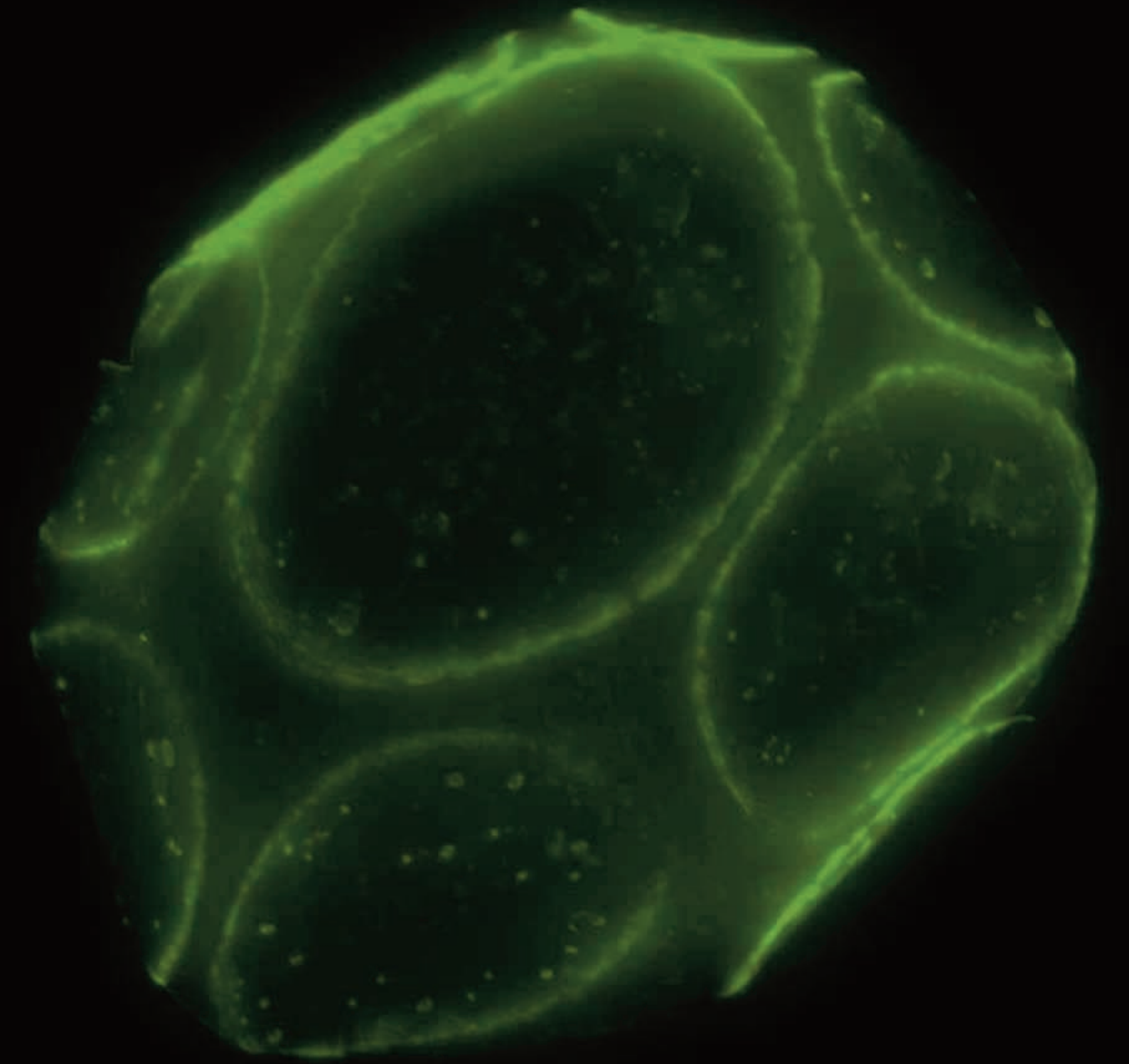
June 2009. Edition 11

GARNish

The official GARNet Newsletter



Plant Cell Walls

Breaking down the Barriers

Also in this issue; Next Generation Sequencing, Study Groups and Making Sense of GM

Editorial

Welcome to another feature-packed issue of GARNish, the GARNet newsletter.

GARNet was set up to serve the Arabidopsis community in the UK and it continues to go from strength to strength. From its roots as a coordinator and provider of plant functional genomics, GARNet's role has evolved with, or even ahead of the changing research landscape so that it has now become a catalyst for plant Systems and Synthetic Biology, and translational research in the UK. It also provides a powerful and coherent voice to promote the interests of UK plant science at national and international levels. Never has this been more important and GARNet's ability to contribute to shaping funding policy and to open new funding opportunities in the current challenging funding climate remains vital. For these reasons I am delighted to report that support for GARNet from BBSRC has been renewed for a further five years. This will allow GARNet to expand it's role and influence in all of the areas above, and comes at a time when GARNet is to take over the administrative lead of MASC (Multinational Arabidopsis Steering Committee). MASC activities have previously been funded by the US and Germany and we are pleased that UK has the chance to play its part in the coordination of Arabidopsis research at the highest level.

Contents

Front cover image kindly suppiled by Paul Knox. Many thanks to all who contributed to this issue, particularly Neil Hall, Paul Knox, Andrew Chapple, Leonor Sierra, Susie Lydon and Stefan Kepinski.

If you have any comments about GARNish or if you would like to contribute an article to the next issue please e-mail ruth@arabidopsis.info.

As ever, the GARNet committee is changing - We thank the departing members, Brendan Davies, Paul Dupree, Jonathan Jones, and Zoe Wilson for their help and support over the last three years. Newly-elected to the committee are Alessandra Devoto (Royal Holloway), Robert Sablowski (JIC), Alex Webb (Cambridge) and myself (Leeds).

In this issue, as part of our continuing focus on enabling technologies for plant science we are pleased to bring you an overview of what has variously been called Next-Generation or Second-Generation sequencing. These continuously improving sequencing technologies have become profoundly useful tools in a number of areas of biology, so if you don't know your SOLiD from your Solexa, this could be the article for you. We also have an update on the challenges and potential rewards facing plant cell wall research and a report on the Mathematics in Plant Sciences Study Group series which has proven extremely effective in fostering a number of new mathematical biology projects. In our now regular outreach and education feature, we have an article on the recently published guide to genetic modification from the charitable trust Sense About Science. 'Making Sense of GM' was written with extensive input from UK plant researchers and is an invaluable resource for those of us engaged in public understanding of science activities as well the public themselves. To round off, our reverse alphabetical tour of plant science research in the UK has reached 'J' meaning that the spotlight falls this time on the John Innes Centre and Sainsbury Laboratory.

Finally, just in case you'd missed it, at the end of June more than a thousand researchers will descend on Edinburgh for the 20th International Conference on Arabidopsis Research (ICAR). This is a fantastic opportunity to hear about all the latest in Arabidopsis research and there is (just) still time to register if you have not already done so. We hope to see you there!

Before I sign off I'd like to thank Ruth for organising another excellent issue of GARNish and wish you all a great summer.

Stefan Kepinski

ICAR 2009

If you haven't already heard, the 20th International Conference on Arabidopsis Research will be held in the vibrant and historic city of Edinburgh, 30th June to 4th July 2009.

Registration for the conference will close on the 15th June so if you haven't already registered to attend, register now by visiting http://arabidopsis2009.com/registernow.html

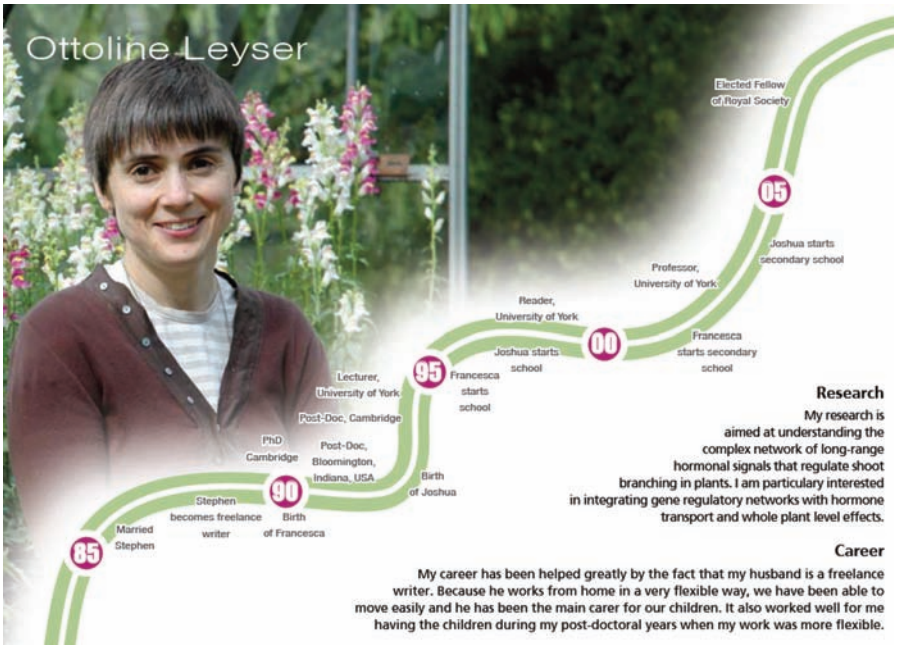
We have a great line up of world-renowned speakers including Enrico Coen, Caroline Dean, Joe Ecker, Jiri Firml, Nicholas Harberd, Alistair Hetherington, Andrew Millar, Ben Scheres, Mark Stitt and Jian-Kang Zhu. For a full programme visit http://arabidopsis2009.com/speakers.html

We look forward to seeing you in Edinburgh.

News and Views

Mothers in Science

As part of her Royal Society Rosalind Franklin award, Professor Ottoline Leyser (University of York) has produced a book entitled Mothers in Science. The aim of this book is to illustrate, graphically, that it is perfectly possible to combine a successful and fulfilling career in research science with motherhood, and that there are no rules about how to do this. On each page you will find a timeline showing on one side, the career path of a research group leader in academic science, and on the other side, important events in her family life. Each contributor has also provided a brief text about their research and about how they have combined their career and family commitments. The book is available for downloaded from http://bioltfws1.york.ac.uk/biostaff/staffdetail.php?id=hmol

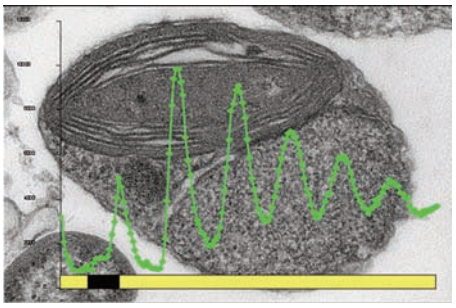


A very small plant system at CSBE

Laura E. Dixon and Andrew J. Millar, CSBE.

Francois-Yves Bouget, Universite Pierre & Marie Curie/CNRS, Banyuls sur Mer, France.

With its new C.H. Waddington Building completed in May 2009, the Centre for Systems Biology in Edinburgh (CSBE) is becoming fully established as an integrated hub for experimental systems biology and computational modelling. A core subject for this work is the plant circadian clock, and most recently, the use of a simpler experimental system to dissect the network of circadian gene regulation and its links to metabolic and signalling pathways. Less complicated, more tractable biology can enormously facilitate Systems Biology's mixture of dynamic modelling and quantitative experiments but plant science doesn't always offer a clear equivalent of the differentiated cell cultures that are much beloved of mammalian systems biologists.



A collaboration with the Université Pierre & Marie Curie's marine biology laboratory in Banyuls, in the South of France, has filled this gap with the marine alga, *Ostreococcus tauri*. This picoeukaryote has a fully-sequenced genome (roughly the size of the yeast genome, [1]) in a cell the size of a bacterium with a startlingly simple cellular organisation. The electron micrograph (courtesy of M.-L. Escande) shows the single chloroplast at top, the mitochondrion lower left (also just one or two microtubules, [2]). *O. tauri* was recently shown to have a circadian clock that controls the cell cycle [3] and through further work in Banyuls, core clock components have been identified from their Arabidopsis homologues. Luciferase reporter gene fusions to the clock genes give high-amplitude circadian rhythms (green trace on figure). Modelling of this reduced clock network is now proceeding with UK and French collaborators.

Of particular interest to the Arabidopsis community, *O. tauri* has a relatively high number of conserved proteins but very few genes in gene families: one bHLH transcription factor, compared to over 150 in Arabidopsis; similarly for other gene families. Mutants in *O. tauri* are very likely to have phenotypes, and the Banyuls group has recently secured EU funding from the ASSEMBLE programme to create a full insertional mutant library. Even more exciting, especially for systems research, is the fact that the homogeneous algal cultures enable cell-based assays that are just not possible in Arabidopsis. Although Ostreococcus research is at an early stage, this candidate 'green yeast' looks poised to provide a fast track for insights into fundamental plant cell biology, far beyond the circadian clock.

[1] E. Derelle, et al. (2006) Genome analysis of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features. Proc Natl Acad Sci USA 103: 11647–11652

[2] G.P. Henderson, et al. (2007) 3-D Ultrastructure of *Ostreococcus tauri*: Electron cryotomography of an entire eukayotic cell. PLoS One 2(8):e749.

[3] Moulager M., et al. (2007) Light-dependent regulation of cell division in Ostreococcus: evidence for a major transcriptional input. Plant Physiol. 144(3): 1360–1369.

Next Generation Sequencing: Be careful what you wish for!

Neil Hall, University of Liverpool, UK

Next Generation Sequencing

Over the last five years the technology used for DNA sequencing has changed radically with the advent of a raft of technologies dubbed second-generation sequencing or SGS. SGS has made genome analysis much cheaper and faster than could previously have been imagined. This disruptive technology has opened doors to new opportunities in the plant sciences. Not only does SGS allow rapid sequencing of crop plants with large genomes but it has also blurred the boundaries between genomic and post genomic science so that sequencing can now be deployed to hypothesis testing applications such as single-nucleotide polymorphism (SNP) discovery, expression analysis and chromatin immunoprecipitation.

What is second generation sequencing?

There are a number of different SGS technologies; all use PCR to amplify DNA in vitro, as opposed to in vivo cloning, however each uses a different chemistry to 'read' the DNA. The three main systems are: 454-FLX from Roche which uses pyrosequencing chemistry, SOLiD sequencing from ABI which uses sequencing by ligation, and finally sequencing by reversible terminators from Illumina (commonly called Solexa sequencing). The throughput, accuracy and read lengths achievable on these platforms are improving rapidly but currently each of these technologies has different strengths and weaknesses.

