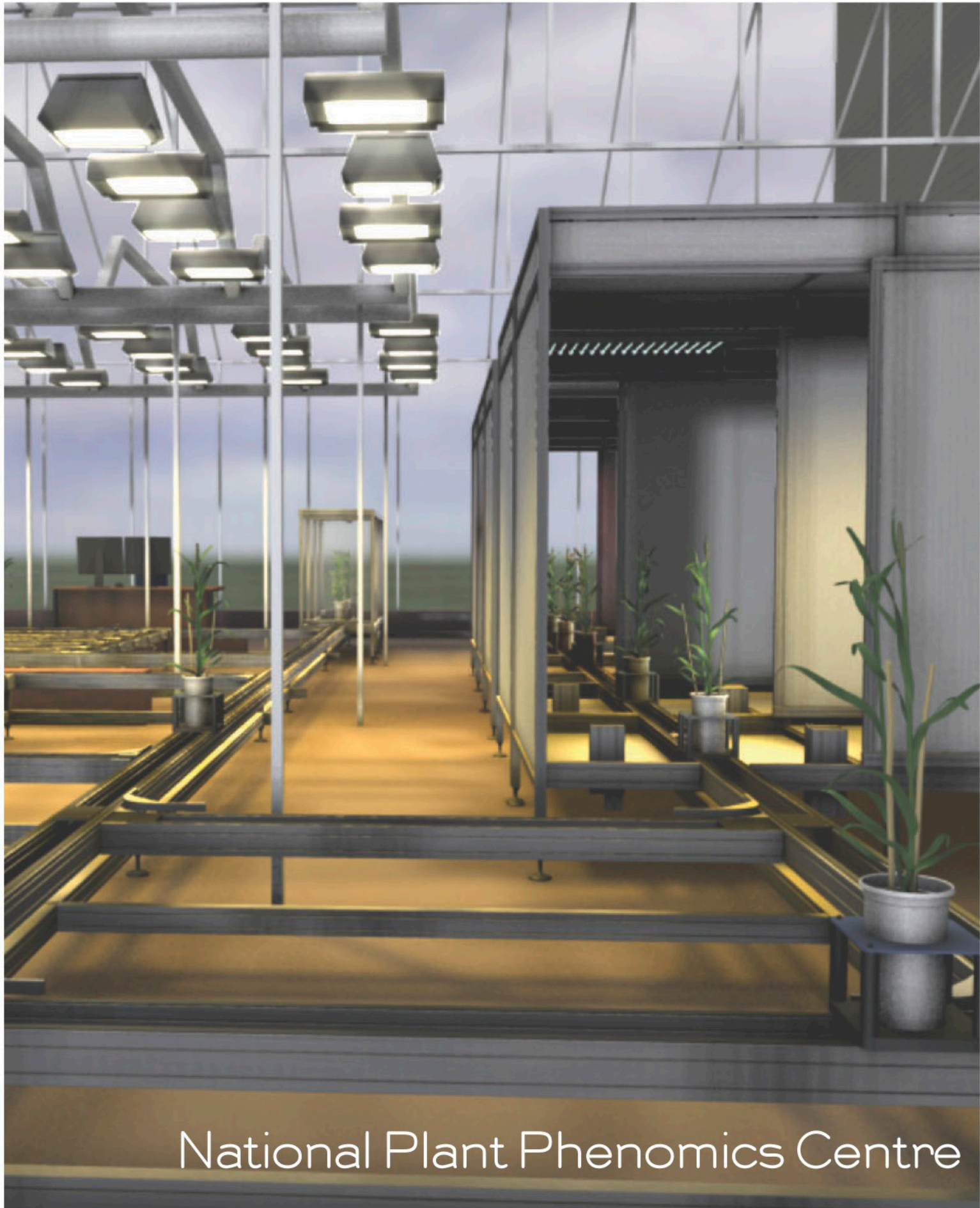


GARNish

December 2011. Edition 16



National Plant Phenomics Centre



Welcome to the December 2011 issue of GARNish!

This is a time when important issues of funding, continuity of community resources and cooperation between all areas of plant science are at the fore. In this respect, the UK Plant Sciences Federation (UKPSF) will have its official launch in late November 2011 (see pg 12). It is hoped that this organization, which operates as a special interest group of the Society of Biology (SoB), will provide a focus for plant science in the UK. With research funding unlikely to increase in the near future, it is essential to have a strong and unified voice. The UKPSF will provide a platform to outline the importance of plant science in everyone's lives, to promote funding that enables both the basic and translational research needed to deliver increased and more sustainable crop yields for food security as well as input to other global challenges such as human health, energy resources, and biodiversity and habitat conservation. The UKPSF website is up and running, and it is well worth taking a look at the developing resources <http://www.ukplantsci.org.uk>. Also, do register on the "Find a Scientist" page so that your research expertise can be broadcast to the community. An important upcoming event for the UKPSF is the inaugural conference (UK PlantSci 2012) to be held at the John Innes Centre (18-19th April 2012, see back cover). Reserve a space in your diaries for this event.

Related to the struggle to gain a portion of the research funding pie, is the need to attract students into plant science (and away from biomedicine!). It is recognised that plants are not well-represented on school curricula making it challenging to attract students to plant-based modules at university. Organisations such as Gatsby Plants are making important contributions to plant science education. Aurora Levesley and colleagues highlight the Gatsby Plants TREE (Tool for Research Engaged Education) resource on page 5. The news on the radio today while I was writing this Editorial focused on unemployment amongst recent science graduates, so another challenge is to guide students in career choices. A book that with this task will help is reviewed on page 16.

Two articles in this issue highlight the value of large data sets and the provision facilities for largescale screening. Next generation sequencing projects are now producing large amounts of data. Not only can the variation in genome sequences between large numbers of *Arabidopsis* accessions be revealed but also the variation in gene expression and its genetic control can be addressed using mRNA-seq (see page 6). The National Plant Phenomics Centre at Aberystwyth University aims to provide a high throughout phenotyping facility, including chlorophyll fluorescence imaging and infrared spectroscopy to image transpiration and root

Contents

News and Views	Pg 3
Gatsby Plants TREE	Pg 5
<i>Arabidopsis</i> population genetics	Pg 6
National Plant Phenomics Centre	Pg 9
UK Plant Science Federation	Pg 12
GARNet 2011 Meeting	Pg 13
Careers Publication	Pg 16
University of Birmingham	Pg 21
University of Essex	Pg 25

Many thanks to all who contributed to this issue, particularly Ruth Bastow, Sarah Blackford, Juliet Coates, John Doonan, Paula Kover, Irene Lavagi, Aurora Levesley, Richard Mott, Phil Mullineaux and Nicholas Smirnovff.

morphology. The progress being made in setting up his facility is described on pg 9. Large data sets and centralised facilities such as these are clearly important to the *Arabidopsis* research community. However, the funding models and sustainability of data repositories (e.g. TAIR and its eventual successor), seed stock centres or providers of services such as sequencing, microarray analysis or metabolomics are issues that require constant evaluation and action. GARNet aims to play a role by acting as a focus and co-ordination point for the community. Indeed, how to maintain the functions of GARNet after the current funding period is being considered.

Other features in this issue include the continuing research spotlight series. The focus is on the diversity of plant science research at Birmingham and Essex Universities (pg 21-27). There is also a report of the last GARNet meeting held at Cambridge. At this meeting I particularly enjoyed the opportunity to get to grips with some of the latest research in epigenetics.

Finally, we should acknowledge to contributions of the outgoing committee members, Alex Webb, Alessandra Devoto, Robert Sablowski and Stefan Kepinski who step down at the end of 2011. Alex Webb served as an energetic and dedicated Chair, playing a key part in establishment of the UKPSF. Jim Murray (Cardiff) will become the new Chair of GARNet in January 2012.

Nicholas Smirnovff

GARNet elections

Not only is December the time to panic about not having done the Christmas shopping, it is also the season for the GARNet Committee Elections.

As part of the long-term development of GARNet, we hold annual elections to select new members of the committee. Advisory committee members generally serve a term of three years and a number of our committee members are reaching the end of their term and will be standing down at the end of 2011. This includes Alessandra Devoto, Stefan Kepinski, Robert Sablowski who we thank for their input and energies. Alex Webb the current GARNet Chair is also standing and we would like to say a huge thank you to Alex for his leadership, direction and enthusiasm. Without Alex we would not have established the UK Plant Sciences Federation (UKPSF).

During November the community nominated the following people to stand for election

Antony Dodd - University of York
John Doonan - Aberystwyth University
Anthony Hall - University of Liverpool
Heather Knight - Durham University
John Runions - Oxford Brookes University
Jurian Ton - University of Sheffield
Carol Wagstaff - University of Reading
Chris West - University of Leeds
Cyril Zipfel - Sainsbury Laboratory, Norwich



It is now up to you to decide who will join the committee. To cast your vote e-mail (ruth@garnetcommunity.org.uk) the names, in order of preference, of the three individuals who would wish to appoint to the committee. Voting will close on the 23rd December 2011.

Petition for science-based GM regulations

In October this year leading plant researchers called for science-based GM regulation in a letter to The Times newspaper.

