukaryotic organisms store chemical energy in the form of oil (triacylglycerol). In plants these are particularly abundant in seeds and are broken down during germination by hydrolases to fuel post-germinative growth. Although triacylglycerol hydrolase has been extensively studied in many prokaryotes and eukaryotes, little is known about lipases from plants. Peter's laboratory is interested in identifying these enzymes and understanding the role they play in regulating oil metabolism in plants. This research involves a combination of approaches to identify and characterise lipases from the seeds of model species such as Arabidopsis, oilseed rape and castor bean. For example, a proteomics study in castor bean has identified an oil body associated lipase and a genetic screen in Arabidopsis is currently underway to identify mutants impaired in the regulation of post-germination oil break down.

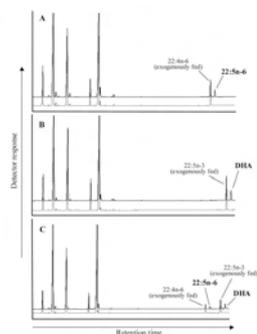
Spotlight on York



Name Alastair Fitter
e-mail ahf1@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/ahf.htm>
Research Area Belowground ecology: functioning of mycorrhizal associations under field conditions; root turnover and the global carbon cycle.

Research Activities

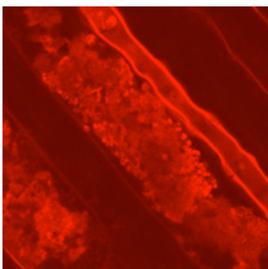
Resource acquisition from the soil is determined both by the architecture of roots and their interactions with mycorrhizal symbionts such as Arbuscular mycorrhizal fungi. These symbiotic associations are responsible for phosphate uptake in many plant species and also confer other nutritional and non-nutritional benefits. To gain a better understanding of how roots acquire resources from the soil Alastair's laboratory is studying the role of mycorrhizal symbioses on root function and their potential role as a rapid pathway of carbon movement from the atmosphere to the soil. The research group also has a particular interest in the molecular and genetic variability of fungal-plant interactions. It is understood that specific plants are colonised by distinct fungal types and the laboratory is investigating if this selectivity affects the success of the plant-fungal combination.



Name Ian Graham
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Website <http://www.york.ac.uk/depts/biol/staff/iag.htm>
Research Area Metabolic engineering.

Research Activities

Plant seeds are able to produce and break down a wide range of products including protein and oils. By understanding the pathways in plant metabolism that control synthesis and degradation of these compounds Ian aims to exploit the potential of crop plants as factories for the production of novel products such as nutraceuticals, pharmaceuticals or renewable and environmentally friendly alternatives to petrochemicals. For example docosahexaenoic (DHA) is an important nutraceutical and the active ingredient in fish oil. Ian's laboratory has discovered a number of genes from marine algae involved in the synthesis of DHA and is now collaborating with industry to evaluate how these genes can be used to engineer DHA production in oilcrops.



Name Angela Hodge
e-mail ah29@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/ah.htm>
Research Area Nitrogen Capture by Plants & Arbuscular Mycorrhizal Fungi.

Research Activities

Plants generally capture the limited nutrient nitrogen in its inorganic form from soil and rely on microbes to release inorganic nitrogen (as NH_4^+) during decomposition of organic material. The distribution of nutrients within the soil is heterogeneous or 'patchy', plants must therefore forage to locate and utilise these nutrient-rich patches. To aid nutrient uptake some plants form associations with specialist mycorrhizal fungi which allows direct access to organic nitrogen sources that would otherwise be inaccessible to the plant. The most common form of mycorrhizal symbiosis is the arbuscular mycorrhizal (AM) association; an association that occurs with two thirds of all land plants. To gain an insight in to how plants detect and utilise nitrogen sources in the soil, Angela's laboratory is focused on how plant roots and arbuscular mycorrhizal fungi respond to nutrient patches in soil using stable isotope techniques.

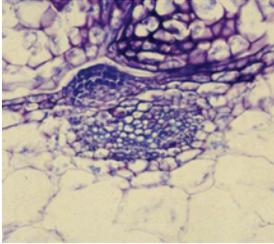


Name Louise Jones
e-mail alj2@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/alj.htm>
Research Area Epigenetic mechanisms in plants.