Sequencing Platform	Read Length*	Total bases per run*	Advantages	Disadvantages
454	500bp	500 million	Very rapid run times Easy data analysis	Cost per base is high Potential for systematic error
ABI-SOLiD	50bp	20 billion	Very high throughput Very high read accuracy	De novo assembly is very diffcult Long run time
Illumina GA	75bp	10 billion	Simple library construction Can use tiny quantities of DNA	Poor accuracy on long reads Expensive instrumentation

Table 1 Advantages and disadvantages of SGS platforms
*Figures shown are those reported by users at the time of writing, but all platforms are increasing capacity rapidly

NGS applications

Assaying genetic diversity

The rate of decrease in the cost of DNA sequencing in the last 10 years has been astonishing. The cost of sequence generation has more than halved every year for the last few years. If this rate continues then full sequencing of a human genome will cost less than $100 within five years; it already costs less than $100,000. In medical research this has led to a number of new experiments that would have been unimaginable just a few years ago. An example is the 1000 human genomes project which aims to study the diversity in 1000 individuals (www.1000genomes.org). These data are primarily being used in genome wide association studies (GWAS) in order to identify candidate SNPs directly by genotyping and phenotyping a large number of individuals. In response, the Arabidopsis community has launched the 1001 arabidopsis genomes project which hopes to generate genetic diversity data for over 1000 accessions, (see www.1001genomes.org), bringing closer the possibility of doing GWAS using natural variants of Arabidopsis.

Mutation screening

As well as identifying SNPs in natural lines, the same technology can be used to identify SNPs in laboratory-generated mutants. Studies demonstrating this have been published in yeast (Smith *et al* Genome Res. (2008)18:1638-42.) and C. elegans (Sarin *et al*. Nat Methods. 2008 5:865-7). In brief, instead of mapping mutant strains, these groups simply re-sequenced the entire genomes to identify the individual point mutations underlying phenotypes of interest. This may seem like taking a hammer to crack a nut, but at the current cost of sequencing this technique is cheaper than more elegant (but more longwinded) methods. Importantly this method can be applied to any organism, including those with less accessible forward and reverse genetic tools, and also to phenotypes that are difficult to map.

Next Generation Sequencing: Be careful what you wish for!

Neil Hall, University of Liverpool, UK

De-novo sequencing

Roche-454 sequencing can achieve read lengths in excess of 500bp which makes it ideal for *de novo* sequencing. In fact, as there is no *in vivo* cloning involved, it is in some respects better than Sanger sequencing as it provides a more even sampling of the genome. Although this technology has mainly been used for sequencing of bacterial genomes it is starting to be used for larger genomes and recently the BBSRC funded full shotgun sequencing of the wheat genome in order identify SNPs that can be used for breeding programmes (http://www.bbsrc.ac.uk/media/releases/2009/090211_wheat_genome_food_security.html).

Expression analysis

Alongside full genome sequencing, SGS has had a major impact in expression studies. The use of direct cDNA sequencing to measure steady state RNA levels has started to become commonplace and it has even been suggested that microarrays are now obsolete (Shendure *et al* Nat Methods. 2008 5:585-7). While the rumours of the death of microarrys have probably been exaggerated, it is true that these technologies have some notable advantage over arrays. Firstly, RNAseq (the new word for sequencing cDNA) has no fixed dynamic range, so you can measure the relative quantities of very highly expressed transcripts and very rare transcripts in the same sample without worries of saturation. Secondly, you do not make any assumptions about what is being expressed whereas arrays will only measure what is on the array. Because of this an early experiment using RNAseq found large holes in the Arabidopsis annotation (Webber *et al* Plant Physiol. 2007 144:32-42). Finally, RNAseq gives digital data while arrays give analogue data in the form of relative intensities. This means that the data can easily be compared between experiments and the statistical analyses needed to interpret the data are simplified.

However, for many experiments arrays will remain the cheap option, especially for people working on model species where the fabrication costs are low, but as sequencing becomes cheaper this may soon cease to be the case.

The informatics tidal wave

A key consideration for any researcher thinking of embarking on an experiment using next generation sequencing should be how they will analyse the data. Some SGS instruments can generate terabytes of raw data in a single run. Even simple processes such as BLAST, would cripple desktop computers if attempted on these datasets and some of the data generated, such as 'colourspace reads', don't even look like DNA sequence. It is easy to be mesmerized by how cheaply gigabases of sequence can be generated and forget that it may take a single talented postdoc months simply to perform a first-pass analysis of the dataset. Five years ago the informatic cost of a genomic experiment would be around 10% of the total cost, now the pyramid has been inverted and it is easily the most expensive component.

Key SGS centres in the UK

For a long time the only UK centre that provided high throughput sequencing on a large scale was the Sanger Institute. Due to its Wellcome Trust funding the Sanger was almost solely a medical research centre and for researchers working in other areas of biological sciences there was little or no access to large-scale sequencing. Since the Sanger Institute has wound down its sequencing service and new technologies have come on-line, more and more medical and university departments in the UK are starting to invest in second generation sequencing instruments and a few of these will offer sequencing as a service. There are also a number of commercial operations that provide this as a service although these are usually significantly more expensive than academic groups. For anyone considering an experiment using this technology, it is important to consider how the bioinformatics will be done prior to starting because, as mentioned above, the bioinformatic analysis of an SGS experiment can be lengthy and potentially costly.

Genome Lab	Technology currently supported	Core funding	Support for bioinformatics	Current funded plant projects
Gene Pool, Edinburgh	ABI-3730 Illumina, 454	MRC NERC	Yes	Various crops Arabidopsis, Algae
AGF, Liverpool	ABI SOLiD 454	MRC NERC	Yes	Wheat, Arabidopsis Kalanchoe
TGAC, Norwich	ABI-3730 ABI SOLiD	BBSRC	Yes	Medicago Tomato

Table 2 Genome sequencing services funded by UK research councils

Next Generation Sequencing: Be careful what you wish for!

Neil Hall, University of Liverpool, UK

The prospect of third generation sequencing

While SGS has very quickly moved from an exciting new technology to a robust and useful tool in a matter of a few years it is quite possible that the field will change quickly again with new technologies dubbed third generation genome sequencing. Third generation sequencing is defined as sequencing of single molecules of DNA, so no amplification is required. This should increase the rate at which sequencing can occur and reduce costs still further. Some recent papers have suggested that this technology will be a reality very soon (Eid *et al* Science, 2009 323:133-8; Stoddart *et al* PNAS 2009 epub.) so that in the foreseeable future DNA sequencing could essentially become a free commodity.

Neil Hall, School of Biological Sciences, University of Liverpool, Liverpool L69 7ZB
+44 (0)151 7954516 neilhall@liv.ac.uk

Genetics 100 Years On

John Innes Centre, Norwich, UK, 9-11 September, 2009
http://www.jic.ac.uk/centenary/events/Genetics100YearsOn/

To help celebrate 100 years of genetics at John Innes, join us for a very special symposium. **Paul Nurse** will open with the Bateson Lecture and **Sydney Brenner** will close with "Genetics 100 Years On".

Sandwiched in between will be reflections on areas of human interest that have been transformed by a genetic approach, examining where they are now, and where they might be in the next 100 years. Come and listen to **David Stern, Stewart Cole, Michael Ashburner, Jonathan Hodgkin, John Doebley, Walter Bodmer, Linda Partridge, Michael Stratton, Chris Tyler-Smith, Leena Peltonen-Palotie, Rico Coen, Eric Wieschaus, Rich Losick, Mark Patshne, Daniel St Johnson, David Baulcombe and Caroline Dean.**

If you are interested in the history of genetics there is a one day meeting immediately preceding the symposium http://www.jic.ac.uk/centenary/events/historyofgenetics/programme.htm, and if you have ever worked at JI there is an **Alumni Day** following the symposium where you can meet up with old friends. http://www.jic.ac.uk/centenary/events/alumniday/programme.htm

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Can you help identify specialist skills that could be lost from the research community?

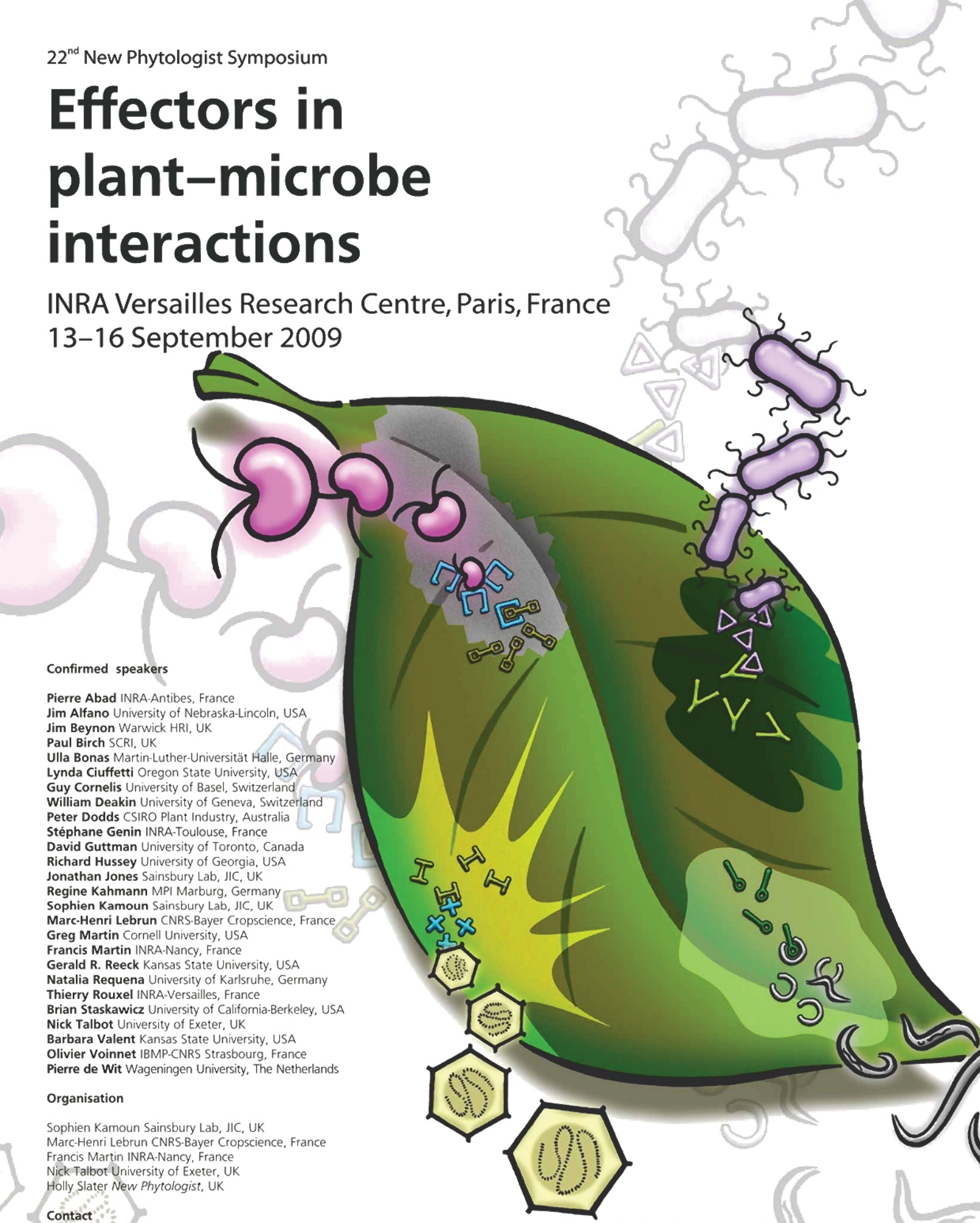
The Biotechnology and Biological Sciences Research Council (BBSRC), in coordination with the Biosciences Federation (BSF), has launched a UK-wide consultation to identify niche areas of expertise that are in danger of being lost from the bioscience research community. The results of this consultation will be used to prioritise investment in the future of strategically important and vulnerable areas of expertise.

All individuals are invited to provide information and evidence to this consulation by completing a questionnaire and submitting it to the BBSRC by 3rd July 2009. A questionnaire can be downloaded from http://www.bbsrc.ac.uk/organisation/policies/reviews/consultations/0905_bioscience_research_skills.html

22nd New Phytologist Symposium

Effectors in plant–microbe interactions

INRA Versailles Research Centre, Paris, France
13–16 September 2009



Confirmed speakers

Pierre Abad INRA-Antibes, France
Jim Alfano University of Nebraska-Lincoln, USA
Jim Beynon Warwick HRI, UK
Paul Birch SCRI, UK
Ulla Bonas Martin-Luther-Universität Halle, Germany
Lynda Ciuffetti Oregon State University, USA
Guy Cornelis University of Basel, Switzerland
William Deakin University of Geneva, Switzerland
Peter Dodds CSIRO Plant Industry, Australia
Stéphane Genin INRA-Toulouse, France
David Guttman University of Toronto, Canada
Richard Hussey University of Georgia, USA
Jonathan Jones Sainsbury Lab, JIC, UK
Regine Kahmann MPI Marburg, Germany
Sophien Kamoun Sainsbury Lab, JIC, UK
Marc-Henri Lebrun CNRS-Bayer Cropscience, France
Greg Martin Cornell University, USA
Francis Martin INRA-Nancy, France
Gerald R. Reeck Kansas State University, USA
Natalia Requena University of Karlsruhe, Germany
Thierry Rouxel INRA-Versailles, France
Brian Staskawicz University of California-Berkeley, USA
Nick Talbot University of Exeter, UK
Barbara Valent Kansas State University, USA
Olivier Voinnet IBMP-CNRS Strasbourg, France
Pierre de Wit Wageningen University, The Netherlands

Organisation

Sophien Kamoun Sainsbury Lab, JIC, UK
Marc-Henri Lebrun CNRS-Bayer Cropscience, France
Francis Martin INRA-Nancy, France
Nick Talbot University of Exeter, UK
Holly Slater *New Phytologist*, UK

Contact

Holly Slater (*New Phytologist*) - newphytsymp@lancaster.ac.uk

New Phytologist Central Office
Bailrigg House
Lancaster University
LA1 4YE, UK.
Tel: +44 1524 594 691
Fax: +44 1524 594 696

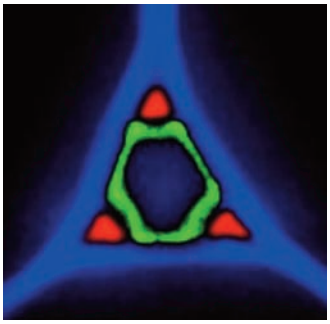
Further details and registration information at

New Phytologist

www.newphytologist.org

Breaking down the barriers: Facing up to the challenge of plant cell walls

Paul Knox, Centre for Plant Science, University of Leeds, UK
http://www.plantcellwalls.net

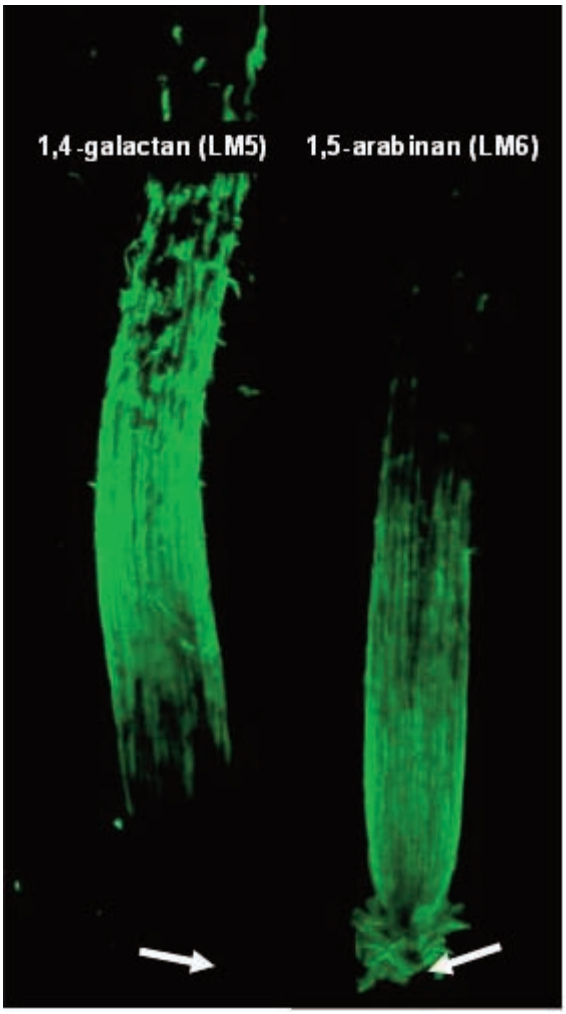


A quick look around will tell you that cell walls are everywhere. Look at this page, look at your desk, look at your shirt and then look at your lunch. Cell walls, being the major biomass component of plants, are everywhere in our world but arguably not proportionally present in current plant biology research. A quick survey suggests that plant cell walls are the focus for less than 5% of the papers published in top plant biology journals in 2008.