At the end of this month, the world's population will reach 7 billion; 1 billion are hungry, and 1 billion more are malnourished (<http://tinyurl.com/3ngkyrt>). In the next decades, there will be more humans. Limited land and water, costly energy for fertilizer, and climate change will ensure that more of them are hungry. Politics, economics and lack of good governance exacerbate the problem, but science and technology can contribute greatly to the solution.



Why then is Europe regulating one part of the solution-GM (genetically modified) crops- as if they are a hazard?

41 leading Swedish plant scientists (see <http://bit.ly/n8lgVc>) have issued an important statement, expressing dismay, bewilderment and anger that legislation of GM crops in the EU is not based on science, ignores recent evidence, blocks opportunities to increase agricultural sustainability, and sustains the dominance of multinationals.

We undersigned British plant scientists endorse the assessment by our Swedish colleagues of the politics and science of GM crops. Irrational and unwarranted obstacles that obstruct the deployment of this useful technology retard innovations that will increase yields and reduce the environmental impact of agriculture. Irresponsible and perhaps well-meaning pressure groups, purporting to protect the environment, are preventing delivery of agrichemical-free solutions to crop pests and diseases. Small companies and the public sector are excluded from providing solutions by excessive regulatory costs, ensuring dominance of the market by multinationals. Pressure groups and organic trade associations who block deployment of GM damage the public interest and prevent the adoption of benign solutions to crop problems, not just in Europe but also in the developing world. We call on these groups to cease and desist from blocking genetic solutions to crop problems, and on Europe to adopt science-based GM regulations. Supporters are endorsing this campaign at <http://bit.ly/q3Folr>.

Jonathan Jones, Giles Oldroyd, Dale Sanders, Maurice Moloney, Sophie Kamoun, Tina Barsby, Wayne Powell

Professor Edwards receives Royal Agricultural Society Award

The Royal Agricultural Society of England's 2011 Research Medal has been awarded to Professor Keith Edwards in the School of Biological Sciences, in recognition of his work using genomics-based technologies to identify, map, isolate, manipulate and express genes of interest to plant breeders. The RASE Research Medal was introduced to acknowledge 'research work of outstanding merit, carried out in the United Kingdom, which has proved, or is likely to be, of benefit to agriculture'. Professor Edwards led the team that recently released genomic sequences covering 95% of all wheat genes, a significant building block in efforts to develop new types of wheat that are better able to cope with drought or salinity and able to deliver higher yields.



JIC researcher recognised for her outstanding contribution to science

Professor Cathie Martin's contribution to science has been recognised by election to the membership of a leading European life sciences organisation, EMBO. Prof. Martin is one of 46 life scientists from 14 countries being acknowledged for their outstanding scientific contributions by awarding them life-long EMBO membership.



Election to EMBO membership is recognition of the commitment to research excellence and the exceptional achievements made by a life scientist. The new EMBO Members join the ranks of 1,500 of the best researchers in Europe and around the world. They are leaders in their research fields and communities. Professor Martin is the sixth current John Innes Centre scientist to be elected to EMBO Membership, an indication of the regard in which John Innes Centre scientists are held by their peers.

Prof. Martin said: "I am really honoured to be elected as a member of EMBO. I look forward to being able to contribute to the shape of European Science through my membership and to work hard at promoting the importance of plant research to finding solutions to the challenges that science and societies currently face." Professor Dale Sanders FRS, Director of the John Innes Centre said: "This prestigious award to Cathie Martin is richly deserved. Cathie has made fundamental contributions to our understanding of factors regulating cell shape in plants and to the way in which plant metabolism can be manipulated to yield nutritionally-enhanced foods."

Prof. Martin's research has focussed on cellular specialisation, and she was the first person to identify the genes that regulate cell shape in plants. In particular, her interests have been in how plants use flowers to attract pollinators, and the roles that specialised cell play in this. More recently, she has been co-ordinating research into how diet helps to maintain our health and reduce the risk of chronic disease, and looking at how crop plants can be fortified to help achieve this.

This year EMBO acknowledges 43 European scientists as EMBO Members and three scientists from the USA as Associate Members. The new members include 11 female scientists and the first EMBO Member from Estonia.

EMBO Director Maria Leptin said: "We are happy to welcome the new EMBO Members into the EMBO community and look forward to the infusion of knowledge that they bring."

EMBO Members apply their expertise and insight to se-

lect the many talented scientists that EMBO supports each year to do the best science. As a result, EMBO Members collectively influence the future directions of life science and strengthen research communities across Europe. By encouraging cross-border interactions, EMBO Members ensure that Europe is a unified community of excellence where top-level life science thrives.

The 46 scientists recognized by EMBO represent a vivid cross-section of the life sciences from molecular biology and plant sciences, to neuroscience, computational neurobiology and cellular immunology.

Funding opportunities

There are a number of funding opportunities available throughout the year and this space just highlights a few. If you would like to have access to a complete list of funding opportunities for UK Plant Science researchers then visit

www.plantsci.org.uk/funding/opportunities/active

ERC Synergy Grants

ERC has introduced a new pilot scheme, called Synergy Grants (SyG), in the 2012 ERC Work Programme. Synergy grants will enable small groups of two to four PIs and their teams to bring together complementary skills, knowledge, and resources, in order to jointly address research problems at the frontier of knowledge going beyond what the individual PIs could achieve alone. Deadline: 25th January 2012. More info available at www.ukro.ac.uk/erc/syg/Pages/open_future_calls.aspx

Leverhulme Early Career Fellowships

Early Career Fellowships aim to provide career development opportunities for those who are at a relatively early stage of their academic careers but with a proven record of research. Fellowships are normally tenable for three years on a full-time basis. Deadline: 8th March 2012. More info available at www.leverhulme.ac.uk/funding/ECF/ECF.cfm

BBSRC Systematics and Taxonomy Scheme

This scheme is designed to provide short-term funding for preliminary research that will form the basis of novel responsive mode proposals with a substantial systematics/taxonomy/phylogenetic component. A total of £250k is available through the scheme which is jointly funded by BBSRC and the Natural Environment Research Council (NERC). The Systematics Association and the Linnean Society are administering the scheme. Deadline: 31st January 2012. More info available at www.bbsrc.ac.uk/funding/opportunities/2012/120131-syntax.aspx

Lectures and slides through the Gatsby Plants TREE

Aurora Levesley*, Richard Collins, Celia Knight
www.gatsbyplants.leeds.ac.uk/tree
 *a.levesley@leeds.ac.uk



A screenshot of the Gatsby Plants TREE Engaged Education) - a shared bank of on-line lectures, downloadable lecture slides, movies and other materials on topical plant science to support lecturers in their teaching.

The TREE aims to bring inspirational, research-led plant science teaching materials together in a one-stop, easy to use web medium, so that the excitement and potential for plant science can be disseminated to a wide audience of undergraduates through plant science educators worldwide.

The TREE builds on the strength of the UK Gatsby Plant Science network and communication between its academic members. The TREE was developed by listening to the needs of lecturers and working closely with them in its construction. Through a series of subject specific meetings, academics, who use their own research and that of others to illustrate concepts and theories in their teaching, shared and reviewed their lecture slides, selected essential content and built a structure for their respective subjects. The innovative TREE structure was thus created and forms an easy to use browse-able framework for key content with the added advantage of the structure defining important areas in modern plant science.

It is our experience that lecturers prefer to build their own custom made lectures from individual lecture slide content, rather than use pre-packaged learning materials. The intuitive TREE structure allows lecturers to do exactly that. The user has the option to browse via 'tree view' or 'map view' or search for a keyword using the search facility, all which help the user find relevant content quickly and may even lead to a serendipitous find relevant to both teaching and research. The TREE currently holds around 1400 lecture slides, 70 movie clips, several practicals and quality links contributed by over 70 academics covering subjects such as plant development, metabolism, cells, lifecycles, reproduction, evolution, environment and biotic interactions. Content is by

no means exhaustive but forms the foundation for each topic. Where a lecture slide is derived from a research paper it is linked to the original



The Gatsby Plants summer school on-line lecture by Dr Robert Zeigler, Director of the International Rice Research Institute, on 'Importance of rice and world food security' and many other lectures may be viewed by registering with the Gatsby Plants TREE at www.gatsbyplants.leeds.ac.uk/tree source for reference and all content which is available for download has been copyright cleared for educational use. A key feature of the TREE is to add lectures each year from the Gatsby Plants summer school, which are delivered by leading plant scientists about their research and deliberately pitched at a level to engage and enthuse undergraduate students. There are currently 25 on-line lectures available in an easy-to-use form that shows the speaker, their slides and a capacity to select parts of the lecture. Recent on-line lectures include 'Importance of rice and world food security' by Dr Robert Zeigler, Director of the International Rice Research Institute and 'Biology to benefit society – science, supply chains and the healing power of plants' by Prof Dianna Bowles, CNAP, University of York, both of which were extremely well received by this year's summer school undergraduates.

The TREE also offers the Plant News with RSS feed and search facility, linking articles, podcasts and videos of current developments and breakthroughs in plant science from leading journals and the media.