Research Activities

RNA silencing is an evolutionary conserved mechanism of targeted mRNA degradation, which is thought to have roles in the control of endogenous gene expression and in the suppression of viruses and transposable elements. RNA silencing is understood to affect these processes via a number of mechanisms including epigenetic changes such as DNA and histone methylation. To try and dissect this epigenetic aspect of RNA silencing Louise is undertaking two main approaches; (1) a forward genetic screen in *Arabidopsis thaliana* to identify novel components of this pathway, and (2) analysis of known candidate genes. The lab has a particular focus on the ARGONAUTE (AGO) gene family which have been implicated in integrating RNA silencing, epigenetic modification and development. Investigations of microRNA (miRNA) function in Arabidopsis are also being conducted by disruption of specific miRNA-mRNA pairings and analysis of the resulting phenotypes.

Spotlight on York



Name Ottoline Leyser
e-mail hmol1@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/hmol.htm>
Research Area Hormonal Control of Shoot Branching.

Research Activities

A unique feature of plant development is the ability to alter body plan in response to environmental conditions. The body plan of plants, like animals, is laid during embryogenesis, giving rise to the primary body axis. In addition plants are able to elaborate this basic architecture post-embryonically via secondary meristems that form new axes i.e. lateral branches. It is this ability to produce lateral branches that gives plants their spectacular plasticity of form. The research in Ottoline's lab is aimed at understanding the role of hormones in developmental plasticity, using shoot branching as an example. Studies are focused on two hormones that inhibit branching, auxin and a novel hormone, which has not yet been chemically defined. By combining genetic, biochemical and physiological data, the aim is to understand how plant hormones integrate environmental, developmental, and genetic inputs to shape the plant body plan.

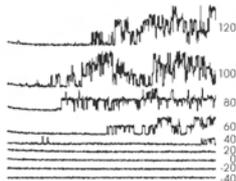


fig1: Recording showing individual cation channels in the tonoplast membrane. Openings become more frequent at positive potentials (shown at right side).

Name Frans Maathuis
e-mail fjm3@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/fm.htm>
Research Area Plant Nutrition and Plant Stress.

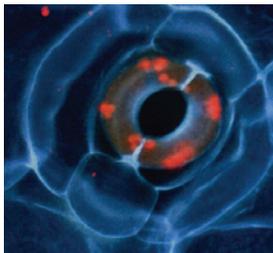
Research Activities

Research in Frans' lab centres on plant nutrition and plant stress. Aspects of plant nutrition being investigated include molecular mechanisms of cation uptake and translocation throughout the plant. Plant stress research focuses on the detrimental effects of high ambient salinity, a global⁺ and increasing problem. The laboratory is particularly interested in the molecular pathways for Na⁺ uptake and how these are regulated by cyclic nucleotide signalling. Transport, physiological impact, nutritional aspects, and toxicity of heavy metals, e.g. Zn²⁺ are all further research interests. A range of techniques are being employed to study these subjects including electrophysiology to characterise ion channels, transcriptomics to identify genes that are involved in plant salt tolerance and cyclic nucleotide signalling, use of reporter genes such as GUS and GFP to determine expression patterns of membrane transporters, and proteomics to study the function of transporters expressed in the plant tonoplast.

Name Simon McQueen-Mason
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Website <http://www.york.ac.uk/depts/biol/staff/sjmm.htm>
Research Area Plant Cell Walls.

Research Activities

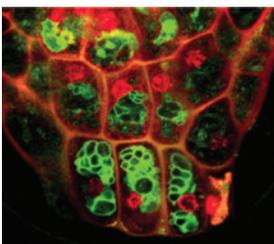
The cell wall is a key feature of higher plants, as well as providing skeletal support it determines much of the development and specialisation of plant structures. Plant cells can increase their volumes at rates exceeding 10% per hour, during this time the wall must remain strong enough to contain the extreme tension from turgor pressure yet flexible enough to accommodate expansion. To understand how the cell wall achieves this, research in Simon's laboratory is largely focused on the molecular basis of the mechanical properties of plant cell walls. The lab is particularly interested in the extension of the wall during cell growth as it is thought that changes in extensibility regulate the rate of expansion. The laboratory is also investigating the remarkable flexibility seen in specialised cell walls, such as those of stomatal guard cells and resurrection plants.



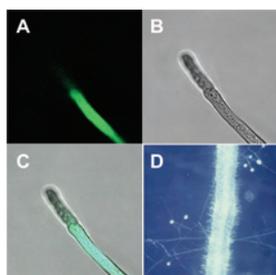
Name Dale Sanders
e-mail ds10@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/ds.htm>
Research Area Plant Membrane Transport and Signalling.