We know plant cell walls are important. They encase, shape, strengthen and defend plant cells. They enable cell enlargement and cell adhesion allowing the regulated growth of robust organs that can penetrate compacted soils or withstand the violent impacts of winds. It is well established that cell walls are highly structurally complex and metabolically dynamic cell compartments and much more than mere physical barriers to contain the interesting and important bits of cells. All this is clear and yet the molecular details of how cell walls are assembled and function in developmental and physiological contexts are far from clear. This lack of molecular understanding compared to other areas of plant biology arises directly from the fact that plant cell walls are constructed largely from polysaccharide and phenolic polymers that have not been readily amenable to analysis or to cell-based, fast high-throughput data generation. In addition they are often highly compacted, insoluble composites and therefore have to be de-constructed to be understood and this is where the current focus on cell walls as benign and sustainable biofuels is having such a positive impact on the field and at the same time revealing the complexity of these materials.

Challenges

Cell wall polysaccharides are diverse and often highly complex in ways that we are only beginning to understand. The current view is that the polysaccharides found in land plant cell walls can be to split into ~8 core polymers: cellulose, xylans, xyloglucans, mannans, galacturonans, galactans, arabinans and arabinogalactans. Several of these polymers are of considerable structural complexity, often possessing structural variants, and can be modified within cell walls. We are just, painstakingly, starting to understand the biosynthetic machinery that constructs individual polysaccharides and to allot specificities to the glycosyltransferases involved – pectin biosynthesis alone requires the action of over 50 glycosyltransferases. An additional challenge is to understand the way that cell walls assemble – a phenomenon underpinned by cross-linking chemistry of considerable complexity. Other major questions that remain unanswered in this field include; how do the diverse assembled configurations of polymers that comprise the cell walls of diverse cell types become integrated into growth-controlling materials? How are cell wall properties and functions coordinated across extending organs such as roots that are responsive to a range of environments? This will be one context where great new strands of excitement will be generated by plant biologists in the future.

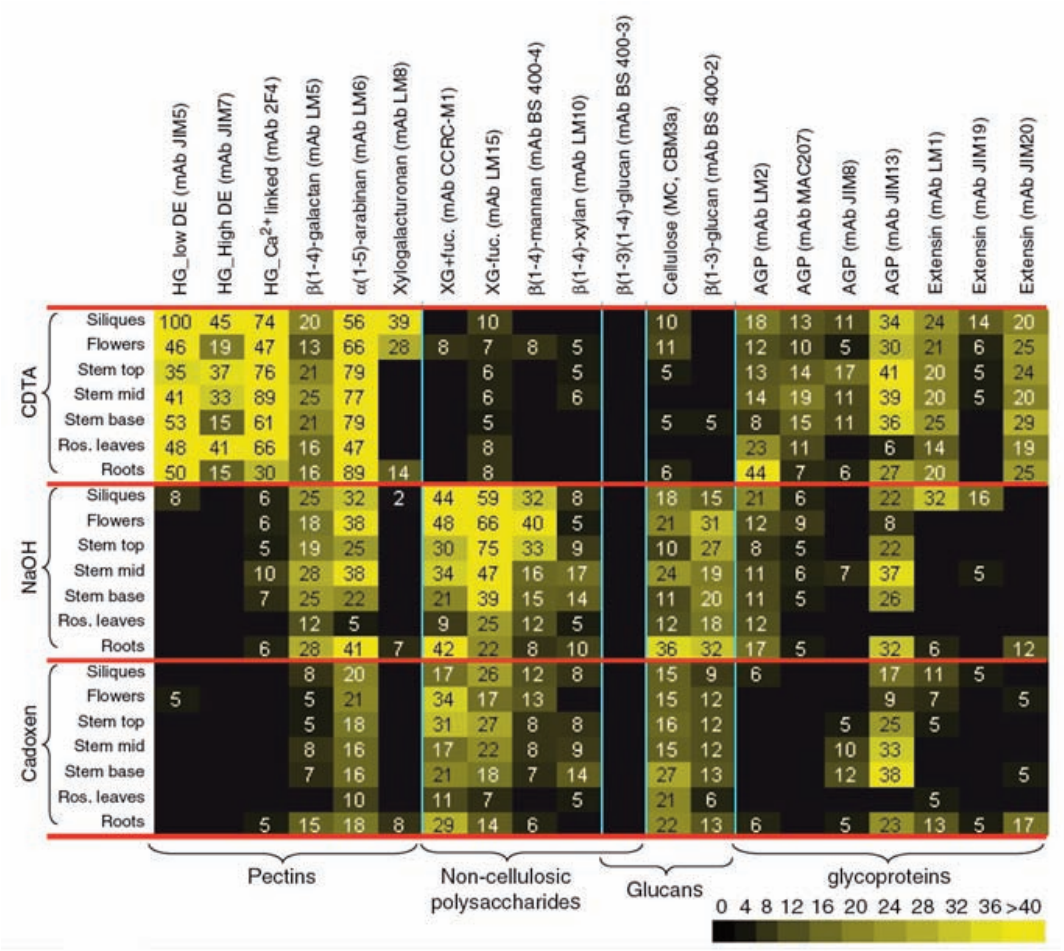


The way forward

We can tackle the sets of proteins that build cell wall polymers and the sets of proteins that can modify, or re-link, or cleave, or attach, or degrade wall polymers. We are now beginning to generate large data sets covering the polysaccharides themselves in biological contexts. Sets of molecular probes capable of the recognition of structural features of cell wall polymers are required for this as the direct *in vivo* tagging of specific features of cell wall polymers is not yet possible. These probes are being assembled for microarray analyses allowing

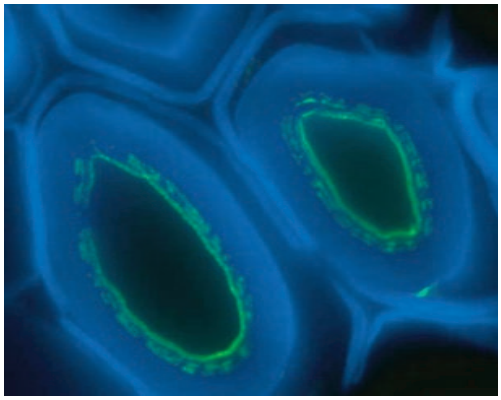
Breaking down the barriers: Facing up to the challenge of plant cell walls

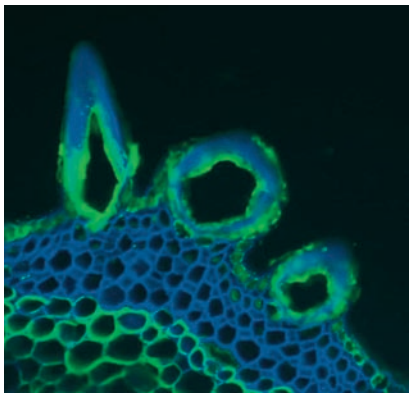
the quick, comprehensive assessment of cell wall polymers. This information can be used to investigate which particular polymer forms are in which cells at which stages of cell development. In addition to this, a considerable gap that is being targeted is how different specific configurations of cell wall polysaccharides impart mechanical properties and respond to mechanical impacts. For example, how do cell wall changes during a cell's progress through an Arabidopsis root apex integrate with physical and mechanical needs? Or in a more applied context - why is a cotton shirt so different from a linen or hemp fibre shirt when all are made from a similar cell wall type?

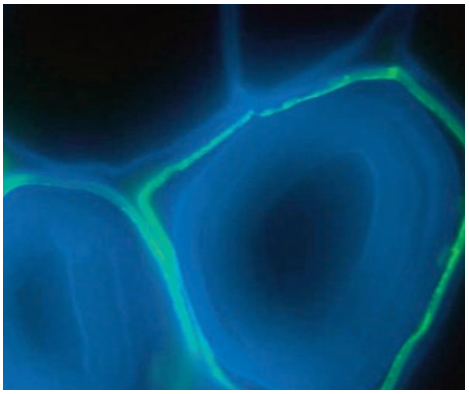


Example of microarray analysis of cell wall polymer occurrence in Arabidopsis organs

We need to understand cell wall structures to optimize their deconstruction as sustainable sources of fuel. We also need to develop our understanding of plant cell and organ biomechanics from the perspective of cell walls as sophisticated and responsive biomaterials. These may be tough challenges but the way ahead is clear and the rewards for their study are likely to be considerable. In addition to providing a real impetus into the biology of plant growth and cell development there will be major outcomes for cell walls enjoyed as foods, fibres and fuels.







Further thoughts

- Paul Knox Cell Wall Lab website: www.plantcellwalls.net
- Moller I et al. (2007) High-throughput mapping of cell wall polymers within and between plants using novel microarrays. Plant J. 50, 1118-1128
- Knox JP (2008) Revealing the structural and functional diversity of plant cell walls. Curr. Opin. Plant Biol. 11, 308-313

Plant Bioinformatics, Systems and Synthetic Biology Summer School

University of Nottingham, UK

27 – 31 July 2009

Selection of topics included in the summer school:

- An Introduction to Bioinformatics Infrastructures
- Structural Bioinformatics
- Data integration for plant systems biology
- Virtual Plants
- Computational Systems Biology
- Mathematical Modeling in Plant Systems Biology
- Comparative and functional genomics
- Bioenergy
- Automated Design in Synthetic Biology
- Design and optimality in photosynthesis and carbon fixation
- Synthetic biology of plants: challenges and accomplishments

Target audience:
Doctoral students from relevant disciplines

Aims:
To introduce cutting-edge research in bioinformatics, systems and synthetic biology, applied to plant biology

Financial support:
Funding for tuition, accommodation, meals & travel is available for a limited number of students from ESF member countries

To register:
http://lobelia.cs.nott.ac.uk/plantsummerschool
Deadline:
15 June 2009
Contact:
plantsummerschool@cs.nott.ac.uk

EUROPEAN SCIENCE FOUNDATION
SETTING SCIENCE AGENDAS FOR EUROPE

The University of Nottingham

CPIB
The Centre for Plant Integrative Biology

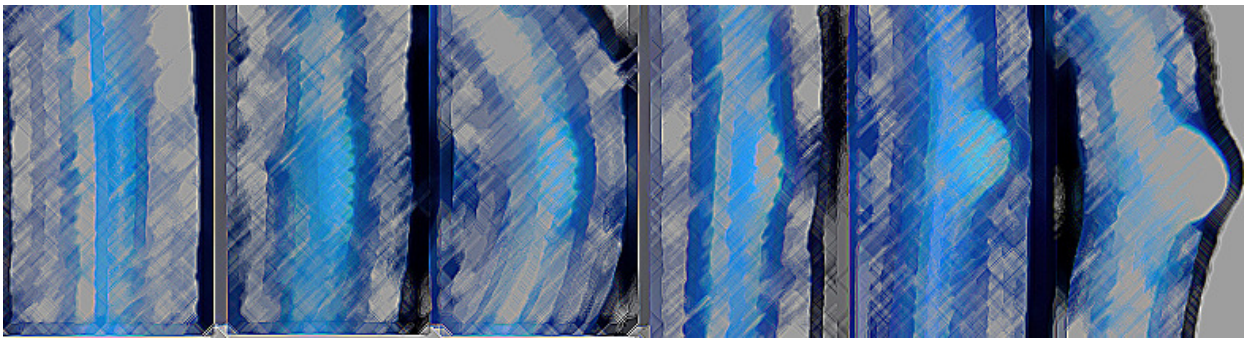
CPIB Summer School 2009

Introduction to biological modelling

University of Nottingham, UK

14-17 September 2009

Co-organised by CPIB, SIGNET, GARNet & STEMN



Target audience

Open to all - PhD students and postdoctoral researchers with a biological background are particularly encouraged to attend.

Aims

- To introduce modelling and quantitative approaches to biologists
- To encourage experimental design which generates data suitable for modelling

Programme overview

Four days combining lectures with supervised hands-on practical exercises using biological examples, allowing participants to try out modelling techniques in a friendly, supportive environment.

Tutors

- Dr Nick Monk (University of Nottingham, UK)
- Dr Markus Owen (University of Nottingham, UK)
- Dr Henrik Jönsson (Lund University, Sweden)

Feedback from the 2008 CPIB Summer School

"Excellent course, has been very useful and stimulated ideas for applying modelling to our research"

"I feel I could communicate better with mathematicians now ... I wouldn't have known where to start before this course!"

"I thoroughly enjoyed the summer school on both a social and scientific level. I would definitely recommend it to colleagues"

Financial support:

Registration is FREE and covers tuition, 3 nights' accommodation in Halls of Residence and all meals.

To register:

email susie@cpib.ac.uk

Deadline:

31st July 2009 – places are limited to 40.

www.cpib.ac.uk/portal/public-content/cpib-summer-school

CPIB
The Centre for Plant Integrative Biology

signet

STEMN

UK Plant Science

There are over 350 plant research groups in the UK, in 42 institutions scattered from Aberdeen to Exeter. Many of these groups are international leaders in their field. To promote the breadth of plant science throughout the UK, and increase awareness of the different types of research being undertaken, GARNet is focusing on geographical areas and institutions across the UK. In this issue we continue our tour around the country highlighting the outstanding research being undertaken at the John Innes Centre and Sainsbury Laboratory.

Spotlight on the John Innes Centre

The John Innes Centre and Sainsbury Laboratory, located on the Norwich Research Park, form an international centre of excellence in plant and microbial science. The scientists use a wide range of disciplines to study biological systems at the genetic, molecular, cellular and whole organism levels via multidisciplinary research programmes. The Centre maintains a mix of fundamental and strategic research, and work on model organisms is integrated with studies on economically important species.