Usage for the TREE and Plant News has grown steadily since the launch of the incomplete site in 2010, with over 850 registered users including from beyond the UK and more than 80,000 hits per month in 2011. Active promotion of the TREE in 2012, continued engagement with the plant science community and developing its sense of ownership will enhance the growth of this educational tool so that it can continue to serve the needs of plant science academics. All lectures and lecture slides are available by registering at: www.gatsbyplants.leeds.ac.uk/tree

We welcome submissions of materials. If you would like to contribute your own copyright owned lecture slides or simply sign up for a Plant News monthly email circular then please contact Aurora Levesley, a.levesley@leeds.ac.uk.

How many Arabidopsis genome sequences do we need?

Richard Mott* and Paula Kover**

*Wellcome Trust for Human Genetics
University of Oxford, OX3 7BN, UK
Richard.mott@well.ox.ac.uk

**Department of Biology and Biochemistry,
University of Bath BA2 7AY, UK
p.x.kover@bath.ac.uk

What makes a good population for dissecting trait variation? This question is being addressed in many model species - *Arabidopsis thaliana*, wheat, flies, worms, mice - and there are broadly three types of population being promoted. One possibility is to knockout every gene systematically on a constant genetic background and observe the consequences. *A. thaliana* has a comprehensive collection of transposon-induced knockouts. A demonstration that knocking out a given gene causes a given phenotype is the gold standard of proof for some researchers. However, knock-outs allows only a comparison between a gene being present or absent. In contrast much of the natural variation in phenotypes of interest are likely to be due to modifications in the function of a gene in a qualitatively and quantitatively, and differently from simply ablating it (for example by changing its level of expression or splicing). Moreover, a knockout may well have subtle pleiotropic effects on many phenotypes. Furthermore, short of phenotyping every knockout for every trait, one must first narrow the search by identifying candidate genes.

This brings us to the alternative: populations containing natural genetic variation, which can be used to identify loci associated with a trait by genetic association. In *A. thaliana*, as in some other species, one can either collect a large number (eventually 1001 (1)) of naturally-occurring inbred accessions, or make a synthetic population of recombinant inbred lines descended a smaller number of accessions. In both approaches one must then sequence or genotype the lines and distribute the seeds from the stock centre to labs for phenotyping in order to perform genetic association.

✱ Natural and synthetic mapping populations

There are theoretical advantages and disadvantages to using natural vs synthetic mapping populations, essentially involving a compromise between allele frequency, population structure and recombination. In a large worldwide population such as *A. thaliana*, very many sequence variants have arisen by mutation and some will have been selected for in favourable environments. Neutral variants will have drifted in and out of the population. The large effective population size of



Figure 1. MAGIC Lines - Image provided by John Doonan University of Aberystwyth

A. thaliana means that a great many recombinations have accumulated, resulting in a situation where the linkage disequilibrium between common variants decays on average to background levels within a few kilobases. This is a good thing, because it means an associated variant, provided it is not a false positive, is likely to be close to the causal variant. However, less positive, is the extensive population structure and large number of rare variants (say with population minor allele frequency under 5%) that arise in natural accessions of *A. thaliana*. Population structure means that distant variants (even on different chromosomes) are sometimes in disequilibrium with each other, causing false positive genetic associations (about 40% of identified associations may be false positives (2)). This can be ameliorated by statistical control for population structure (3), but at the cost of reducing the power to detect associations (4). In addition, rare variants affecting a phenotype are hard to detect or map accurately, first because they are unlikely to account for much of the phenotypic variation, and second, if they are of recent origin, they are likely to be in linkage disequilibrium with much of the surrounding genome.

Synthetic populations have complementary characteristics - they control for allele frequency (the minor allele frequency should never be much under $1/N$, where N is the number of founders) and population structure is broken up. However, the extent of recombination is less, being limited to those accumulating in meioses during the generations of crossing and selfing used to make the population. Thus mapping resolution (which depends ultimately on the density of recombinants) is lower, but there is a better chance of detecting causal loci (no rare variants) and there are fewer false positives (little population structure).

✱ MAGIC lines

A set of Multiparent Advanced Genetic Inter Cross (MAGIC) lines descended from $N=19$ geographically

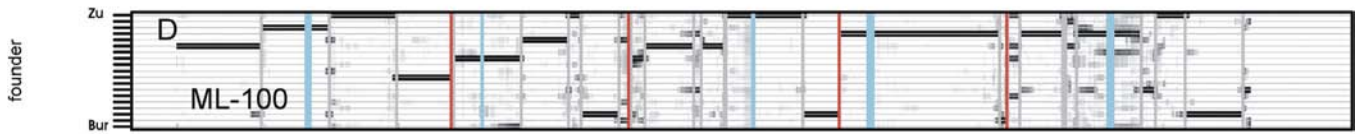


Figure 2. The genome mosaic for the MAGIC line ML-100 expressed as a posterior probability from a hidden Markov model run across 1200 SNPs. The vertical axis represents the 19 possible founders, n alphabetical order. The x-axis is genome location across the 5 chromosomes (divided by red bars, with blu indicating centromeres). The probability for a founder at each locus is represented by a grey bar, the shade of grey varying from white ($P = 0$) to black ($P = 1$). Figure taken from 5.

dispersed *A. thaliana* accessions has been recently created (5), funded by BBSRC. We have now deposited seeds for 700 MAGIC lines at the stock centre, and genotyped the lines at 1200 SNPs. Recently we sequenced the founder genomes (6). In this article we describe some of our findings about the composition of the founder genomes and their likely consequences on the use of the MAGIC lines. We don't discuss how to project this information into the MAGIC lines themselves, except to note that since the genomes of the MAGIC lines are mosaics of the founders (Figure 2) we can infer the MAGIC genomes: this is currently underway.

The 19 accessions that are founders of the MAGIC lines include the reference genome Col-0, for which a high quality genome sequence is already available (The Arabidopsis Genome Initiative, 2000; TAIR). We sequenced the other 18 genomes using Illumina GA-II short-read technology in a project also funded by the BBSRC. In most of the accessions we obtained 27-60x coverage in aligned reads from two paired-end libraries with different insert sizes (36bp paired end

reads with 200bp inserts, 52bp paired end reads with 400bp inserts). We developed a novel informatics pipeline, IMR/DENOM that combines iterative mapping of reads to the reference with de-novo genome assembly to generate genome assemblies for each accession. Comparison with sequence data from the accessions Bur-0 and Ler-0 indicates that the accuracy in single-copy regions of the genome is about 1 substitution error per 10kb, and about 1 error 10 kb in repetitive regions (Figure 3). However, there will be some undetected copy number variants and genome rearrangements which are hard to find with short read data.

RNA-seq data

Our collaborators Richard Clark at the University of Utah obtained RNA-seq data from seedlings from each of the 19 accessions (in biological duplicate), and Gunnar Raetsch (MPI Tubingen, Germany) re-annotated the protein coding genes in each accession. They used a combination of *de-novo* computational gene prediction combined with alignment of the RNA-seq reads. The latter information is key, for example when determining when alternate splicing occurs. Thus we have produced a set of 19 reference genomes for *A. thaliana*, each with its own gene annotation. What we found was quite surprising. If we had simply transferred the gene annotations in the reference Col-0 to each accession, then about one third of the genes would appear to be significantly disrupted (e.g. by a premature stop codon) in at least one accession. However, the RNAseq evidence suggested that in most cases, the splicing pattern of an affected gene changed in such a way that the new transcript was still functional. In other words, using the default reference gene annotations to predict the effects of sequence variation is fraught, and the only sure way to correct the annotations requires transcript data (6).

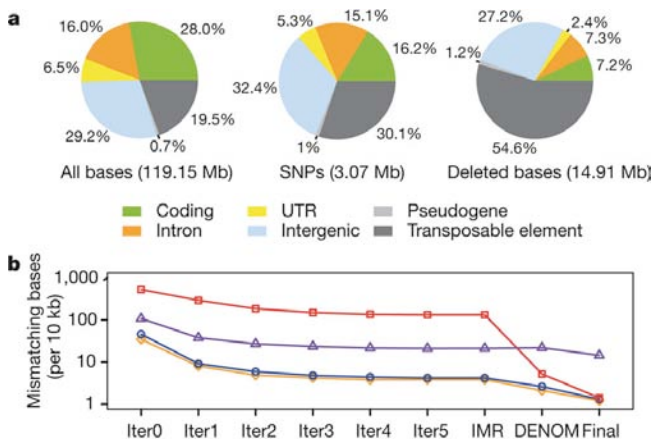


Figure 3. a, Classification of sequence, SNPs and indels in the 18 sequenced genomes based on the Col-0 genome. b, Assembly accuracy (y axis; base substitution errors per 10 kb) measured relative to four validation data sets at each of eight stages in the IMR/DENOM assembly pipeline (x axis). Bur-0 survey (blue line): 1,442 survey sequences (about 417 bp each) in predominantly genic regions; Bur-0 divergent (red line): 188 sequences (each about 254 bp) highly divergent from Col-0; Ler-0 nonrepetitive (orange line): a predominantly single-copy 175-kb Ler-0 sequence on chromosome 5; Ler-0 repetitive (purple line): a highly repetitive 339-kb Ler-0 locus on chromosome 3. Iter, iteration. Figure taken from 6.