Research Activities

Cations play essential roles in many biological systems; as cofactors of enzymes and transcription factors, as osmotic, as energy transducers and stabilisers of phosphate-containing metabolites. In addition others ions such as calcium have evolved important roles in cell signal transduction. As sessile organisms, plants often face problems in obtaining these critical nutrient ions from the soil, this has even required some plants to evolve strategies to grow in potentially toxic concentrations of some cations – especially heavy metals. Work in Dale's laboratory focuses on the plant transport systems responsible for uptake of these nutrients ions from the soil and their distribution within and between cells. Studies include the characterisation of heavy metal transporters with respect to their specificities and physiological functions; of particular interest is their capacity to enhance the concentration of essential micronutrients such as zinc in food. Recent work has also involved the discovery and characterization of a novel calcium-permeable, vacuolar channel that plays a role in seed germination and in stomatal closing.



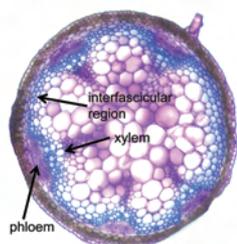
Spotlight on York



Name Michael Schultze
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Website <http://www.york.ac.uk/depts/biol/staff/ms.htm>
Research Area Genetic basis of the arbuscular mycorrhiza development.

Research Activities

Symbiosis between plant roots and a specific group of fungi leads to the development of arbuscular mycorrhizas ("fungal roots"). Fungal hyphae grow inside and around the plant root and help the plant to obtain mineral nutrients from the soil. In return, the fungus receives sugar nutrients from the plant. In the absence of a host plant, these mycorrhizal fungi are unable to grow and multiply. Michael's laboratory is carrying out research to understand how this type of plant-microbe symbiosis is controlled at the genetic level. Research areas include; a screen in *Medicago* for genes that are necessary for symbiosis to be successful. This work will hopefully allow a better understanding of why beneficial fungi such as arbuscular mycorrhizas, can gain access to plant roots while pathogenic fungi causing disease are repelled by the plant's defence system.



Name Neil Taylor
e-mail ngt2@york.ac.uk
Website <http://www.york.ac.uk/depts/biol/staff/ngt.htm>
Research Area Regulation of Cellulose Synthesis.

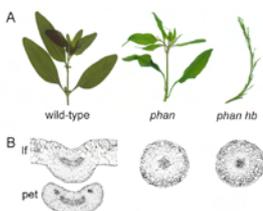
Research Activities

Cellulose is central to plant development and growth. Cellulose deposition in secondary ('woody') cell walls contributes to the mechanical properties allowing upright growth and the provision of channels for water transport to the aerial parts of the plant. Despite the importance of cellulose little is known about its synthesis. Work in Neil's laboratory aims to increase our understanding by studying three genes in *Arabidopsis* that are essential for cellulose synthesis in the secondary cell wall. These genes encode proteins which interact in a large plasma membrane bound complex that synthesises cellulose. Research is currently focused on understanding the regulation of these genes at the transcriptional level, as well as studying the assembly and targeting of the cellulose synthase complex and its regulation once inserted into the plasma membrane.

Name Richard Waites
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Website <http://www.york.ac.uk/depts/biol/staff/rw.htm>
Research Area Plant Cell Walls.

Research Activities

As leaves emerge from shoot apical meristems, and petals from floral meristems, they flatten perpendicular to an upper (adaxial) - lower (abaxial) axis. As plant development continues layers of different cell types differentiate asymmetrically along this ab-adaxial axis. Mutants that lack either abaxial or adaxial cell types produce radial organs that fail to flatten and produce a symmetrical arrangement of remaining cell types, indicating that the juxtaposition of abaxial and adaxial cell types is essential for lateral growth and the specialised shape of leaves and petals. To investigate how abaxial and adaxial cell fate is determined during leaf and petal development Richard's research is centered on the *PHANTASTICA (PHAN)* gene which encodes a MYB-related transcription factor, required for several aspects of leaf development in a diverse range of plant species. By investigating genes that interact with *PHAN*, or are targeted by it, Richard aims to gain a better understanding of how adaxial and abaxial fate is specified and its role in plant development.



Useful Websites

Oligogo

<http://oligogo.botany.wisc.edu/>

A web based primer design site for *Arabidopsis* gene families.

This website identifies and displays members of a gene family from a single AGI code. Once a family is identified Oligogo searches for T-DNA insertion lines in the genes of interest and provides an excel table of primers for genotyping. Oligo also provides primers for RT-PCR.