2009 sees the centenary of the founding of the John Innes, and a series of events are planned to mark the occasion, including a 'Genetics 100 Years On' Conference, Alumni Day and Discovery Day, when the JIC will be opening its doors to the public.

The JIC is a registered charity and a company limited by guarantee, and the JIC is an institute of the BBSRC. The JIC leases the land and buildings it uses from the John Innes Foundation (JIF), an independent charity. The Sainsbury Laboratory was founded in 1989 on the JIC site as a joint venture between the Gatsby Charitable Foundation, the University of East Anglia, the BBSRC and JIF. The laboratory has a worldwide reputation for its research in molecular plant pathology and genetics.

Name Ian Bancroft
e-mail ian.bancroft@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/ian-bancroft/
Research Area Brassica genomics and oilseed rape genetics

Research Activities

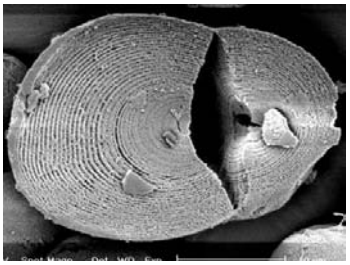
The Bancroft group aims to understand the genetic regulation of key traits of relevance to the sustainability of the UK oilseed rape crop. They are studying the control of seed storage product accumulation and canopy architecture in oilseed rape, using Arabidopsis as a model. Although many of the structural components of the lipid biochemical pathways have been cloned from Arabidopsis and other plants, little is known about control mechanisms or environmental interactions. Oilseed rape has a poor harvest index due to a relatively large proportion of biomass being committed to stems, but little is known about its control. To gain insight into the control of these traits, the group use quantitative genetic approaches and are exploiting the natural variation in 6 recombinant inbred populations that they have recently developed in Arabidopsis. In parallel, the Bancroft group are taking a similar approach in oilseed rape using several mapping populations the aim of this work is to assess the contribution in oilseed rape of genes encoding components of the putative regulatory pathways. In addition, the group is aiming to understand genome structure, function and evolution in the Brassicaceae and are developing comparative genomic approaches to address this.

Name Mike Bevan
e-mail michael.bevan@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/michael-bevan.asp
Research Area Sugar signalling and gene expression patterns and networks; cereal and grass genomics

Research Activities

All organisms need a supply of nutrients to support growth and development. Sugars such as glucose are universal nutrients as they provide carbon skeletons for energy supply, storage and the synthesis of most metabolites. Work in the Bevan group is looking at how the supply of carbon from photosynthesis is integrated with growth and development in the plant. The aim is to define new regulatory pathways linking the perception and transduction of metabolic signals to growth and developmental responses using genetic screens in the model plant Arabidopsis. Large populations of Arabidopsis mutants have been generated, including a population of Ds gene trap insertion lines created as part of the GARNet project, and a large number of these lines are being screened systematically for a variety of growth and developmental phenotypes. Information from this has helped develop the AtiDB Arabidopsis functional genomics database. The Bevan group are also studying the genomics of important crop species, in particular wheat, as well as Brachypodium, an emerging model system for grasses and cereal crops.

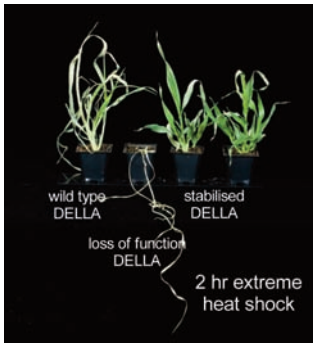
Spotlight on the John Innes Centre



Name Steph Bornemann
e-mail stephen.bornemann@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/stephen-bornemann/
Research Area Plant and microbial enzymology

Research Activities

The Bornemann lab studies a number of plant and microbial enzymes using a multidisciplinary approach. Interests include developing methods to study the surface specificity of starch synthase isoforms *in vitro* with a view to understand their individual contributions to the wide diversity of starch granule properties *in vivo*. To this end, the group has recently developed a surface plasmon resonance approach to monitor polysaccharide synthesis in real time on a surface using a model system. This allows the turnover number of the enzyme on the surface to be determined and, in addition, atomic force microscopy is used to measure the rigidity of these carbohydrate surfaces. The group is also interested in the atomic details of how a protein kinase is able to interpret calcium spiking and control the development of nitrogen fixing nodules in legumes.



Name Margaret Boulton
e-mail margaret.boulton@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/margaret-boulton/
Research Area Understanding how plants survive abiotic stress

Research Activities

Plants have evolved mechanisms to survive environmental stress. Given an increasingly unpredictable climate, it is important to understand these mechanisms and to ensure that they operate effectively in the crops of the future. Thus, genes identified as important in the survival of, and response to, abiotic stress in model systems are being characterised in crops. An example of these translational (model to crops) studies comprises the DELLA proteins of Arabidopsis that are part of the gibberellin signalling pathway and are negative regulators of plant growth. DELLAs were recently shown to be integrators of multiple environmental signals and to be important in promoting long term survival of abiotic stress. The accumulation (or stabilisation) of Arabidopsis DELLAs in plants experiencing adverse conditions aids their survival by two mechanisms: the active restraint of growth and the increased expression of enzymes important for detoxification of reactive oxygen species. The Boulton group has shown that the cereal DELLA orthologues, agriculturally important as the dwarfing (*Rht*) genes associated with the Green Revolution, are also involved in tolerance of short term (extreme heat) and long term (salt) stress conditions. A key area of research is to develop a mechanistic understanding of the molecular nature of plant growth and stress tolerance in crops which contain only a single DELLA gene compared to the five DELLAs present in Arabidopsis. These studies, coupled with analysis of the genetic diversity of the *Rht* locus in wheat, will inform the incorporation of appropriate dwarfing alleles in wheat.

Name Lesley Boyd
e-mail lesley.boyd@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/lesley-boyd/
Research Area Genetics and biology of cereal fungal pathogen interactions

Research Activities

The work of the Boyd lab investigates the genetics and biology of cereal fungal pathogen interactions, with past work focusing on the wheat-yellow rust interaction. A major focus of the group has been the genetic and biological dissection of wheat yellow rust resistance. National and international programs have characterised the genetic biodiversity of yellow rust resistance in national wheat germplasm collections. Microscopic studies have examined the biology of the wheat-yellow rust interaction, with particularly focus on durable sources of resistance in wheat. New areas of research include the genetics and biology of non-host resistance, using the wheat-*Magnaporthe grisea* and *Puccinia triticina* systems, and Systemic Acquired Resistance (SAR) in cereals, modelled on DIR1-mediated SAR found in Arabidopsis. Markers developed for yellow rust race-specific R-genes have provided tools for marker assisted selection breeding and are currently being used to stack these R-genes, along with partial QTLs for yellow rust resistance into French wheat. A major interest of the group has been the characterisation of the microphenotypes of durable sources of yellow rust resistance in wheat, facilitated by developing a light microscopy procedure that allows examination of yellow rust development in adult plant tissues. Much of the work undertaken in the Boyd group has involved collaborations with scientists from less developed countries and a program is being established that will allow an expansion of collaborative projects that support international development, co-ordinated by Lesley Boyd.

Spotlight on the John Innes Centre

Name James Brown
e-mail james.brown@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/james-brown.asp
Research Area Genetics of disease resistance and pathogen adaptation to crops

Research Activities

There is a constant struggle between plants and their parasites: as plants evolve to become resistant to disease, parasites evolve to overcome that resistance. Consequently, crops in agriculture are exposed to a constantly changing population of different genotypes and species of parasites. The Brown lab studies the adaptation of pathogens to crops and researches ways of developing high-yielding crop varieties which are resistant to disease. Most of the work is on fungal pathogens of cereals, especially *Septoria tritici* blotch of wheat, Ramularia leaf spot of barley and powdery mildew of cereals and cucurbits. In recent work, the group have identified numerous genes for resistance to Septoria and characterised the interaction between Septoria resistance and yield, investigated the evolution of effector and fungicide resistance genes in powdery mildew fungi, and analysed the fitness cost of disease resistance using Arabidopsis as a model. The group collaborates closely with plant breeding companies, and James Brown coordinates current LINK projects on Septoria and Ramularia. The group also uses mathematical and computer modelling to investigate the coevolution of hosts and parasites. Recent work has shown that diversity in host and parasite genes is maintained by ecological factors that operate at the population level, not simply by genetic factors, such as fitness costs, that affect hosts or parasites at the level of individual organisms.

Name Mary Byrne
e-mail mary.byrne@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/mary-byrne/
Research Area Genetics of plant architecture

Research Activities

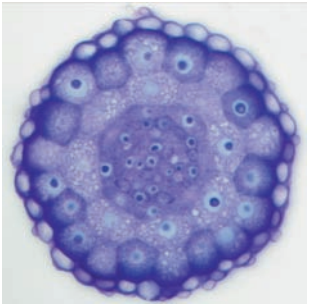
Mary Byrne's lab is interested in the genetic basis of plant shoot architecture. Most organs of the shoot are specified post-embryonically. This developmental habit is the result of establishment and maintenance of a stem cell population the shoot meristem. Stem cells in the central region of the meristem give rise to peripheral region cells that are recruited to form lateral organs of the shoot such as leaves. Early in leaf development patterning growth is established, and this occurs via signalling from the meristem and via signalling within the developing leaf. The aim is to understand the genetic pathways that regulate shoot meristem function and the events that determine leaf shape, and how variation in regulation of these aspects of plant development leads to diversity of plant form. The main goals of the group's research are to identify genes that are involved in meristem function and leaf shape; establish networks that interconnect these regulatory genes; determine conserved and divergent pathways in distant plant groups. This approach uses molecular genetics to study development in the model dicot species *Arabidopsis thaliana*, and the model monocot species *Brachypodium distachyon*. Comparative analysis of these two species will define pathways that are shared and regulatory pathways that are divergent between these evolutionarily distinct flowering plant groups.

Name Rico Coen
e-mail enrico.coen@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/enrico-coen/
Research Area Plant development and evolution

Research Activities

The Coen group is seeking to understand how diverse biological forms develop and evolve. A combination of molecular, genetic, imaging and modelling approaches are being used to understand how genes and growth interact to create specific shapes during development and how this is related to patterns of evolutionary diversity. Antirrhinum and Arabidopsis are used as a models to study evolution and development of organ size, shape and symmetry. The group has explored the use of optical projection tomography (OPT) to gather quantitative data on three dimensional morphology and gene activity at various growth stages. A novel method of time-lapse imaging has also been developed to capture seedling growth at the cellular level, to compile a comprehensive dynamic map of growth and patterning through leaf development. By collecting detailed genetic and physiological data through the process of organ growth and development, the Coen group is developing accurate computer models of plant growth and evolution.

Spotlight on the John Innes Centre

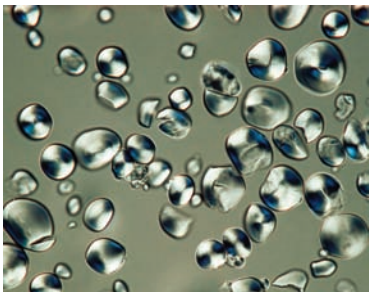


Name Silvia Costa
e-mail silvia.costa@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/silvia-costa.asp
Research Area Genetic basis of the cell fate switch

Research Activities
Plants are remarkable because they can form new organs from old ones, and it is intriguing why some but not all organisms are able to regenerate missing body parts. For plants, this capacity is important for survival in natural conditions and is also useful for horticultural propagation. In the laboratory the group are interested in understanding the regenerative capacity of plants by investigating how plant cells are able to retain their totipotency and switch fate when external stimuli change. Silvia Costa is using a combination of molecular, cell biological and genetic techniques to investigate how plants can switch the fate of cells, using Arabidopsis as a model organism.

Name Caroline Dean
e-mail caroline.dean@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/caroline-dean/index.htm
Research Area Vernalization and the molecular control of flowering time

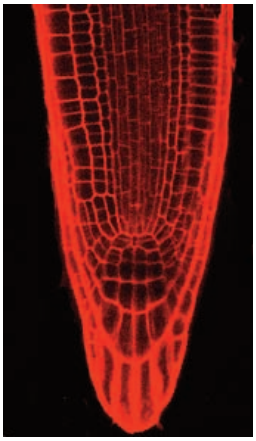
Research Activities
The Dean lab is investigating the molecular control of flowering time, focusing specifically on the acceleration of flowering by prolonged cold, a process known as vernalization. *Arabidopsis thaliana* is being used as a model system to analyse genes conferring a vernalization requirement, and identify and characterise genes that mediate the vernalization response. A central regulator in flowering and vernalization is FLC, which represses the floral transition, and the Dean lab is focussing on pathways that promote and repress *FLC* expression. *FLC* regulation provides an excellent system in which to define conserved chromatin regulatory pathways, and the aim is to understand the molecular basis of these different pathways, how their interaction antagonistically regulates a common target and how this interaction changes throughout the life-cycle and during the evolution of different flowering variants. Knowledge emerging from this system will be translated into manipulating vernalization in different plants, in particular wheat, barley and Brassica.



Name Kay Denyer
e-mail kay.denyer@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/kay-denyer/
Research Area Starch metabolism in cereals

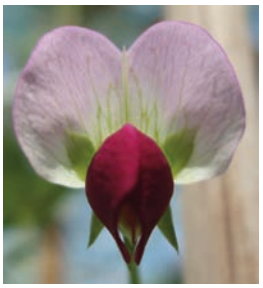
Research Activities
The Denyer lab aims to understand how starch is synthesised and degraded in plant cells in general and cereal endosperm cells in particular. Cereal grains are very rich in starch, they are economically important and there is a wide variation in starch properties between and within cereal species. Specific questions being investigated by the group include, starch granule initiation – is there a glycogenin-like protein in plants? What is the structure and mode of action of the different isoforms of starch synthase? How are the size and shape of starch granules determined? In addition, the pathway of starch synthesis in cereal endosperm is different from that in other plant organs and the evolution of this unique pathway of primary carbohydrate metabolism is of major interest. The lab uses a range of disciplines including biochemistry (enzymology, protein structure and function, starch structure and composition), genetics (forward and reverse genetics, chemical genetics), and molecular biology (gene identification, phylogenetics) and a range of cereal species including barley, wheat and rice.

Spotlight on the John Innes Centre



Name Liam Dolan
e-mail liam.dolan@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/liam-dolan/
Research Area Cellular development and evolution

Research Activities
Plants first appeared on land around 460 million years ago, and members of the Dolan lab are using their knowledge of the development of model plants such as Arabidopsis, Brachypodium and Physcomitrella to investigate the events that led to the evolution of the large and complex plant body from the first small pioneers of the land. The aim of research in the Dolan lab is to dissect the mechanisms that underpin the development of plant bodies with special emphasis on cells involved in rooting functions. A combined cellular, genetic, phylogenetic and computational approach is being taken. This research will lead to an understanding of how regulatory changes gave rise to the diversity of cell type and body plans that have evolved since plants first grew on land. Important regulatory genes are being identified that may be useful tools with which to modulate rooting traits in crops in the future.