Overall, in our genomes there are about 3.3 million variable sites (Figure 2), of which about 10% are indels or structural variants and 45% are private (unique) to a single accession. Each accession differs from the reference at about half a million sites, of which about 5% are private. We looked at the ancestry of the accessions, focusing on just the 1.25 million variants that were not private to an accession and where we had complete data in all accessions (private variants don't

Arabidopsis population genetics

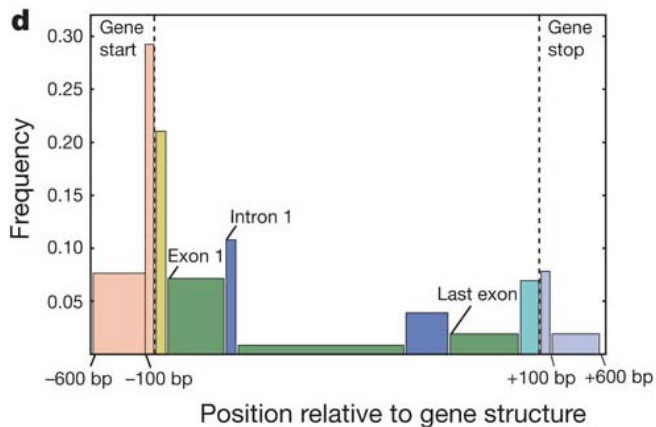


Figure 4. Frequencies of nucleotide-variant eQTLs in protein-coding genes, classified by component (bar widths are proportional to the components' average physical lengths): red bars, upstream; yellow bars, 59 untranslated region; green bars, coding sequence exons; blue bars, introns; cyan bars, 39 untranslated region; grey bars, downstream. Figure taken from 6.

tell us about co-ancestry). What we found was that across the genome the local history of the accessions varies dramatically, so that any given pair of accessions is about as likely to be closely as distantly related. This means most of the common variation predates much of the accumulated recombination in the genomes. Whilst selection may well have adapted these accessions to different environments (our sample included accessions from Africa as well as Northern Europe), it suggests the mechanism involved the re-use of ancient variation as well as the accumulation of new mutation private to each accession's recent lineage.

From the RNAseq data we found much heritable accession-specific gene expression and splicing patterns, and showed that the genetic variant most strongly associated with variation in expression was very likely to be concentrated in the promoter region up to 100bp upstream of the gene in question (Figure 4). In the case of alternative splicing (here limited to intron retention events), the most associated variant tended to be with 1kb of the affected intron. These results suggest that in some cases we have identified causal variants affecting gene expression, and that it may be possible to map causal variants precisely in the MAGIC lines by incorporating this sequence data.

It remains to be seen how the extent and patterns of variation we have observed in the 19 genomes compares with that in the larger number of accessions being sequenced around the world (7). It will also be interesting to compare the genetic mapping properties of the MAGIC lines with those of association in natural accessions. It has been suggested one should use synthetic lines and natural accessions to map the same trait simultaneously (2). A key question will be the extent to which variation is common between the popula-

tions and so can be used to replicate findings. These comparisons are underway. In any event, the GARNet community is soon likely to have a wealth of tools for genetic mapping in *A. thaliana*. Watch this space.

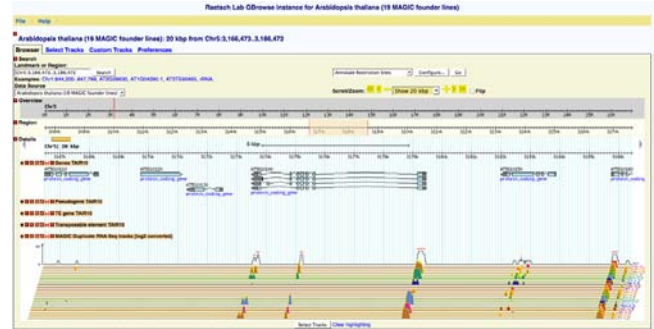


Figure 5. Screenshot of genome browser

Our data are available from <http://mus.well.ox.ac.uk/19genomes> (Figure 5)

1. D. Weigel and R. Mott (2009) *Genome Biol* 10 (5), 107
2. J. Bergelson and F. Roux (2010) *Nat Rev Genet* 11 (12), 867
3. H.M. Kang, N.A. Zaitlen, C.M. Wade *et al.* (2008) *Genetics* 178, 1709
4. S. Atwell, Y.S. Huang, B.J. Vilhjalmsson *et al.* (2010) *Nature* 465 (7298), 627
5. P.X. Kover, W. Valdar, J. Trakalo *et al.* (2009) *PLoS Genet* 5 (7), e1000551
6. X. Gan, O. Stegle, J. Behr *et al.*, *Nature* 477 (7365), 419
7. J. Cao, K. Schneeberger, S. Ossowski *et al.*, *Nat Genet* 43 (10), 956

The National Plant Phenomics Centre. New developments at Aberystwyth University

John Doonan*, Anyela Camargo-Rodriguez, Alan Gay, Catherine Howarth, Martin Swain and John Draper

IBERS

Aberystwyth University
Aberystwyth, SY23 3EB, UK
*john.doonan@aber.ac.uk

Recent advances in DNA sequencing technology now provide the means to define the individual genomes across whole populations of plants and animals. This raises the question: How we can best exploit this cornucopia of information to improve agricultural productivity? A number of looming crises, collectively discussed under the umbrella term of “Food Security”, are expected to arise as results of human population pressure, rising living standards and expectations, land loss/degradation and climate change (1, 2) and lend increasing urgency to the topic. Providing practical answers will be an enormous challenge but, based on previous experience, one promising avenue is to ensure that we maintain (and aim to increase) the rate of crop plant improvement by linking the improvements in genotyping to parallel improvements in phenotyping.

Why automated phenotyping?

Our capacity to genotype organisms, including plants, now vastly exceeds our ability to phenotype those same individuals. Genotyping can provide molecular resolution at the nucleotide level and can be scaled to deal with whole populations at reasonable and ever decreasing cost. Phenotyping on the other hand is less scalable, is often subjective or it measures attributes such as yield (or even profit) that are complex and difficult to relate to the underlying genetic variation. This has been termed the phenotyping bottleneck (3) and has long been recognised by plant biotech companies who have invested heavily in automation, mainly to characterise candidate transgenes. These systems were first used in the horticultural industry and were ideal for handling large numbers of fairly uniform plants, each group differing in a transgene, producing objective quantitative data. These quantitative non-destructive approaches also hold promise for the more complex task of relating trait variation to the underlying genetic variation and, with improved automation, imaging and high performance computing, such platforms have been being built or are currently under construction at several sites in Europe and across the world.

The NPPC at Aberystwyth

In the UK, the National Plant Phenomics Centre at Aberystwyth is due to open in May 2012 (Figure 1). The

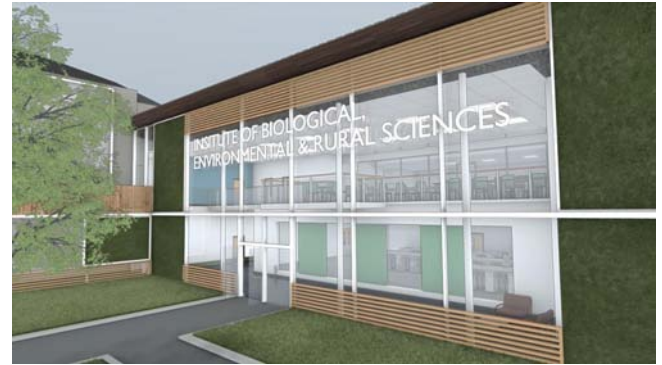


Figure 1. The new IBERS building currently under construction on the Gogerddan campus, Aberystwyth University. This will house the National Plant Phenomics Centre and the Translational Genomics Facility facilitating the integration of genomics with phenomics.

NPPC represents a major infrastructural development, funded by Aberystwyth University (AU), the Welsh Government and BBSRC, providing state-of-the-art capabilities for objective plant phenotyping under controlled environment conditions using high throughput robotics, automated high content imaging systems combined with computing technologies. This investment builds on previous experience at AU in public good plant breeding where traditional methods in field and glasshouse phenotyping have been used to produce many of the grass and oat varieties that are currently used on UK farms. Varieties bred at AU currently make up 70% of the oat acreage and 28% in forage seed sales in the UK, representing significant added value to the UK economy. Recent work on breeding high sugar grasses will provide new dual use crops and breeding of dedicated bio-fuel crops and has great promise to deliver green chemical feedstocks and energy from non-arable land. As with almost all our crops, these species have considerable and largely underexploited genetic potential. The NPPC will support public good breeding programmes in the UK and will make phenomic facilities available to academic researchers investigating fundamental problems in plant biology as well as to commercial and regulatory organisations. A recently awarded Framework 7 grant, the European Plant Phenomics Network, provides for international access, funding collaborative pilot projects from across Europe as well as supporting technology development and the integration of phenomics with other ‘omics’. A national research network is planned to promote the development of phenomics throughout the UK (see Box 1).