Botany Array Resource

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

A user friendly web based resource that facilitates analysis of gene expression data. It contains microarray data from NASC Arrays and AtGenExpress. Tools for querying data include Expression Browser; generates e-northerns, Expression Angler; fishes for genes with similar expression patterns and Promomer; identifies over represented words in a promoter or group of promoters. Reference:- Plant J. 2005 Jul;43(1):153-63.

4. Plant GEMs Amsterdam 2005 Plant Genomics European Meetings

20. - 23. September
www.plantgems.org

Plant-GEMs, the Plant Genomics European Meetings are annual meetings on the subject of genomics in all its aspects and sponsored by four national Plant Genomics programmes in Europe and the European Research Area Network Plant Genomics. The fourth Plant-GEM will take place at the Congress Centre RAI in Amsterdam, The Netherlands, from September 20 - 23, 2005

Programme

TUESDAY, September 20

Registration & Opening reception

Opening session

Chair: Willem Stiekema

WEDNESDAY, September 21

Session 1: Highlights in Genomics

Chair: Marc Zabeau, Belgium

Session 2: Genome Structure, Evolution and Comparative Genomics. Chair: Javier Paz-Ares, Spain

Session 3: Genomics Assisted Breeding
Chair: Francesco Salamini & Roberto Tuberosa, Italy

Session 4: Nutrigenomics
Chair: Raoul Bino, Netherlands

THURSDAY, September 22

Session 5: Genetic Networks Underlying Biological Processes. Chair: Ruth Bastow, United Kingdom

Session 6: Epigenetics, small RNAs and Chromatine Structure. Chair: Olivier Voinnet, France

Session 7: Function of "Unknown Genes"
Chair: Ian Small & Michel Caboche, France

Session 8: Plant Genomics and Environment (abiotic and biotic). Chair: Pablo Vera, Spain

FRIDAY, September 23

Session 9: Bioinformatics
Chair: Klaus Mayer, Germany

Session 10: Natural Variation
Chair: Maarten Koornneef, Netherlands/Germany

Session 11: Plant Systems Biology
Chair: Dirk Inzé, Belgium

Speakers (confirmed)

Altmann, Thomas	Baulcombe, David
Bhalerao, Rishikesh	Bino, Raoul
Colot, Vincent	Cooper, Mark
Faure, Sebastian	Folstar, Peter
Greirson, Claire	Gruissem, Wilhelm
Inzé, Dirk	Jong de, Hans
Loake, Gary	Loudet, Olivier
Martienssen, Robert	Meinke, David
Morgante, Michele	Müller, Michael
Parker, Jane	Paz-Ares, Javier
Pereira, Andy	Perez, Pascual
Scheres, Ben	Schiex, Thomas
Schoof, Heiko	Schulze-Lefert, Paul
Shinozaki, Kazuo	Stiekema, Willem
Stitt, Mark	Town, Chris
Traas, Jan	Zabeau, Marc

Abstracts

Posters will be on display throughout the congress. A number of abstracts will be selected for oral presentation. Please submit your abstract for a poster or oral presentation via the website.

Registration

Before July 15, 2005:

Registration € 400, Student € 300

After July 15, 2005:

Registration € 500, Student € 400

The registration fee includes admission to all sessions, poster sessions and exhibition, opening reception, coffee/tea, 3 lunches, conference materials and a copy of the abstract book.

Hotel Accommodation

RAI Hotel Service has made a selection of hotels near the Amsterdam RAI and in the city centre of Amsterdam. Demand for hotel rooms in Amsterdam is very high in September. **Our advice is to make your reservation as soon as possible, but before June 15 at the latest!** You can book your hotelroom via the website.

Local organisers

Willem Stiekema, Sjef Smeekens, Ben Cornelissen, Raoul Bino, Robert Hall, Andy Pereira, Christine Bunthof

Sponsors

Centre for BioSystems Genomics, Netherlands Genomics Initiative, ERA-NET Plant Genomics, Garnet, GABI, Genoplante, Spanish Ministry of Science and Technology, Keygene NV, RijkZwaan Nederland, City of Amsterdam

More information & contact

More information: <http://www.plantgems.org>

Centre for BioSystems Genomics (CBSG)