Name Claire Domoney
e-mail claire.domoney@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/claire-domoney/
Research Area Legume seed protein synthesis and regulation

Research Activities
The Domoney lab is researching genetic and biochemical aspects of legume seed quality and nitrogen accumulation that are applicable to the development of improved crops for sustainable agriculture. Metabolite analysis is being used to identify the pleiotropic effects of mutations in protease inhibitors and other 'antinutritional' proteins, for which functions have not been defined. Variation in genes encoding enzymes of senescence-related processes is being studied for its significance to nitrogen reassimilation, and relevance to crop end use. Dissecting the function of individual genes is based on natural variation and TILLING mutant isolation. The lab is also investigating the link between plant stress and the profile of metabolites, to provide information on the effect of drought-stress on the metabolome.

Name John Doonan
e-mail john.doonan@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/john-doonan/index.htm
Research Area The molecular and cellular basis of cell growth and proliferation during plant development

Research Activities
Using *Arabidopsis thaliana* as a model system, the Doonan lab seeks to understand how cell division is regulated during plant growth. Cyclin-dependent protein kinases (CDKs) are key regulators of cell cycle progression and also influence cell growth through the reversible phosphorylation of key structural and regulatory proteins in both the nucleus and cytoplasm. Several key targets of CDK regulation have been identified, including components involved in protein translation and the microtubule cytoskeleton that are involved in cell growth and cell division. Recently, the group has been exploring the extensive variation in organ size found in many species to define the constraints acting on cell proliferation in wild species such as Arabidopsis and Brachypodium as well as in agronomically relevant species such as wheat.

Name Allan Downie
e-mail allan.downie@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/allan-downie/
Research Area The interactions between Rhizobium bacteria and legume roots

Research Activities
The expression of "nodulation" genes in the bacteria is activated by signals from plant roots and as a result the bacteria synthesise chemical signals (Nod-factors) that induce a nodule meristem and enable the bacteria to enter this meristem via a plant-made infection thread. In addition to Nod factors, the bacteria make other chemical signals that enable individual bacterial cells to sense how many other bacteria are surrounding them. This ‘quorum sensing’ allows bacteria to determine whether there are enough of them, i.e. a quorum, to initiate the change towards acting in a multicellular fashion.

Spotlight on the John Innes Centre

Name Allan Downie
Research Area The interactions between Rhizobium bacteria and legume roots

Research Activities Continued

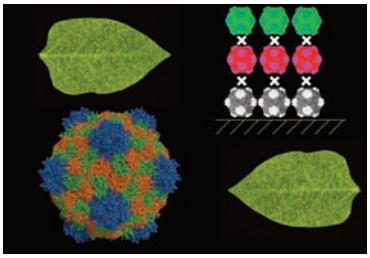
Rhizobium genes induced by quorum-sensing regulation affect several characteristics including the transfer of nodulation and nitrogen fixation capacity to other bacteria, legume infection, attachment and biofilm formation on roots, and stress responses. The Downie lab is aiming to understand how the network of quorum-sensing regulation is coordinated, understand root attachment and biofilm formation in relation to various bacterial surface polysaccharides and secreted proteins, and understand how rhizobia respond to different extracellular stresses regulated by a specialised group of RNA polymerases.

Nod-factors made by Rhizobium bacteria activate a signalling cascade in root cells leading to activation of gene expression for nodule development. The group have demonstrated that Nod factors induce two distinct calcium responses in root hairs, a rapid calcium influx and oscillations in intracellular calcium, particularly around the nuclear region, and are interested in understanding how the plant cells generate these responses and how the changes in calcium are interpreted and lead to induction of gene expression.

Name Noel Ellis
e-mail noel.ellis@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/noel-ellis/
Research Area Pea genetics and diversity

Research Activities

Legumes include a diverse group of economically important crop plants; they possess a number of unique qualities that cannot be studied, or would be very difficult to study, in other plants. Of these, pea is the main European legume field crop and it is amenable genetically with a rich resource of mutants. The Ellis lab has made major contributions to comparative genetics in legumes, focussing on pea genetics and genomics. This has included the development of resources for comparative and genetic linkage mapping which have been developed to aid the isolation of agronomically and developmentally important genes from pea. The group has also described the pattern of genomic diversity in the JIC Pisum collection. These resources have been deployed in the understanding of the genetics of plant architecture, especially pea leaf development. Plants can have simple leaves, with just one blade, like *Arabidopsis thaliana*, or compound leaves, like many legumes. The pea leaf (*Pisum sativum*) is a variant of the typical legume pinnate compound leaf in that it has terminal tendrils. A recent paper has described the gene involved in tendril formation.



Name Dave Evans
e-mail dave.evans@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/dave-evans/
Research Area Bionanoscience

Research Activities

The Evans lab is researching the use of plant viruses as nanobuilding blocks, nanoscaffolds and nanotemplates. The programme in this exciting, developing, multidisciplinary field sits at the interface of biology, chemistry, materials science and medicine. Biological nanoscience is concerned with well-defined structures with dimensions of 1-100 nm. Nanotechnology allows the fabrication of a range of materials and devices including nanoelectronics, biosensors, and drug delivery devices.

Cowpea mosaic virus (CPMV) particles are 28 nm diameter icosahedra with well characterised physical, genetic and biological properties. The properties of CPMV make it a natural, robust, nanoscale building block for use in nanotechnology. The Evans lab has shown that inorganic, organometallic and organic moieties can be chemically linked to the virus surface and that the virus particles can be assembled into two- and three-dimensional arrays on solid supports in a controlled fashion. In addition, the mineralisation of the virion external surface, using virus chimaera technology, and internal cavity, utilising capsids devoid of RNA, is being assessed as a means to generate monodisperse, nanospheres and nanoparticles with unique properties. Ultimately, such systems will be developed for applications in nanoelectronics, biological assays, biosensing and biomedicine.

Spotlight on the John Innes Centre

Name Rob Field
e-mail rob.field@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/rob-field/
Research Area Carbohydrate chemistry

Research Activities
The Field group is diverse in its activities, which range from organic synthesis to mechanistic enzymology and chemical biology. However, the common theme that runs throughout is carbohydrates. The group is developing novel chemical and enzymatic approaches for the preparation of sugar nucleotides, oligosaccharides and glycosylated natural products. Target synthesis of plant cell wall oligosaccharides to enable biosynthesis and self-assembly studies is being studied, as are the structure and mechanisms of enzymes involved in lipopolysaccharide and secondary metabolite biosynthesis. Carbohydrate-coated surfaces ("glycochips", gold nanoparticles and fluorescent quantum dots) are used to identify and quantify protein-carbohydrate and pathogen-carbohydrate interactions, and chemical genomics and chemical proteomics tools are used to dissect events in cell and developmental biology, such as root hair development in *Arabidopsis thaliana* and starch metabolism in barley seed germination.

Name Wendy Harwood
e-mail wendy.harwood@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/wendy-harwood/research.htm
Research Area Understanding and exploiting transformation systems in plants and crops

Research Activities
The main focus of interest in the Harwood lab is in improving the technology for the genetic modification of barley and increasing understanding and control of the genetic modification event. The group also works to address some of the safety issues surrounding the use of GM crops and on the development of methodology for the analysis of GM crops to detect possible unanticipated consequences of transgene insertion. In addition, the BRACT project (Biotechnology Resources for Arable Crop Transformation) is providing transformation resources for the main UK crops (www.bract.org). The BRACT project aims to meet the increasing need of the UK research community for crop transformation systems to elucidate gene function. Areas of expertise include both particle bombardment and Agrobacterium-mediated transformation of cereals, genetic and molecular analysis of transgenic plants and field trials.

Name Saskia Hogenhout
e-mail saskia.hogenhout@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/saskia-hogenhout/default.htm
Research Area The molecular basis of the interactions among plants, phloem-feeding insects and insect-transmitted plant diseases.

Research Activities
Research in the Hogenhout lab centres on the emerging and important field of Molecular-Plant-Microbe-Insect Interactions (MPMII). Insects and other arthropods vectors carry more than half of plant viruses described to date, and several important groups of bacterial plant pathogens. By definition, studies on MPMII are interdisciplinary and require expertise with at least three unrelated organisms. Research in the Hogenhout lab has focussed on phytoplasmas and rhabdoviruses. Phytoplasmas and rhabdoviruses replicate in plants and insects and establish beneficial and pathogenic interactions with these hosts. A major objective is to gain a better understanding of how phytoplasmas and rhabdoviruses manipulate plants and insects, and determine host range. It is possible that they interact with conserved proteins allowing efficient spread in both hosts. Bioinformatics, genomics, functional genomics, biochemistry, and microscopy are used to identify and characterize pathogen and host proteins involved in these interactions. The availability of model systems (Arabidopsis and Drosophila) is an aid to research progress, and obtained knowledge can be transferred to agriculturally important organisms. This research is leading to a greater understanding of fundamental cellular and developmental pathways of plants, and molecular aspects of plant-microbe interactions, plant-insect interactions and insect-microbe interactions.

Spotlight on the John Innes Centre

Name Judith Irwin
e-mail judith.irwin@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/judith-irwin/
Research Area The genetic mechanism responsible for variation in vernalization response in *Brassica oleracea*

Research Activities

Vernalization is important in agriculture, allowing the development of spring and winter sown varieties and thus extending the geographical range of many crops. The Brassica genus includes species with many morphological forms that are cultivated for use as vegetables, oils, fodder and condiments, and much of this morphological diversity can be attributed to variation in flowering time. Arabidopsis genotypes have been studied to understand how and why vernalization affects flowering time. Elucidation of the mechanism controlling this variation in Brassica will allow the determination of why some Brassica varieties are more or less responsive to different periods of cold. This knowledge will be used to address key questions about the impact of climate patterns on the availability of UK-produced quality Brassica vegetables.

Name Stanislav Kopriva
e-mail stanislav.kopriva@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/stanislav-kopriva/
Research Area Molecular basis of nutrient use efficiency and control of nutrient uptake and assimilation.

Research Activities

The Kopriva lab's research in plant nutrition is focused on understanding the molecular basis of nutrient use efficiency and control of nutrient uptake and assimilation, concentrating on assimilation of sulfate. The lab is studying the signals responsible for interconnection of sulfate assimilation with carbon and nitrogen metabolism and response to biotic and abiotic stress. Control of nutrient efficiency is also a key area of research. The control of traits known to affect sulfur use efficiency, e.g. accumulation of sulfate or control of sulfur partitioning between primary and secondary metabolism are being analysed, and new control mechanisms are being investigated using natural variation in growth at low nutrient supply. Kopriva's lab has analysed sulfur metabolism in the model moss *Physcomitrella patens* resulting in the discovery of new forms of the key enzyme in sulfur assimilation. Mining of the newly sequenced genomes of marine microalgae has also provided a large number of new enzyme variants and fusions that might be used for improvement of plant sulfate assimilation.

Name Chris Lamb
e-mail chris.lamb@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/chris-lamb.asp
Research Area Plant disease resistance: mechanisms and signal networks

Research Activities

Plants have evolved a battery of defence mechanisms that in aggregate provide protection against a wide range of potential pathogens encountered throughout the plant life cycle. However, in the artificial setting of agriculture, disease, although the exception, can be costly and even devastating.

The major focus of the group is the dissection of signal mechanisms underlying the activation of inducible defences against pathogens and pests. New knowledge and understanding, emerging from these studies will allow the development of novel approaches to enhance durable resistance of crops to pathogens and pests, thereby helping to secure the future supply of safe, nutritious food world-wide and reduce environmental load in diverse agricultural systems.

The model plant species *Arabidopsis thaliana* is used for a combination of genetic and molecular approaches for the study of plants' responses to pathogen attack. Specific areas of research centre on the genetic dissection of systemic acquired resistance and systemic signal networks, the analysis of stress signalling genes and on the genetics of non-host resistance.

Spotlight on the John Innes Centre

Name David Laurie
e-mail david.laurie@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/david-laurie/
Research Area Flowering and adaptation in cereals

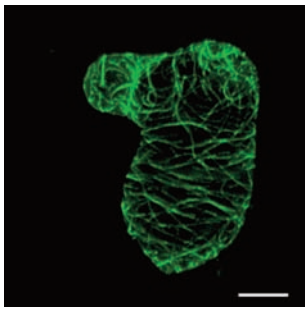
Research Activities

Plants have evolved sophisticated mechanisms to ensure that they flower when the chances of pollination, seed development and seed dispersal are highest. For most plants this means that flowering is restricted to a particular time of year. The timing of flowering is also very important for crops as it has major impacts on yield and quality. But how does a plant "know" what time of year it is? Many plants, including cereals, use environmental cues, particularly the length of the day (photoperiod) and extended periods of low temperature (vernalization). During domestication the ways in which crops use these signals has been altered by selection so that they can now be grown in regions outside the ecogeographical limits of their wild ancestors. Research in the Laurie lab is focussed on the response to photoperiod in barley and wheat. Understanding how wheat and barley recognise and respond to environmental cues, and understanding how variation can provide adaptation to different environmental cues will provide knowledge and resources that plant breeders can use to enhance adaptation and sustainability of production, both in current environments and in new environments arising from climate change. Model plants, particularly Arabidoipsis, are used to investigate whether the genetic basis of flowering time is conserved by comparing the regulatory pathways of cereals and Arabidopsis with those of their common ancestors. Knowledge of this facilitates the identification of important genes in cereals.

Name Michael Lenhard
e-mail michael.lenhard@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/michael-lenhard/
Research Area The genetic and regulation of organ growth in plants

Research Activities

Plant organ size is remarkably uniform within and between individuals of a given species, yet can vary widely between different species. Understanding the genetic controls of organ size in plants is not only desirable from a scientific point of view, but also promises to open up novel opportunities for manipulating economically important characters. Thus, the major aim of research in the Lenhard lab is to elucidate genetic and molecular mechanisms that underlie the regulation of organ growth in plants. Arabidopsis has been used to isolate several genes that regulate the size of leaves and flowers, and the mode of action of these genes in controlling growth at the organ scale is now under investigation. Flower size and morphology are important adaptive traits, especially in outbreeding species that rely on insect pollinators, and it has been frequently observed that an evolutionary switch to self-pollination is accompanied by a reduction in floral size and display. One such transition has been seen in the Brassica genus Capsella, and this is being investigated to identify the genes responsible for the difference in organ size.



Name Clive Lloyd
e-mail clive.lloyd@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/clive-lloyd/
Research Area The role of microtubules in plant growth and form

Research Activities

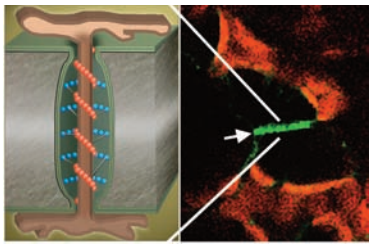
The form of a plant is dependent upon cell walls, both the orientation of the new cross-wall that divides cells and the side-walls that stretch as cells undergo directional expansion. The Lloyd lab studies the microtubule arrays that support these key morphogenetic processes, focussing on the regulatory role of microtubule-associated proteins. The group are especially interested in the dynamic behaviour of the cortical microtubule array and observe it undergoing rotary movements that are likely to regulate the movements of cellulose synthases and hence the patterning of cellulose microfibrils in the wall. The lab also study how microtubule (MT) organization and dynamics are changed in helical mutants that undergo twisted growth. The group has also developed an *in vitro* Arabidopsis system for the differentiation of suspension cells into xylem tracheary elements. Researchers are utilising RNAi to investigate how microtubule-associated proteins regulate the bunching of MTs and hence the characteristic sculpturings of the secondary cell wall.