Box 1

UK-PPN - A plant phenomics network for the UK

John Doonan (john.doonan@aber.ac.uk)

Tony Pridmore (tony.pridmore@nottingham.ac.uk)

Ruth Bastow (ruth@garnetcommunity.org.uk)

Malcolm Bennett (malcolm.bennett@nottingham.ac.uk)

Martin Parry (contact@mlparry.com)

Chris Rawlings (chris.rawlings@bbsrc.ac.uk)

Julie Scholes (j.scholes@sheffield.ac.uk)

The UKPPN aims to provide a forum for scientists and plant breeders interested in the development and application of automated objective approaches to plant phenotyping under both controlled environment and field conditions. The first public meeting of the UK Plant Phenotyping Network was held at Sutton Bonnington, University of Nottingham, this October. Interactions between research biologists, breeders, engineers, computational scientists and mathematicians will be required to integrate and exploit advances in robotics, imaging and computing to enable sensitive, non-destructive, high-throughput analysis of plant growth, function and performance. It is envisaged that this network will facilitate these interdisciplinary interactions by means of organizing workshops, summer schools and meetings, develop a community consensus on key issues and provide representation at both a national and international level for UK scientists working or interested in this area. For more details, please contact Susie Lydon (susie@cpib.ac.uk) or any of the organising committee.

NPPC facilities



Figure 2. The SmartHouse, a state of the art climate-controlled greenhouse, will contain robotics for plant handling with automated imaging and analysis

areas on a programmable conveyor system (Figure 3) that has a capacity of over 800 carriages. Each carriage can accommodate one large plant (up to 2m tall) or a tray of small plants. Automation (of plant handling) has several advantages that are often overlooked during experimental design and costing. Large plants and their pots are heavy – 800 cereal pots might weigh 2-3 tons, which would normally preclude routine analysis. The ability to move plants fre-

quently can effectively reduce local environmental gradients, reducing the level of replication needed, while the movement itself can mimic aspects of the outdoor environment. Almost all phenotyping experiments to date, even low throughput ones, lack adequate published metadata, so one of the aims of phenomics will be to establish standards analogous to those commonly used in other branches of large scale biology. Environmental, nutrient and watering controls enable the application of single or combinatorial stresses, allowing the dissection of Genotype x Environmental interactions. The Centre therefore has the ability to characterize typical mapping populations under a number of defined conditions.

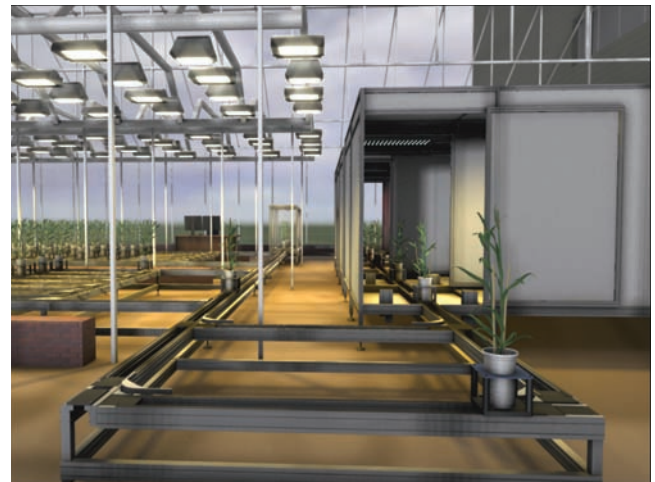


Figure 3 A computer-stimulated view of plants moving into the imaging stations within the SmartHouse. The full video can be viewed at <http://www.phenomics.org.uk/>. Images by See3D Ltd : www.see3d.co.uk

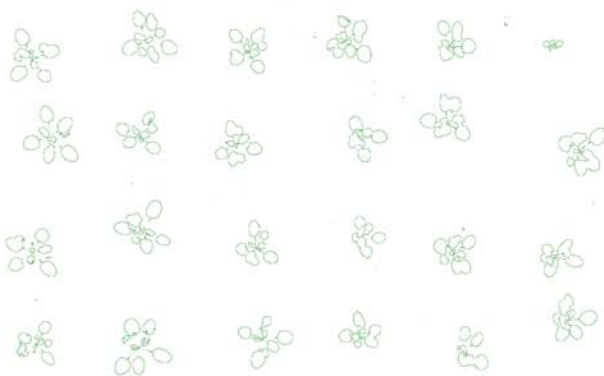
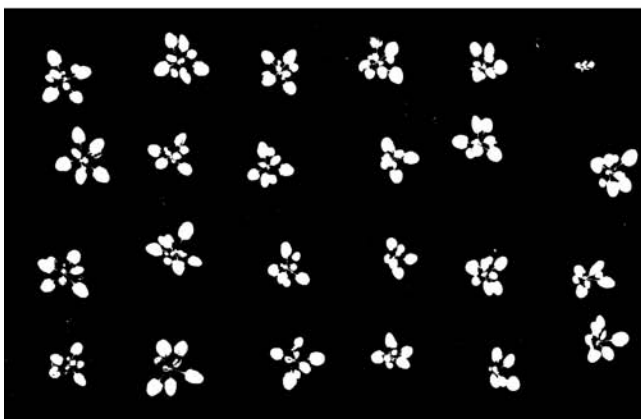
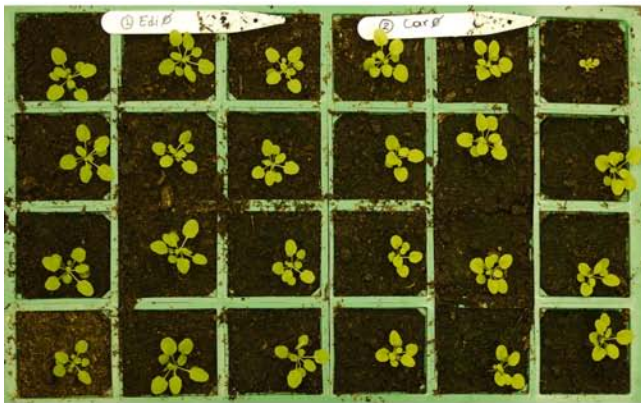
quently can effectively reduce local environmental gradients, reducing the level of replication needed, while the movement itself can mimic aspects of the outdoor environment. Almost all phenotyping experiments to date, even low throughput ones, lack adequate published metadata, so one of the aims of phenomics will be to establish standards analogous to those commonly used in other branches of large scale biology. Environmental, nutrient and watering controls enable the application of single or combinatorial stresses, allowing the dissection of Genotype x Environmental interactions. The Centre therefore has the ability to characterize typical mapping populations under a number of defined conditions.

Imaging techniques and sensors at the NPPC facilities

The Centre provides an array of different imaging techniques and sensors to record plant development and physiology non-destructively and dynamically. Initially the types of imaging available will be:

1. Infra-red thermography of shoots (for mapping changes in plant temperature and stomatal activity).
2. Fluorescence (for photosynthetic function and detection of fluorescent tags).
3. NIR for soil columns with automatic removal of the root cover (for water content and root tracking).
4. Visible, (for morphology, growth estimates etc.).
5. NIR imaging (tuned to detect water content).

In all imaging except 3, both top and side view images can be acquired simultaneously, and all imaging except the thermal imaging is equipped with zoom lenses. An overhead laser scanner is incorporated into unit 3 to allow high resolution 3d surface reconstruction of



small plants. In addition to these established methodologies, a key research priority will be to develop new high throughput methodologies, both non-destructive and destructive as well as modelling, to increase the range of characters that can be assessed (Figure 4).

Integration with other genome wide analyses will be key to exploiting the full value of phenomics so dedicated data analysts will assist users in managing and manipulating their experimental results. This will require the development of widely acceptable trait ontologies that are acceptable for use in both controlled environment and field.

Timeline for NPPC operation

The Smarthouse is built. The robotics and imaging equipment are currently being installed with expected completion in April 2012. Commissioning and testing will occur during summer and autumn of 2012 with first experiments commencing in 2013.

What will the NPPC offer

Different service levels will be provided in the NPPC ranging from collaborative projects (aimed primarily at Academic researchers) to full service projects (Academic and Industrial researchers and Regulatory Agencies). Further details will be posted on the website in due course. Since we aim to place phenomics on a similar footing to the other more established "omic" technologies, academic users will be encouraged (after a suitable interval) to make experimental data and its associated metadata available to the community to facilitate and encourage the development of the technology and associated informatic tools.