Congress Secretariat Plant GEMs

P.O. Box 98, 6700 AB Wageningen, The Netherlands

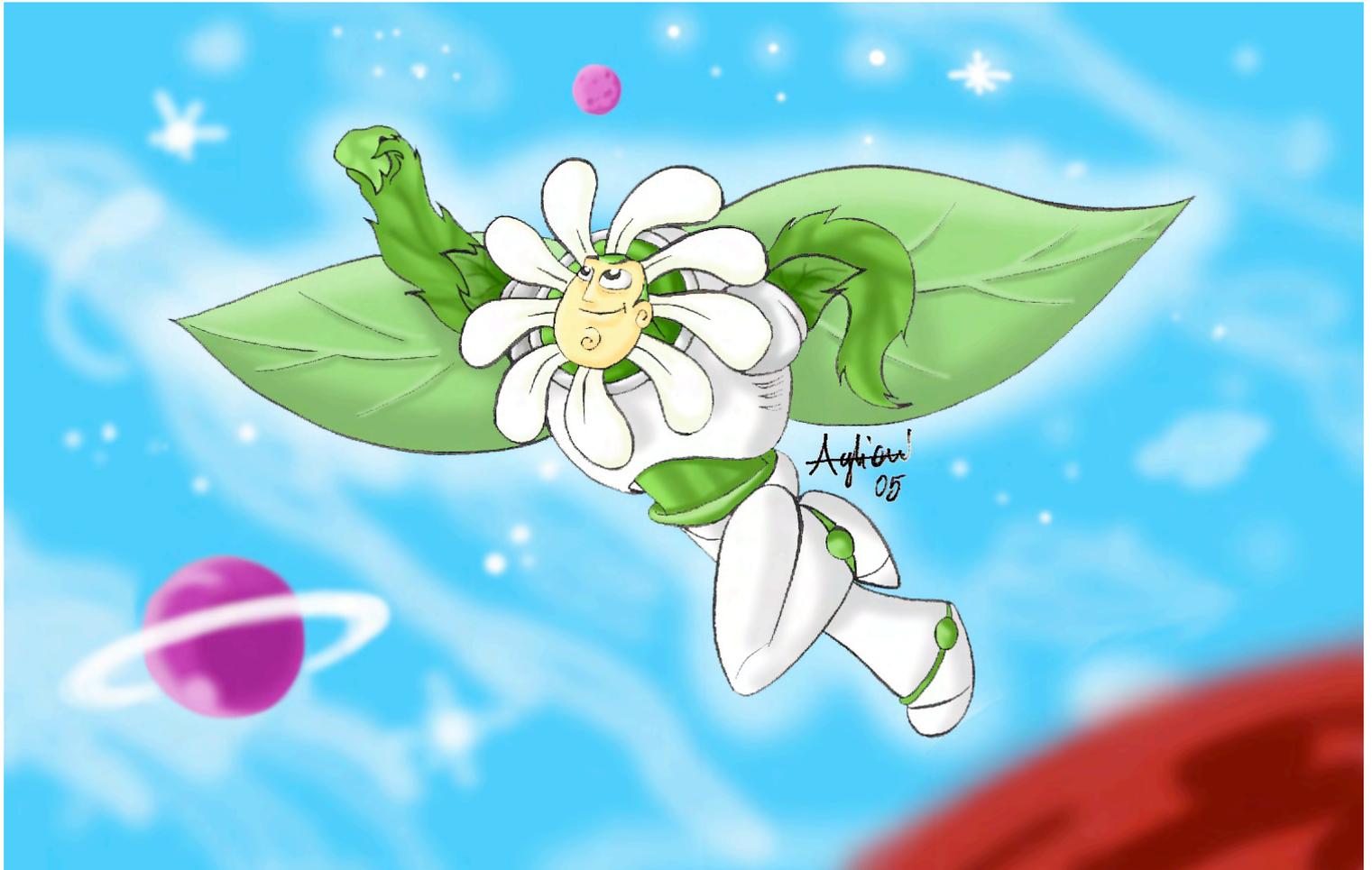
E-mail: secretariaat.cbgs@cbgs.nl

Fax: 31 317 477266

GARNet 2005 “To 2010 and Beyond”

John Innes Centre

Norwich, UK



5-6 September 2005

Speakers to include

Nam-Hai Chua

David Baulcombe

Bob Pruitt

Ottoline Leyser

Wayne Powell

Graham King

Also

UK Arabidopsis, Brassica and Cereal Forum

Rockefeller University

Sainsbury Laboratory

Purdue University

University of York

NIAB

Rothamsted Research