Spotlight on the John Innes Centre

Name Cathie Martin
e-mail cathie.martin@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/Cathie-Martin.asp
Research Area Dietary flavonoids and health

Research Activities

One of the main areas of interest in the Martin lab, is understanding the regulation of flavonoid synthesis in plants and investigating the role of dietary flavonoids and related phenolics in health promotion and prevention of disease. This involves a unique co-operation between plant breeders, plant geneticists, epidemiologists, cardiologists and clinicians across Europe. The project focuses on the relationship between flavonoid content in whole foods and risk factors for cardiovascular disease and stroke, defined cancers and age-related degenerative diseases, especially those associated with obesity and the metabolic syndrome. It uses, for the first time, whole plant material, which is isogenic except for its flavonoid content.



Name Andy Maule
e-mail andy.maule@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/andy-maule/
Research Area Structure/function determination of plant cell-to-cell communication and its role in pathology and stress responses

Research Activities

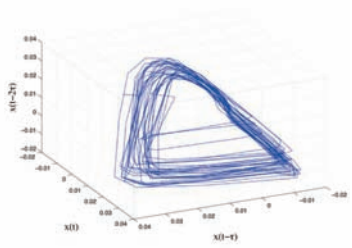
The Maule lab is pursuing a detailed analysis of components of the cell-to-cell trafficking pathway through plasmodesmata. Plasmodesmata are membrane rich symplastic channels through plant cell walls that regulate the flow of large molecules from cell to cell. These molecules can be transcription factors that control growth and development, small RNAs that regulate defence against pathogens (especially viruses), or the macromolecular structures that are viruses themselves. Hence understanding the nature of plasmodesmata will throw light on diverse areas of plant growth and defence. Indeed, since viruses in plants are retained within the symplastic environment understanding how they exploit plasmodesmata is key to understanding virus disease. Interestingly, some fungi may also use plasmodesmata as doorways to cell invasion. The primary focus of the work is the identification of new plasmodesmal components using proteomics, cell biology and genetics. To date several new families of plasmodesmal proteins have been identified and their role in the control molecular flux established. The challenges now are to identify how these proteins are regulated and the nature of the processes that trigger changes in flux, and how these and other plasmodesmal proteins operate in concert to shape plant biology.

Name Graham Moore
e-mail graham.moore@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/graham-moore/
Research Area Wheat genetics and comparative genomics and chromosome pairing

Research Activities

The Moore Group is investigating chromosome pairing in wheat and related species, which is under the control of the *Ph1* locus. The *Ph1* locus prevents pairing and recombination of chromosomes that are not true homologues. This failure in chromosome exchange (introgression) prevents breeders from exploiting the diversity of wild relatives within their breeding programmes, so the ability to turn *Ph1* off and on would be of major importance to wheat breeding. Understanding the make-up of the Ph1 complex and the mechanism by which it controls specificity of chromosome pairing during meiosis could open up a large pool of desirable traits such as salt tolerance, drought resistance and disease resistance that would be otherwise unavailable.

Spotlight on the John Innes Centre



Name Richard J Morris
e-mail richard.morris@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/richard-morris/
Research Area Mathematical modeling

Research Activities
The Morris group employs a variety of mathematical and computational techniques to address problems of biological relevance for plant research. A particular emphasis is on signal processing in biology, such as molecular recognition, calcium signaling or flowering time control. The approaches range from standard numerical, physical modeling techniques to methods of artificial intelligence, machine learning, computational geometry, computer vision, evolutionary algorithms and especially information theory. The group has expertise in shape analysis, optimization, graph theory, statistics, protein structure, ODEs, PDEs, and algorithm design and implementation in most high-level programming languages.

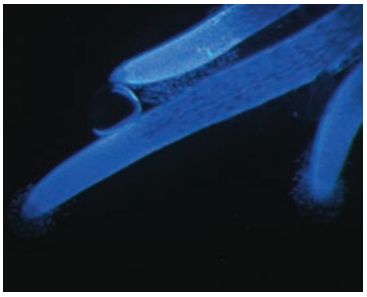
Name Paul Nicholson
e-mail paul.nicholson@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/paul-nicholson/
Research Area Resistance to facultative pathogens of cereals and the role of mycotoxins in pathogenicity

Research Activities
The Nicholson lab is investigating facultative pathogens involved in disease complexes of the stem-base and heads of cereals. Emphasis is placed on study of the genetics and mechanisms of resistance to Fusarium species and developing methodologies to enable identification and characterisation of resistance. Arabidopsis is used to gain insight into potential signalling pathways important in host resistance. Results are translated into crop systems to determine whether these pathways also function in wheat and barley. This will provide candidate genes for exploitation by scientists and plant breeders. The two most important Fusarium species, *F. graminearum* and *F. culmorum* both produce trichothecene mycotoxins, predominantly deoxynivalenol or nivalenol and these are differentiated on the basis of their chemotype. The role of chemotype in host-pathogen interaction is being investigated to establish the basis of the balanced selection that maintains both chemotypes in the population. These studies are also aimed at understanding the basis of trichothecene function within plants. In addition, the lab is investigating temporal and spatial regulation of toxin biosynthesis during host colonisation to determine the effect of host and environmental factors on toxin accumulation in plant tissues. The lab is also studying the genetic basis of seedling and adult plant resistance to the stem-base disease eyespot, caused by two closely related species of Oculimacula. This work combines disease assessment of populations with genetic mapping to produce markers suitable for use by plant breeders.

Name Giles Oldroyd
e-mail giles.oldroyd@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/giles-oldroyd/
Research Area Legume/rhizobial symbiosis

Research Activities
Many plant species acquire a significant amount of their nutritional needs through symbiotic interactions with micro-organisms. Using *Medicago truncatula* as a model plant, work in the Oldroyd lab focuses on two symbiotic interactions of legumes: the mycorrhizal association that aids in the uptake of nutrients from the soil and is particularly important for plant acquisition of phosphates and the rhizobial symbiosis that provides a source of nitrogen to the plant. In both cases the establishment of these interactions involves a molecular communication between the plant and the micro-organisms, with diffusible signals being released by both the mycorrhizal fungi and the rhizobial bacteria. Research is focused on understanding how legumes perceive these diffusible signals and transduce this information for the activation of developmental processes associated with accommodating these symbionts. The signalling processes in the plant utilize calcium as a secondary messenger and the Oldroyd group is particularly focused on understanding how calcium changes are induced following recognition of the symbiont and how the calcium signal is transduced to gene expression changes.

Spotlight on the John Innes Centre



Name Anne Osbourn
e-mail sanne.osbourn@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/anne-osbourn/
Research Area The molecular basis of plant-microbe interactions

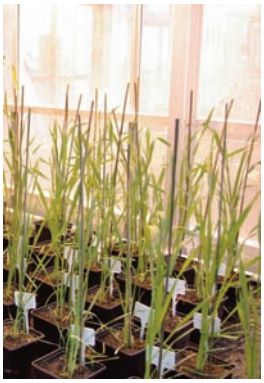
Research Activities

Plants produce a huge array of natural products (secondary metabolites). These compounds are exploited by humans as sources of drugs, flavouring agents, fragrances and for a wide range of other applications. The natural function of plant-derived natural products is in ecological interactions, where they provide protection against attack by herbivores and microbes and serve as attractants for pollinators and seed-dispersing agents. They may also contribute to competition and invasiveness by suppressing the growth of neighbouring plant species (a phenomenon known as allelopathy). The Osbourn lab investigates the molecular basis of interactions between plants and other organisms, with particular emphasis on natural products and plant defence. Primary interests are in understanding the function and synthesis of plant-derived natural products and the origins of metabolic diversity. This research impacts on other fundamental aspects of biology such as chromosome structure and gene regulation, genome plasticity, diversification of function of enzymes and multi-component pathways and adaptive evolution. The Osbourn group works with crop and model plants, using a wide range of multidisciplinary approaches that include genetics, genomics, computational biology, cell biology, protein and small molecule biochemistry. Anne Osbourn also coordinates the Science, Art and Writing (SAW) initiative. Through creative use of science in the classroom, SAW inspires artistic and scientific endeavour. Children realise that science and the arts are interconnected and they discover new and exciting ways of looking at the world. SAW projects are accessible to all ages and abilities. They stimulate exploration, enquiry and creativity. And they are fun! http://www.sawtrust.org

Name Lars Østergaard
e-mail lars.ostergaard@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/lars-ostergaard/
Research Area Fruit development in Brassica and Arabidopsis

Research Activities

Brassica and Arabidopsis are members of the diverse Brassicaceae family and are estimated to have diverged approximately 20 million years ago. This close relationship is also reflected in their similar overall fruit morphologies. The outside of both fruit consists of two seed pod walls that are separated along their entire length by a thin structure called the replum. At maturity, the pod walls detach from the replum, allowing the seed to be released. The Østergaard lab is researching the genetic and hormonal regulation of fruit development and has recently demonstrated the crucial importance of correct hormone distribution for fruit tissue specification. This knowledge provides a clear direction for future strategies to control seed dispersal that should be generally applicable to diverse Brassica crop species to reduce seed loss. Oilseed rape (*Brassica napus*) contributes 15-20% to the total UK crop output every year. However, the overall yield could be significantly improved by the inhibition of unsynchronised seed dispersal known as pod shatter, which leads to annual losses of 11-25%, and contamination of the following years' crop, inhibiting crop rotation practices. Molecular and genetic comparisons of the mechanism of fruit development in Arabidopsis and Brassica suggest that using experience from Arabidopsis fruit development to modulate this trait in oilseed rape will be successful. Research is focussing on gaining additional knowledge of the pod shatter mechanism to enable the improvement of conventionally modified crops through marker-assisted breeding combined with a "candidate gene" approach.



Name Chris Ridout
e-mail christopher.ridout@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/christopher-ridout.asp
Research Area Control of pests and diseases in cereals and brassicas

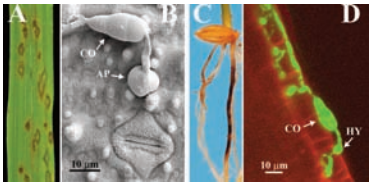
Research Activities

The aim of the research carried out in the Ridout group is to gain a better understanding of plant pathogen interactions for application in industry and the wider community. This involves working with plant breeders and biotech companies on an increasing range of projects. Current work is on the characterisation of pattern recognition receptors (PRRs), which detect conserved pathogen associated molecular patterns (PAMP's) in bacteria, oomycetes and fungi. PAMPS are essential, conserved molecules in microbial pathogens, that cannot be mutated or lost. Thus, PRRs could enable durable, broad-spectrum disease control in crops. Other projects include research on Turnip Yellows virus of oilseed rape, to understand how it is transmitted by aphids and to investigate its impact on oil quality, and projects on take-all and stem rust in wheat.

Spotlight on the John Innes Centre

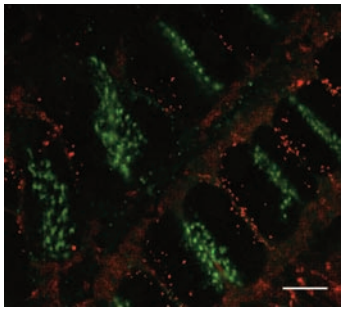
Name Robert Sablowski
e-mail robert.sablowski@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/robert-sablowski/sablowski.htm
Research Area Meristem and floral organ development

Research Activities
Plants produce new organs such as leaves throughout their lifetime. The cells required to build new organs are recruited from pools of actively dividing cells called the meristems. This continuous supply of new cells is sustained by small groups of self-renewing cells that reside at the core of the meristems and are functionally similar to stem cells in animals. The Sablowski group has been interested in how regulatory genes control the different cellular activities required for meristem maintenance and organ initiation. One approach to this problem is to reveal the changes in gene expression that are set in motion by regulatory genes, exemplified by work on the gene expression program controlled by the floral organ identity gene AGAMOUS in the early stages of organ development. Another approach is to use live imaging and modelling to understand how floral organ identity genes and some of their targets (such as JAGGED) control local growth and cell division to produce the shape of early floral organs. Current work also aims to understand how the meristem responds to stresses that cause DNA damage - based on the expectation that genome integrity is particularly important in cells that function as the long-term source of new cells to sustain plant growth.



Name Ane Sesma
e-mail ane.sesma@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/ane-sesma/
Research Area Organ-specific development and post-transcriptional gene regulatory mechanisms required for plant colonisation in the rice blast fungus *Magnaporthe oryzae*

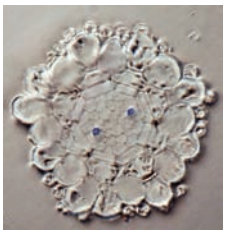
Research Activities
Magnaporthe oryzae (rice blast fungus) causes disease on a wide variety of grasses including rice, wheat and barley. The process of infection of leaves by *M. oryzae* has been extensively studied. Research has shown that it can undergo a different set of programmed developmental events that are typical of root-infecting pathogens. The Sesma lab is now working on the genetic dissection and comparative analysis of different pathways of plant attack by *M. oryzae*. The group is also looking at post-transcriptional gene regulatory mechanisms that control fungal plant infection. They are investigating the role of an RNA-binding protein required for the maturation and transport of mRNA precursors implicated in the synthesis of secondary metabolites (often called natural products) and infection-related development. This research area has also a broader relevance for understanding the link between natural products and cell differentiation processes in fungi.



Name Peter Shaw
e-mail peter.shaw@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/peter-shaw/
Research Area Organisation of interphase chromosomes and the nucleolus

Research Activities
Peter Shaw's group is investigating the relation between organization and activity in the nucleus, in particular how transcription is related to and regulated by chromosome territory organization and chromatin dynamics. These studies are being carried out using wheat and related cereals, because of their large nuclei, relatively good cytology and importance as crop plants, and in Arabidopsis because of its excellent genetic and genomic resources. A long-term collaborative project is in understanding meiotic homologue pairing, in particular the mechanism of Ph1, which controls the specificity of pairing in wheat and which is a major factor restricting the introgression of novel traits into wheat from related species by plant breeding. Another area in the lab focuses on the nucleolus and related sub-nuclear bodies, particularly Cajal bodies, which are involved in snRNA and siRNA metabolism, and which the group have shown to be mobile, dynamic structures. The nucleolus has well established functions in assembling ribosomes; analysis of the nucleolar proteome and 'RNA'ome has revealed the nucleolus is involved in other, previously unsuspected functions including mRNA surveillance and nonsense mediated degradation.