For further information about the NPPC please visit <http://www.phenomics.org.uk/> or contact Prof John Doonan

1. M.S. Swaminathan (2010) Achieving food security in times of crisis. *New Biotechnology* 27, 453-460
2. I.M.S. Swaminathan (2011) Doubling food production to feed the 9 billion: A critical perspective on a key discourse of food security in the UK. *Journal of Rural Studies*
3. E. Finkel (2009) With 'phenomics' plant scientists hope to shift breeding into overdrive. *Science* 325, 380-381

Figure 4: Arabidopsis accession Edi-0 and Can-0 processed using LenmaTec Software

UK Plant Sciences Federation (UKPSF)

*Ruth Bastow
GARNet, School of Life Sciences,
University of Warwick,
Wellesbourne, CV35 9EF, UK
*ruth@garnetcommunity.org.uk

Escalating pressure for food security and renewable energy requires a detailed understanding of the biology and ecology of plants, and this need has never been greater. Although the UK plant science community is amongst the world leaders in advancing our scientific knowledge and wisdom, the sector is currently fragmented into groupings focussed on species or research areas. This has resulted in a lack of comprehensive dialogue between those undertaking high quality basic and applied plant research, end users and policy makers and a subsequent lack of cohesive strategy.



To achieve its full potential and address grand challenges, the UK plant science community must coordinate and align activities. It must cultivate a collegiate and communicative research base to build a viable research pipeline from the lab to the field that will inspire the next generation of plant researchers.

The UK Plant Sciences Federation has therefore been established to provide one voice for everyone involved in Plant Science research and development, education and training.

After a consultation with a number of stakeholders across the plant science sector, the UKPSF was formally established as a special interest group of the Society of Biology in Sept 2011. At present it consists of over 20 member organisations including research communities, teaching organisations, learned societies, industry, plant breeders and agriculturalists (see Box 1) and was officially launched on the 23rd November 2011 at Charles Darwin House in London

The UKPSF will provide a central focus and structure to increase interactions and improve communication across the plant science community, formulate

a coordinated strategy and vision for UK plant science that can be used to inform policy, and promote effective plant science teaching at all levels. These goals will be essential to nurture the next generation of plant scientists and to establish a secure public and privately funded context in which they can work.

If you would like to learn more about the UKPSF or if your organisation is interested in becoming a member organisation of the UKPSF please contact Jackie Caine (jackiecaine@societyofbiology.org) or Ruth Bastow (ruth@plantsci.org.uk).

Box 1

UKPSF Member Organizations

Association of Applied Biologists
AHDB - Agricultural Horticultural Development Board
BASIS
Bayer
Biosciences KTN
British Crop Production Council
British Ecological Society
Biochemical Society
British Society of Plant Breeders
The British Society for Plant Pathology
GARNet
Gatsby Plants
Genetics Society
Linnean Society
MONOGRAM – Cereal and Grasses Research Community
SAPS – School and Plant Science
SCI Horticultural Group
SEB – Society of Experimental Biology
Syngenta
The Rosaceae network
The Royal Microscopical Society
UK-BRC – Brassica Research Community
UK-SOL – Solanaceae Research Community
Unilever
VEGIN – Vegetable Genetic Improvement Network



Mark Downs (CEO of the Society of Biology) opening the UKPSF Launch

GARNet 2011

*Irene Lavagi and Ruth Bastow
GARNet, School of Life Sciences,
University of Warwick,
Wellesbourne, CV35 9EF, UK
*irene@garnetcommunity.org.uk



The 2011 GARNet annual meeting took place at the Murray Edwards College, Cambridge. Over 100 researchers came to the University of Cambridge to enjoy two intensive days of fascinating talks and workshops.

Day 1: Dynamics of DNA and chromatin structure

The first session of the meeting was Dynamics of DNA and chromatin structure and this covered a wide range of topics. David Baulcombe (University of Cambridge, UK) described the involvement of short RNAs in mechanisms affecting chromatin modification that may be linked to defence mechanisms against invading DNA from viruses or transposable elements. Steve Jacobsen (University California Los Angeles,

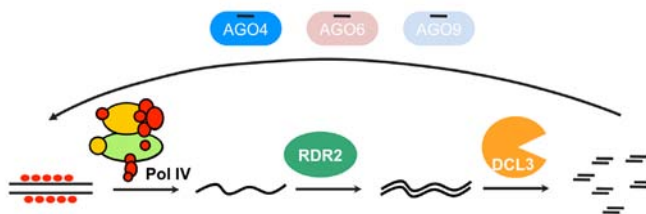


Image provided by David Baulcombe

USA) outlined the work carried out in his laboratory using genetic and genomic techniques to study DNA methylation showing that the initiation and maintenance of methylation require different mechanisms. Recent studies have determined that in addition to gene silencing methylation serves to regulate replication of transposable elements. Caroline Dean (John

Innes Centre, UK) discussed the role of chromatin dynamics in vernalization. The epigenetic silencing of FLC, a MADS box transcriptional repressor, by a conserved Polycomb mechanism is key to vernalization. This understanding has in turn shown that differences in epigenetic silencing of FLC are important in the differing degrees of vernalization response in Arabidopsis accessions adapted to different climates. Jon-Myong Kim (RIKEN Plant Science Centre, Japan) highlighted the role of histone deacetylase 6 (HDA6) in epigenetic gene silencing. Many transposable elements affected by HDA6 were localized to the heterochromatin region around centromeres on all chromosomes. It was proposed that silencing of transposable elements on heterochromatic regions by HDA6 is required for structural and functional maintenance of chromosomes.



Image provided by Frank Johannes

Vincent Colot (Ecole Normale Supérieure, Paris, France) described the use of epigenetic recombinant inbred lines (epiRILs) obtained by crossing two parents with near identical genomes but contrasting DNA methylomes to investigate transgenerational epigenetic variation. Frank Johannes (University of Groningen, The Netherlands) also made use of epiRILs to study the inheritance of epigenetic changes and their role in complex traits at the population level. Ortrun Mittelsten-Scheid (Gregor Mendel Institute, Vienna, Austria) described the environmentally induced chromatin changes in response to heat stress and their effects on subsequent generations. Matthew Jones (University California, Davis, USA) described the role of the Jumonji domain Protein JMJD5, a histone demethylase that positively affects the expression of clock genes expressed at dawn, highlighting how the clock modulates transcription via histone modifications. Anna Amtmann (University of Glasgow) concluded the session describing a newly identified member of a histone deacetylase complex in Arabidopsis and its involvement in abscisic acid (ABA) response via the modification of the acetylation status of ABA biosynthesis genes. The establishment of a priming protocol consisting of a short salt treatment of Arabidopsis seedlings and subsequent salt shock of mature plants followed by ChIPSeq (Chromatin Immunoprecipitation and Sequencing of the DNA associated with the pulled down proteins) have provide a great insight into how plants assess and deal with osmotic stress.

GARNet 2011 Dynamic Biology Meeting

Workshop: Opportunities for industrial engagement



Image provided by Dan Godfrey (BBSRC). If you would like to learn more about any of the schemes, please contact dan.godfrey@bbsrc.ac.uk

A workshop on opportunities for industrial engagement gave the opportunity for the GARNet delegates to learn about and discuss the current possibilities of involvement and exchange between industry and academia. Dan Godfrey (BBSRC, UK) described the current BBSRC schemes that enable knowledge exchange between industry and academia. Tom Jenkins (KTN, UK) highlighted the function of the KTN in supporting and assisting research partners in industry engagement through a variety of funding initiatives. Matthew Hannah (Bayer Crop Science, Belgium) covered a variety of academic projects in which Bayer have been involved in the past and showed the high impact of Arabidopsis research at the level of patents by specific aspects (e.g. abiotic stress). Peter Werner (KWS UK Ltd, UK) gave an overview of the current schemes that enable industrial engagement with academia from the perspective of a private company.

Day 2: Dynamics of transcription

On the second day, Elliot Meyerowitz (The Sainsbury Laboratory, Cambridge, UK) opened the ses-

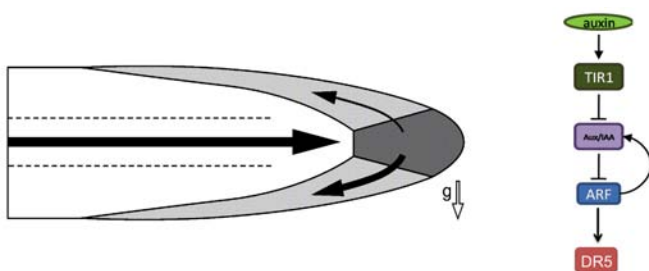


Image provided by Malcolm Bennett

sion describing the computational models developed by his group to investigate the morpho-dynamic control of the gene expression pattern in the shoot apical meristem, including the expression of *CLAVATA1*, *CLAVATA3*, *WUSCHEL* and the control exerted by cytokinin and auxin. Malcolm Bennett (University of Nottingham, UK) presented results obtained via the employment of a novel Aux/IAA-based reporter, DII-VENUS and a mathematical model to quantify auxin redistribution following a gravity stimulus, yielding a high spatio-temporal resolution map, which has allowed the group to postulate the existence of a 'tipping point' mechanisms that operates to reverse the asymmetric auxin flow at the mid-point of root bending. Katherine Denby (University of Warwick, UK) described network inference and how time series gene expression data can be used to infer gene regulatory networks. Comparing network models generated from a high-resolution time series transcriptome profile of Arabidopsis leaves inoculated with the fungal pathogen *Botrytis cinerea* with models from transcriptional profile of senescing leaves led to the identification of core regulatory components of stress responses in Arabidopsis.