Spotlight on the John Innes Centre



Name Alison Smith
e-mail alison.smith@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/alison-smith/
Research Area Starch and sucrose metabolism in relation to plant growth

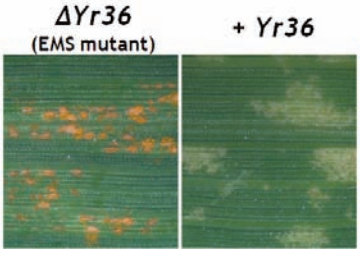
Research Activities

The aim of the research in the Smith lab is to discover the nature and control of pathways of sucrose and starch metabolism in plants, and to relate these aspects of primary metabolism to plant growth and productivity. Forward and reverse genetic approaches in Arabidopsis have been used to define the pathways of starch synthesis and degradation in leaves. Recent research is focused on how storage and utilisation of starch is controlled in relation to growth over the day-night cycle. Initial results show that starch degradation at night is a major determinant of productivity, and that the rate of degradation is controlled by a mechanism that uses information from the circadian clock. Other research on the function of starch storage in plants, building on results from Arabidopsis, includes investigation of starch degradation in germinating barley seeds using a combination of chemical genetics and reverse genetics and exploration and exploitation of variation of starch structure and properties in barley and wheat. The Smith lab also studies how sucrose is metabolised to provide the carbon for biosynthesis and growth in non-photosynthetic cells. The research uses a large collection of mutants impaired in aspects of sucrose utilisation in Arabidopsis. The Smith lab also has interest in using a collection of starch- and sucrose-metabolism mutants in Lotus to study starch storage and sucrose metabolism in relation to regrowth, perenniality and nitrogen fixation.

Name John Snape
e-mail john.snape@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/john-snape/index.htm
Research Area Genetic analysis of crop plants

Research Activities

The Snape lab is working on the development of conventional and novel methods of genetic analysis and their application to understand the genetic control of agronomic characters in crop plants, particularly cereals, and their application in crop improvement programmes. Current projects include the identification of traits and genetic markers to reduce the nitrogen requirement and improve the grain protein concentration of winter wheat, optimising grain shape for improved processing quality and enhancing wheat field performance and response to abiotic stress with novel growth-regulatory alleles. The group is also developing biotechnologies for cereal improvement, particularly molecular maps, doubled haploid methods and transformation systems.



Name Cristobal Uauy
e-mail cristobal.uauy@bbsrc.ac.uk
Website http://www.jic.ac.uk/profile/Cristobal-Uauy.asp
Research Area Identification and deployment of genes underlying wheat QTL of agronomic importance

Research Activities

The study of quantitative variation is of special interest to agricultural scientists since it tries to explain the variation and inheritance of many of the most important traits related to food and fibre production. These traits are characterized by their large environmental dependency and the multiple genes controlling them, known as quantitative trait loci (QTL). However, the molecular mechanisms underlying these traits are not well understood since there are a limited number of plant QTL in which the underlying gene has been cloned. Work in the Uauy lab is seeking to identify genes underlying wheat QTL with significant agronomic impact and facilitate their effective deployment into modern breeding varieties. Using map-based cloning, genes that determine QTL for complex traits such as senescence, grain nutrient content and broad-spectrum yellow-rust resistance have been identified. Two TILLING populations in tetraploid and hexaploid wheat have been developed as a resource for researchers undertaking wheat functional genomics. Current research is focussed on identifying genes responsible for key yield QTLs in UK wheat germplasm and the development of genetic resources to enable effective translational research from model to crop species. Enhancing the pipeline to translate new knowledge into improved wheat varieties for growers, industry and consumers is a key focus. As part of this strategy, Cristobal Uauy holds a joint appointment with the National Institute of Agricultural Botany at Cambridge for pre-competitive germplasm improvement.

Spotlight on the John Innes Centre

Name Philippe Vain
e-mail philippe.vain@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/philippe-vain/index.htm
Research Area Understanding and exploiting transformation systems in model and crop plants

Research Activities
The main research interests of the Vain lab are to develop clean and efficient transformation systems that are better understood in terms of transgene integration, structure, expression and stability. The technologies and know-how developed using key species such as *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Brachypodium distachyon* and rice contribute to the further improvement and exploitation of plant transformation systems. The Vain lab also has key interests in designing new strategies and standard operating procedures to conduct large scale and generational transgenic studies in plants, addressing biosafety considerations, and in monitoring trends in plant transgenic science and technology. Recent work includes the production of mono- and dicotyledonous plants free of undesirable selectable marker genes (such as antibiotic resistance genes) using the pCLEAN vector system; the development of transgenic strategies for nematode resistance in rice and cooking banana; and the development of a T-DNA tagging system for insertional mutagenesis in *Brachypodium distachyon* (BrachyTAG programme). *Brachypodium distachyo*n is a new model system for bridging research into temperate cereal crops, such as wheat and barley, and for promoting research in novel biomass grasses. The BrachyTAG programme represents the first T-DNA mutant resource available worldwide for Brachypodium. T-DNA stock lines can be obtained online at www.BrachyTAG.org.

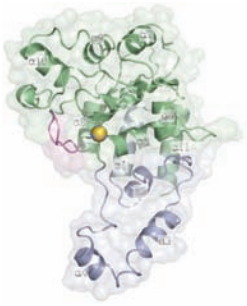
Name Trevor Wang
e-mail trevor.wang@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/trevor-wang/
Research Area Carbon partitioning and secondary metabolism in the model legume *Lotus japonicus*

Research Activities
The Wang lab is using the model legume, *Lotus japonicus*, to investigate carbon partitioning especially to nodules, and the biosynthesis of selected natural products. Numerous mutants have been generated using both forward and reverse genetics, especially mutants in starch metabolism and sucrose breakdown. Using such mutants the group have defined some of the roles of sucrose synthases and cytosolic invertases in this model plant. All of this research makes extensive use of a reverse genetics TILLING platform set up by the group in collaboration with the Sainsbury Laboratory and now being developed into a biological and bioinformatics resource for the wider plant scientific community via the RevGenUK project http://revgenuk.jic.ac.uk. This provides an integrated reverse genetics platform for several model plant species.

Name Philip Wigge
e-mail philip.wigge@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/philip-wigge/index.htm
Research Area Temperature perception and primordia fate determination

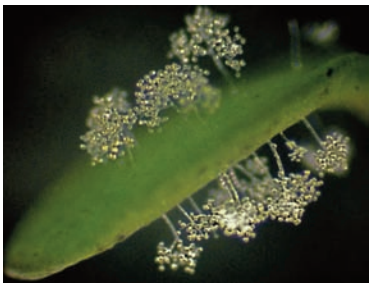
Research Activities
The Wigge lab is studying how plants sense changes in environmental conditions, particularly ambient temperature, and how these signals are integrated into development. Forward screens in Arabidopsis have been used to identify key regulatory components of the temperature sensing pathways. Many of these mutant lines have altered growth, indicating their importance in integrating temperature sensing signals into plant development. A second area of interest for the lab is how primordia fate is determined and factors that provide spatial information. Primordia fate specification and the relative contributions of vegetative versus floral signals have a profound effect, not just on flowering time, but also on the entire architecture and growth habit of the plant. The integration of these signals to control growth and development is still poorly understood. Arabidopsis is an ideal multicellular system for studying transcriptional switches and regulatory networks at the transcription factor and epigenetic level, and ways to represent and model different types of biological switch, particularly continuously variable switches. As well as Arabidopsis, the group also works on these problems in the model grass species *Brachypodium distachyon.*

Spotlight on the Sainsbury Laboratory



Name Mark Banfield
e-mail mark.banfield@bbsrc.ac.uk
Website http://www.jic.ac.uk/staff/mark-banfield/
Research Area Molecular interactions at the host:pathogen interface

Research Activities
The Banfield group primarily investigates molecular interactions at the host:pathogen interface, with a particular focus on 'effector' proteins that are translocated into host cells during infection. These proteins interfere with host cell processes, presumably to the benefit of the pathogen. The lab works on proteins from both mammalian and plant pathogens (and their respective hosts). The experimental method of choice is structure determination by X-ray crystallography, using a wide variety of other biophysical techniques appropriate to answering relevant biological questions. In plants, effector proteins can not only have a 'virulence' function (promoting disease) but can also be specifically recognised within plant cells leading to localised cell death (so-called 'avirulence' function as it restricts pathogen growth). The latter function forms part of the plant innate immune system. Using protein biochemistry and structural biology the group is aiming to further understanding of effector function/evolution in plant pathogens.



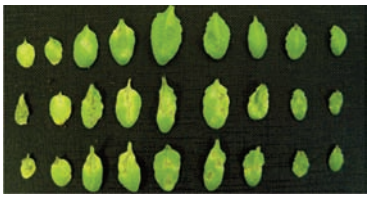
Name Sophien Kamoun
e-mail sophien.kamoun@sainsbury-laboratory.ac.uk
Website http://web.mac.com/sophien/KamounLab/default.htm
Research Area Effector biology in filamentous plant pathogens

Research Activities
Unravelling the biochemical activities of effectors to understand how pathogens successfully colonize and reproduce on their host plants has become the driving paradigm in the field of plant pathology. The Kamoun lab studies effector biology, mainly in the *Phytophthora infestans*-Solanaceae pathosystem. The long-term objective is to dissect the molecular mechanisms that enable filamentous pathogens, such as the oomycete *P. infestans*, to successfully infect plants and the plant processes that are perturbed by the effectors of this pathogen. The group aims to understanding how pathogen effectors function, how they evolve, and how they traffic into host cells.

Name Jonathan Jones
e-mail jonathan.jones@sainsbury-laboratory.ac.uk
Website http://www.tsl.ac.uk/research/jonathan-jones/
Research Area Plant Defence

Research Activities
Pathogen effector molecules, that can either suppress host defences, or activate them if recognized by a Resistance (R) protein, provide profound insights into plant/pathogen interactions. The identification and analysis of bacterial effectors (and avirulence proteins) has led to major advances in understanding how phytopathogenic bacteria cause disease (or fail to do so). With advances in DNA sequencing and other genomics methods, potentially devastating crop pathogens such as rusts, powdery mildews and downy mildews are now “within range” for genomics-based approaches. This provides opportunities to reveal new biological mechanisms and to accelerate recruitment of new sources of host resistance variation for crop improvement.
The main goals of the group are to investigate the effector complements of Arabidopsis downy mildew (*Hyaloperonospora arabidopsidis, [Hpa]*) and various races of white rust (Albugo) species that infect Arabidopsis, Brassica and other brassicaceae. This approach takes advantage of genomics and other tools for investigating Arabidopsis biology, and of recent advances in oomycete genomics, and an ERA-PG project coordinated by Jim Beynon. In January 2009 the laboratory was awarded European Research Council funding to expand the *Albugo* project; this has enabled 3 additional postdoctoral and assistant appointments. A central hypothesis in this proposal is that using one-effector-at-a-time delivery with the Effector Dectector Vector (EDV) system (Sohn *et al* Plant Cell 19:4077-90 [2007]), this funding will allow researchers to gain insight into the extent to which “non-host resistance” (NHR) in Arabidopsis to brassica strains of *Albugo*, is explained by effector-triggered immunity, or by failure of the effector complement to suppress disease.
In addition, the group continue with studies on various aspects of plant/bacteria interaction, particularly the recognition of AvrRps4 by RPS4, and have identified a putative “guardee” that appears to be required for RPS4 function. Researchers are also investigating the roles of auxin and DELLA proteins in resistance and susceptibility. Jonathan recently obtained a BBSRC grant to use new genomics tools to accelerate cloning resistance genes from wild potato relatives for potato blight resistance.

Spotlight on the Sainsbury Laboratory



Name John Rathjen
e-mail john.rathjen@sainsbury-laboratory.ac.uk
Website http://www.tsl.ac.uk/research/john-rathjen/index.htm
Research Area Plant immunity against pathogenic bacteria

Research Activities

The Rathjen lab is interested in plant immunity. Plants have sophisticated means to sense environmental cues and translate these signals into appropriate responses. Plant-pathogen interactions are characterised by extreme specificity. This specificity has arisen as a result of millions of years of host and parasite co-evolution. The group's aim is to characterise such interactions at the molecular level. The principle model is the interaction of *Pseudomonas syringae* bacteria with Arabidopsis, tomato and the wild tobacco, *Nicotiana benthamiana*. Initial perception of bacteria is due to recognition of bacterial elicitors called PAMPs, for pathogen-associated molecular patterns. The group along with Thomas Boller's lab identified the receptor kinase BAK1 as a central regulator of PAMP-triggered immunity in both Arabidopsis and *N. benthamiana*. BAK1 forms a complex with FLS2 shortly after elicitation. Bacteria respond to PAMP perception by secreting about 30 virulence effector proteins into the host cytoplasm, where they target key host molecules to abrogate signalling. The group identified the LysM receptor kinase, CERK1, as an important target for bacterial pathogenicity. The effector AvrPtoB binds to CERK1 leading to its ubiquitination and subsequent degradation. However, on resistant tomato plants, AvrPtoB is recognised by an effector recognition complex composed of Pto kinase and the nucleotide binding-leucine rich repeats protein Prf. Recently, the lab discovered that Pto disables AvrPtoB by phosphorylating it within its E3 ligase domain, potentiating Prf-dependent recognition of the effector. Kinase-deficient Pto mutants were not able to disable AvrPtoB, leading to loss of the Pto-Prf complex. The search for important effector targets, which underlie host immunity to bacteria continues.

Name Cyril Zipfel
e-mail cyril.zipfel@sainsbury-laboratory.ac.uk
Website http://www.tsl.ac.uk/research/cyril-zipfel/index.htm
Research Area Plant-microbe interactions

Research Activities

Higher eukaryotes can recognize invading microorganisms by detecting conserved molecules referred to as PAMPs (pathogen-associated molecular patterns) by pattern recognition receptors (PRRs). The mechanisms underlying this innate immune recognition and subsequent signalling have been extensively studied over the last decade in insects and mammals, but much remains to be discovered in plants. *Arabidopsis thaliana* provides an excellent model system to study PAMP-triggered immunity (PTI), and detects a variety of PAMPs, including conserved domains of bacterial flagellin and EF-Tu, or their peptide surrogates, flg22 and elf18, respectively.

The significance of PAMP-triggered immunity (PTI) against bacteria is demonstrated by the fact that successful bacterial pathogens have evolved to avoid PAMP recognition or to suppress PTI-signalling by secreting effectors into the host cells. Although many resistance (R) proteins have been identified and many genetic or biochemical approaches to dissecting effector-triggered immunity (ETI) initiated, there is only limited knowledge about plant PRRs and PRR signal transduction.

We need to understand PTI properly not only because of its intrinsic interest, but because many of the pathogen effector targets will be PTI components. Furthermore, there are more PRRs to discover in order to fully understand the molecular interplay between host and pathogen that directs the outcome of infection. The Zipfel lab is using a combination of forward- and reverse-genetics, as well as biochemical and proteomic approaches to understand how PAMP is perceived, what signalling events is triggers, and what contribution PAMP perception makes to plant immunity.

Fifth epso Conference

Plants for Life

Olos (Lapland), Finland
18-22 April 2010

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Science and society

Food security and safety – challenges ahead

Achieving sustainability

Crop genomes for sustainable agriculture
Breeding tools and strategies

Achieving quality

From plant architecture to traits
From photosynthesis to solar fuels
Tree biology for multiple uses
From metabolites and recombinant proteins to plant-made-pharmaceuticals
Plants with improved nutritional quality and value

Strengthening the functioning of ecosystems

Plant health
Climate change and plant production
Landscape genomics
Biodiversity

Confirmed speakers

Jim Barber, Mike Bevan, Wout Boerjan, Jörg Bohlmann, Thomas Boller, Paula Bramel, Barbara Burlingame, Reinhart Ceulemans, Paul Christou, Philippe Ciais, Jean-Christophe Glaszmann, Wilhelm Gruissem, Timothy Hall, Richard Hobbs, Dirk Inzé, Stefan Jansson, Jaana Husu-Kallio, Cris Kuhlemeier, Jane Langdale, Leena Manonnen, Stephen Mayfield, Karin Metzlaff, Maurice Moloney, Kirsi-Marja Oksman-Caldentey, Per Pinstrup-Andersen, Riita Puupponen-Pimiä, Bill Rutherford, Bernhard Schmid, Ulrich Schurr, Anker Sørensen, Eva Stöger, Chiara Tonelli, Robbie Waugh, Rod Wing, Tom Whitham

Coordinators: Karin Metzlaff, EPSO and Kirsi-Marja Oksman-Caldentey, VTT, Finland

Information and registration at www.epsoweb.org

What could a mathematician do for you?

written by Susie Lydon, University of Nottingham, CPIB, Sutton Bonington Campus.

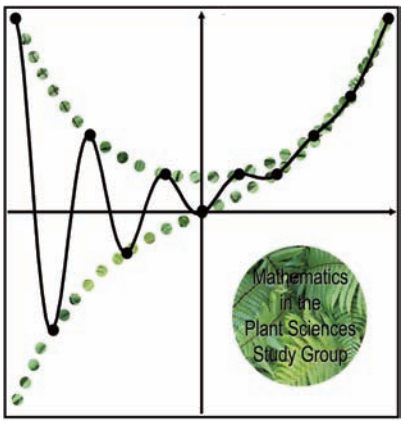
With the 'systems approach' to biology high on the agenda and interdisciplinary research becoming ever more prevalent, how can a plant scientist with no mathematical links get a kick-start in using modelling in their research? The answer is the Mathematics in the Plant Sciences Study Group (MPSSG) series.

Study Groups are a well-established mechanism for mathematicians to apply their skills to real world problems. Mathematicians at Oxford University have been holding study groups with industry since 1968, and the Mathematics in Medicine study group series, established in 2000, has been successful in building collaborations between theoreticians and researchers in the life sciences.

The Mathematics in the Plant Sciences Study Groups, co-organised by the Centre for Plant Integrative Biology (CPIB) at Nottingham, GARNet and the Spatio-Temporal Modeling Network on Plant Systems (STEMN), follow the format established by other study group series. On day one of the four day workshop, five plant scientists present a problem within their field which is amenable to modelling or statistical approaches. The forty or so applied mathematicians, computational modellers and statisticians attending listen to all the presentations, and then decide which problem to apply their skills to. Modellers are free to choose any problem to work on, and to move between problems mid-workshop (and indeed to 'phone a friend' if special skills are needed and a colleague's input would be of value!). The groups each convene to a meeting room, armed with flipcharts and whiteboards, and spend the rest of the workshop tackling the problem. The study group approach is intense, with long days and regular updates to the whole meeting required – but this often results in a great deal of progress made in a very short time.

The inaugural MPSSG took place at Nottingham in December 2007, followed by the second (also at Nottingham) in January 2009. Problems tackled so far have covered a broad range of biological topics and physical scales: from biosynthesis and signalling pathways, and floral organ development, through to the mechanics of processes in germination and abscission, genetic diversity in weed species, and relating variation in genotype to yield in crop landraces.

So did the plant biologists who took the plunge in the first MPSSG in 2007 think it was worth it? Mike Holdsworth, who co-presented a problem relating to the mechanics of Arabidopsis seed germination with colleagues Tara Holman, Darren Wells and Michael Wilson at the University of Nottingham, feels that the benefits began with submitting the problem in the first place. He feels that the process of formulating a problem description for modellers "forces you to think outside the 'trendy experiment' box and think about what you actually need to find out, rather than what will get funding or get into a high-impact journal(!)". Mike also found the workshop itself a refreshing experience: "interacting with non-biologists completely changes your focus, as they ask questions pertinent to their mechanisms of discovery, not yours". For Mike, the process has been very fruitful, leading to two grant applications (one successful, one under review), two new PhD students, and new collaborations with engineers, computer scientists and mathematicians.



Pete Iannetta (SCRI, Dundee), who presented a problem relating to genetic diversity within the arable weed *Capsella bursa-pastoris* was attracted to the Study Group approach by the dual benefits of "working with scientists possessing expertise complementary to my own" and "publishable information being acquired within a short time frame". The progress made during the workshop led to his adoption of a new statistical tool introduced to him by modellers, which is now feeding into a publication. Having seen the study group process in action, he is now keen to return with another problem! Other problem contributors from the first MPSSG note that it has led to several publications and, in one case, a patent application.

With the third MPSSG planned for 14-17 December 2009, the organisers are keen to hear at any time from plant scientists who would like to get involved. Problems are subject to a selection process, and the earlier discussions with the organisers begin, the more opportunity there is for problems to be refined into a form which will maximise progress at the study group itself. If you would like to get involved in the next MPSSG, please contact Marcus Tindall (m.tindall@reading.ac.uk) Ruth Bastow (ruth@arabidopsis.info) or Susie Lydon (susie@cpib.ac.uk).

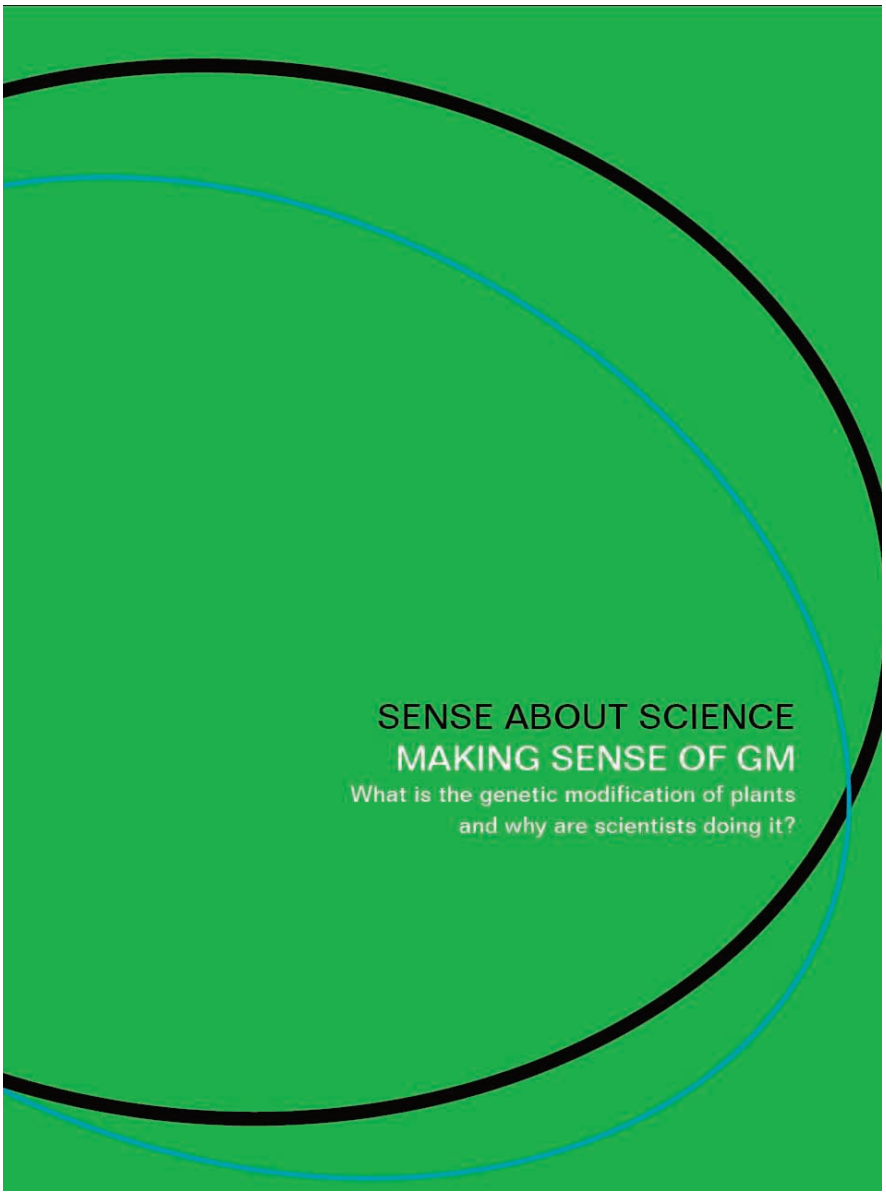
Making sense of GM

Leonor Sierra, Scientific Liaison, Sense About Science

There have been more Google searches on GM crops in the past two years in the UK than anywhere else in the world and the issues surrounding GM are being revisited in the public discussion. However, Sense About Science, found that when people contacted them, it was difficult to point them towards anything that could give them a direct way into the debate that wasn't overwhelmingly technical or full of polemic.

Sense About Science is a UK charity that equips people to make sense of science and evidence. We have a database of over 3,000 experts from academia and industry, Evidence Base, who help us respond to enquiries from journalists, politicians, schools and others. They also work with us on different projects, providing insights on a range of issues – including radiation, chemicals and peer review –and tools that they would use and that are useful for people to question topical issues they are confronted with.

In February 2009, we released the guide Making Sense of GM – What is the genetic modification of plants and why are scientists doing it? We worked with scientists and agriculturalists to launch a fresh public discussion that puts GM back into the context of plant breeding techniques and to directly respond to the public's questions and misconceptions, such as what is GM? What is the likely impact on the environment? Are people eating GM foods and what would happen if they did? We also worked with the directors of the leading UK plant research institutes who pointed out that unless there is a well-informed discussion about GM, it won't be possible to judge what crop technologies can contribute to food security and natural resource and climate change management. The document also discusses what GM can and cannot do and how GM is a plant breeding technique rather than a social or economic system, despite much of the discussion centring on whether or not it can solve world hunger.



Since the release of the guide we have been thrilled about how many farmers, horticultural groups, schools, librarians and others have contacted us to request copies of the publication and who told us how useful they found it.

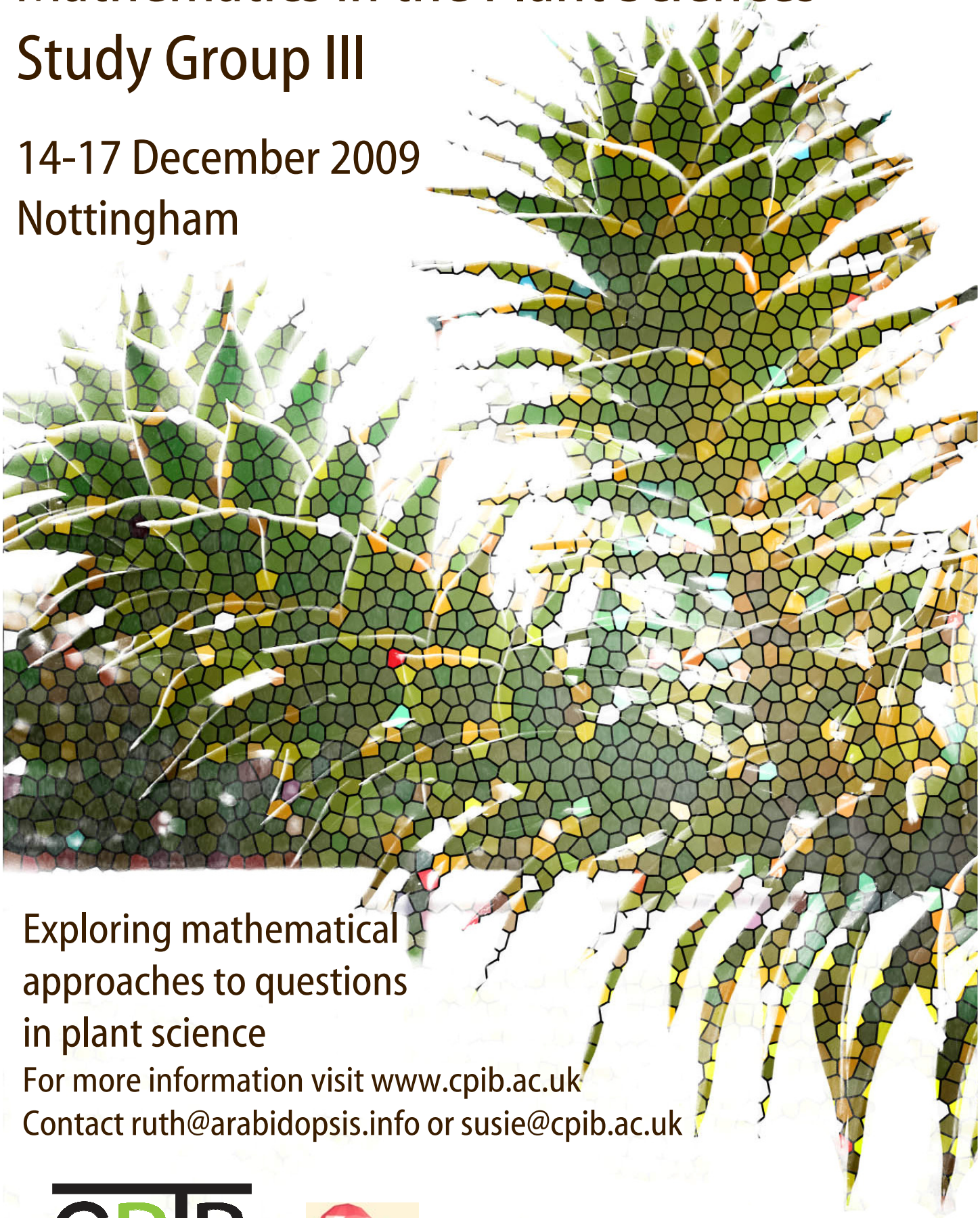
We believe it is important that the people that work on these technologies talk out about what GM is and the work they are doing, so that public discussion does not lose sight of the science behind the stories and what we know about GM.

If you run public engagement activities or talk with the public about GM, and you could use some copies of the guide please get in touch by emailing lsierra@senseaboutscience.org. The guide Making Sense of GM can also be downloaded for free as a PDF from: http://www.senseaboutscience.org.uk/index.php/site/project/16/.

If you would like to join our database and offer your support, please fill in the form located at: www.senseaboutscience.org/support.

Mathematics in the Plant Sciences Study Group III

14-17 December 2009
Nottingham



Exploring mathematical approaches to questions in plant science

For more information visit www.cpib.ac.uk

Contact ruth@arabidopsis.info or susie@cpib.ac.uk

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