Intracellular dynamics

In the second half of the morning, dedicated to the Intracellular Dynamics session, Joerg Kudla (University of Muenster) presented the work from his group on calcineurin B-like proteins (CBLs), a group of calcium sensor proteins, and their exclusive interactors, the serine-threonine kinases CBL-interacting proteins (CIPKs). The preferential complex formation of individual CBLs with a defined subset of CIPKs was reported to be responsible for the temporal and spatial specificity of calcium signals in plants. Wolf Frommer (Stanford University, USA) described the use of glucose sensors in fluorescence resonance energy transfer (FRET) microscopy approaches that led to the recent discovery of the SWEET protein family, a novel class of sugar transporters exploited by fungal and bacterial pathogens upon infection for pathogen nutrition. Information on several types of protein nanosensors from the Frommer lab can be obtained from <http://dpbweb.stanford.edu/sites/www.dpb.ciw.edu/files/frommer/nanosensors/index.html> and the nanosensor plasmid clones can be ordered through www.addgene.com

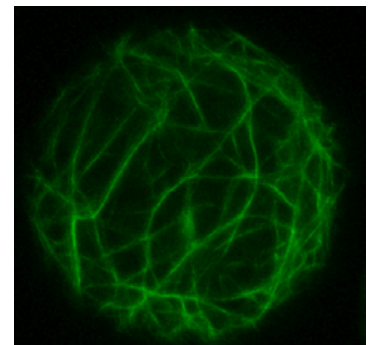


Image provided by John Runions

Jan Traas (ENS Lyon, France) presented 3D me-

GARNet 2011 Dynamic Biology Meeting

chanical models which are generated from measuring the geometry of floral meristems via multiangle reconstruction and segmentation. These 3D models are used as templates to reproduce, with mathematical approaches, the growth patterns observed during flower development. A microtubule control of cell wall anisotropy has been identified and in conjunction with the hormone-based control of growth patterns, it appears to be associated with the outgrowth of organs at particular locations. John Runions (Oxford Brookes University, UK) discussed the findings on the different lateral diffusion rates of the different classes of plasma membrane proteins that led to the hypothesis that the cell wall itself, rather than the cytoskeleton as previously postulated, inhibits such diffusion. Daniel Gibbs (University of Nottingham) described how the response to hypoxia is regulated by the N-end rules pathway of proteolysis (NERP) in plants. It was discovered that many important hypoxia-response genes are constitutively up regulated in plants deficient in components of NERP, which is in common with wild type plants grown in hypoxic conditions. A homeostatic model was proposed, with the hypoxia-response being initiated through the stabilization of transcription factors with respect to NERP under low oxygen conditions.

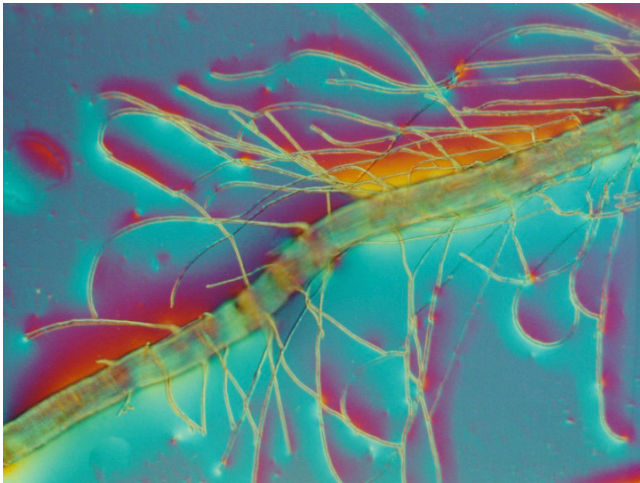


Image provided by Claire Grierson

Cellular dynamics

In the afternoon Cellular Dynamics session, Mike Blatt (University of Glasgow) presented OnGuard, a mathematical programme to model ion cell fluxes and Guard Cell Dynamics (GCD), a dynamic computational model with predictive power for cellular physiology that takes advantage of the wealth of biophysical and kinetic knowledge accrued from guard cell transport, signalling and homeostasis. Richard Morris (John Innes Centre, UK) presented a spatiotemporal model for the perinuclear calcium wave oscillations, a mechanism known to

play a key role in the specificity of downstream events in the symbiotic relationship between both legumes and rhizobial bacteria and legumes and mycorrhizal fungi. Claire Grierson (University of Bristol, UK), described the integration of different approaches including mathematical modelling, agent-based simulation and laboratory experiments to investigate the influence of auxin on the polarity of root hair cells. Jiri Friml (VIB/University of Ghent) presented data on the localization of PIN proteins, the auxin efflux catalysts, suggesting a cellular mechanism for cell polarity maintenance that involves the active picking up of cargo by endosomes rather than simply receiving it as previously thought. Jesper Gronlund (University of Warwick, UK) described the exploration of different methods for cell type specific analysis in Arabidopsis leaves including laser-capture microdissection (LCM), fluorescence-activated cell sorting (FACS) and future use of INTACT to obtain a transcriptional map of the different Arabidopsis leaf cell types. David Newman (University of Cardiff) talked about regulation of stomatal lineage by D-type cyclins (CYCDs).

The 2011 GARNet Meeting provided an excellent opportunity for plant scientists to discuss current advances and future challenges in plant biology. The GARNet 2011 Dynamic Biology meeting showcased plant epigenetics, plant systems biology, plant cell biology and the emerging high-resolution spatiotemporal modelling of plant processes illustrating how mathematical modelling is shaping plant science.

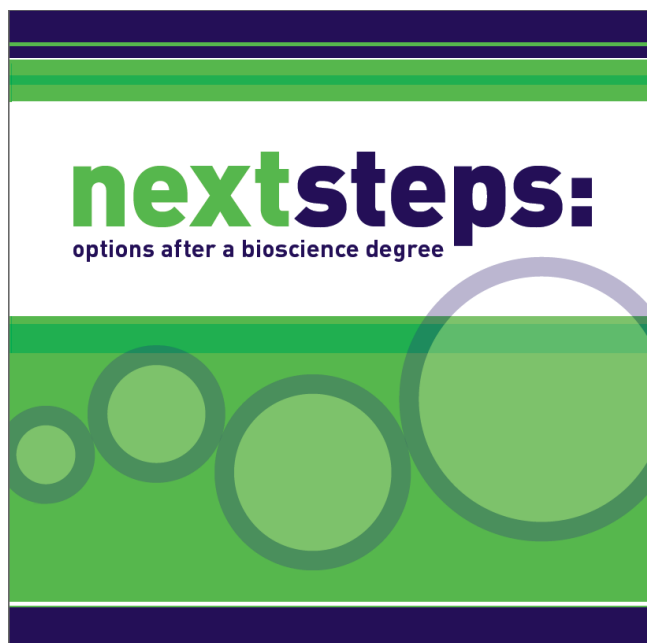
Next steps. Options after a bioscience degree

Sarah Blackford*

Head of Education and Public Affairs

Society of Experimental Biology

* s.blackford@lancaster.ac.uk



Universities are about to change forever. More accurately, from September 2012 English universities will have to source the majority of their teaching funding from their undergraduate student 'customers' in the form of student loans from the government. And with degree course fees rocketing up to £9000 per year student expectations are likely to soar with them. They will want some 'bang for their bucks' and in order to help them to compare the university markets the government has demanded that each university produces a KEY INFORMATION SET or KIS which contains a standardised set of information to be published on every university's website from September 2012. The KIS includes:

- student satisfaction
- course information
- employment and salary data
- accommodation costs
- financial information, such as fees
- students' union information

Whilst it is the course information which will be the main focus for university academics ensuring they make their degrees enticing to prospective students, as a practising HE careers adviser (within my role as head of education & public affairs at SEB), it is the employment and salary data which is of most inter-

est to me and which may become of more interest to you in future. Course content, of course (!), will be uppermost in most student's minds when they make their choices, but they (and their parents) are likely to become increasingly concerned about employment and salary data as they contemplate how they are going to pay off their loans (estimated up to £50,000). See a recent article which was published in Science career magazine about student finance - http://sciencecareers.sciencemag.org/career_magazine/previous_issues/articles/2011_10_28/caredit.a1100121

Specialised careers book for biologists

With this in mind, teaching staff are more likely to be quizzed by their students during the course of their degree about future careers and prospects. Students tend to be very discipline-focussed and want to know what biologists do in 'real life'. You can use anecdotal examples of previous students you know of who have forged successful careers as (for example) research scientists in academia or industry, teachers, consultants, managers and accountants. You can also refer them to the official statistics which are published each year by the HE Careers Service Unit (HECSU) www.hecsu.ac.uk/research_reports_what_do_graduates_do_november_2010.htm (page 12). You will be pleased to hear that, in addition to these avenues of careers information, further help is now at hand in the shape of a comprehensive careers book for bioscience undergraduate students.

Since its launch only one and half months ago in September 2011, two thousand copies of Next Steps - Options after a bioscience degree have already been sent out to university departments, careers advisers and individuals on their request, and with only 3000 copies left the reprint is imminent. Why is this book so popular? Next Steps is the first careers publication specifically aimed at bioscience undergraduates with a comprehensive list of resources, job sites and ideas for successful job seeking. It contains example CVs, job sector information and explains the career planning process to bioscientists. Postgraduate study is very popular with this student cohort so we have included a section which covers master's degrees, PhD studentships, medical-related, teaching and more generic further qualifications which they can consider. It explains the process of entry onto postgraduate courses and graduate training programmes which vary considerably amongst job sectors.

If you teach, and have responsibility for bioscience undergraduate students this book should help you to become more informed about the ins and outs of career planning so that you will be better equipped to deal with student enquiries. Whilst it is true that you can

A Careers Publication for Biology Undergraduates



British Ecological Society



Organised biannually by the Society of Biology and some of its affiliated member organisations, the Life Sciences Careers Conference is aimed at bioscience undergraduates and postgraduates. It features a programme of talks, CV workshop and exhibition. The next event will take place in London, March 2012 (date and venue to be confirmed). <http://www.societyofbiology.org/education/careers/lsc2011-2012lsc>

always send them off to the university careers service (which is still advisable), being able to give them some guidance and a physical book in their hand on the spot will probably be appreciated. A well-informed student is more likely to be better placed to apply for and enter the job market after their degree than one who is not given any help at all. Most do not make use of their careers service so if they can get help within their own department from tutors who are able to take a few minutes to show them this book or direct them to the on-line pdf it should not only assist students individually but it may also contribute to better employment statistics. This, in turn, will improve your KIS results when it's time for students to assess their course and deliver their verdict. The future starts here: www.sebiology.org/education/docs/Next_steps_web.pdf



The booklet 'Next Steps. Options after a bioscience degree' was conceived and written by seven learned societies:

Biochemical Society (www.biochemistry.org)
British Ecological Society (www.britishecologicalsociety.org)
British Pharmacological Society (www.bps.ac.uk)
Physiological Society (www.physoc.org)
Society of Biology (www.societyofbiology.org)
Society for Endocrinology (www.endocrinology.org)
Society for Experimental Biology (www.sebiology.org)



SALZBURG 2012

SEB ANNUAL MAIN MEETING 29TH JUNE - 2ND JULY

Plant Sessions

Improving photosynthesis

Organized by: Steve Long (University of Illinois) and Richard Leegood (University of Sheffield)

Confirmed speakers: John Sheehy (IRRI), Julian Hibberd (Cambridge, UK), Dean Price (Canberra, Australia), Lisa Ainsworth (Illinois, USA), Martin Parry (Rothamsted Research), Christoph Peterhänsel (Hannover, Germany), Paul Quick (IRRI), Andreas Weber (Düsseldorf, Germany), Michel Havaux (CES, France), Howard Griffiths (Cambridge, UK), Cheryl Kerfeld (DOE Joint Genome Institute & UC Berkeley), Maureen Hanson (Cornell, USA), Christine Raines (University of Essex)

Evolution of physiological traits

Organized by: Colin Osborne (University of Sheffield)

Confirmed speakers: Bill Martin (Heinrich-Heine-Universität, Düsseldorf, Germany), David Beerling (University of Sheffield, UK), Lisa Donovan (University of Georgia, USA), Howard Griffiths (University of Cambridge), Pascal-Antoine Christin (University of Lausanne), Paul Falkowski (Rutgers University), Taylor Field (University of Tennessee), John Raven (University of Dundee), Erika Edwards (Brown University), Lawren Sack (UCLA), Jonathan Leake (University of Sheffield)

Chloroplast biogenesis

Organized by: Enrique Lopez (Royal Holloway, University of London) and Paul Jarvis (University of Leicester)

Contact: E.Lopez@rhul.ac.uk; rpj3@leicester.ac.uk

Plant hormone signal transduction and the control of agronomic traits

Organized by: Claus Schwechheimer (Technische Universität München)

Confirmed speakers: Peter Hedden (Rothamsted Research), Shinjiro Yamaguchi (RIKEN, Yokohama), Salomé Prat (CSIC Madrid), Paul Nicholson (John Innes Centre), Patrick Achard (IBMP, Strasbourg), Mike Holdsworth (University of Nottingham), Marcel Quint (IPB, Halle), Luz Irina Calderon-Villalobos (IPB, Halle), Lars Ostergaard (John Innes Centre)

Induced resistance against biotic attack

Organized by: Mike Roberts (Lancaster University), Jurriaan Ton (Sheffield University)

Confirmed speakers: Katherine Denby (Warwick University), Corné Pieterse (Utrecht University), Sergio Rasmann (University of Lausanne), Dale Walters (Scottish Agricultural College), Matthias Erb (Max Planck, Jena), Klaus Schlappi (Max Planck, Köln), Victor Flors (University of Jaume I), Harrold van den Burg (University of Amsterdam), Brigitte Mauch-Mani (University of Neuchâtel), Monica Höfte (Ghent University), Vivianne Vleeshouwers (Wageningen University)

The environmental control of development

Organized by: Karen Halliday (University of Edinburgh) and Miriam Gifford (Warwick University)

Confirmed speakers: Mikhail Semenov (Rothamsted Research), Cris Kuhlemeier (University of Bern), Marc Knight (Durham University), Steve Penfield (University of York), Lionel Dupuy (The James Hutton Institute), Christian Fleck (University of Freiburg), Ida Ruberti (Istituto Biologia e Patologia Molecolari CNR), Paul Devlin (Royal Holloway, University of London), Phil M Mullineaux (University of Essex)

Cell Sessions

Generating New Biological insight from Complex Data: Methodology, Data Gathering, Inference, Modelling, Validation, Integration and Solutions

Organized by: The Cell Committee

Molecular Plant Cell Dynamics

Organized by: Ive De Smet (University of Nottingham)

Confirmed speakers: Zhiyong Wang (Department of Plant Biology, Carnegie Institution for Science, USA), Jozef Samaj (Palacky University Olomouc, Czech Republic), Stephanie Robert (Umea Plant Science Centre, Sweden)

Quantitative Imaging

Organized by: John Girkin (Durham University) and Paola Borri (Cardiff University)

Confirmed speakers: Dr Alistair Elfick (University of Edinburgh)

Regulation of Transcription by Metabolism

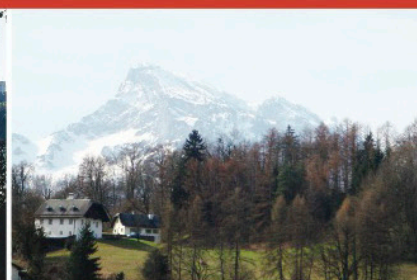
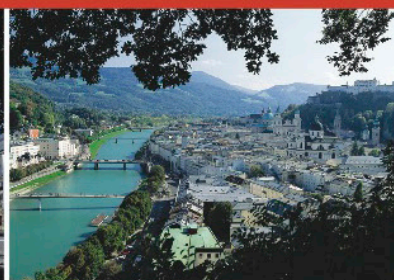
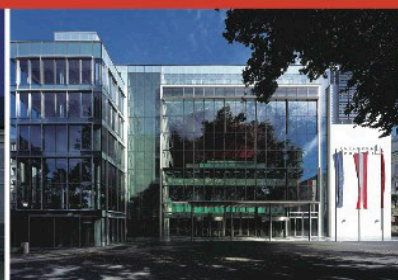
Organized by: Alex Webb (Cambridge University)

Confirmed speakers: Professor Bruce Kemp (St Vincent's Hospital University of Melbourne), Professor Alison Smith (John Innes Centre, Norwich UK), Professor Johannes Hanson (Umea Plant Science Centre, Sweden), Professor Frédéric Gachon (Lausanne University)

New insights into plant nuclear envelope proteins and their interactions

Organized by: David Evans (Oxford Brookes University), Katja Graumann (Oxford Brookes University), Iris Meier (The Ohio State University), Christophe Tatout (Université Blaise Pascal)

Confirmed speakers: Professor Iris Meier (Ohio State University), Dr Kentaro Tamura (Kyoto University), Professor Moreno Diaz de la Espina (Centro de Investigaciones Biológicas (CSIC)), Professor Hank Bass (Florida State University), Professor Eric Richards (Cornell University), Dr Sue Armstrong (University of Birmingham)



29th New Phytologist Symposium

Stomata 2012

Manchester Conference Centre, Manchester, UK
2–4 July 2012



Confirmed speakers

Sally Assmann Penn State University, PA, USA
Dominique Bergmann Stanford University, CA, USA
Mike Blatt University of Glasgow, UK
Tim Brodribb University of Tasmania, Australia
Jennifer McElwain University College Dublin, Ireland
Julie Gray University of Sheffield, UK
Rainer Hedrich Würzburg University, Germany
Alistair Hetherington University of Bristol, UK
Hugo Jan de Boer Utrecht University, The Netherlands
Tracy Lawson University of Essex, UK
Josette Masle ANU, Canberra, Australia
Keith Mott Utah State University, UT, USA
Colin Osborne University of Sheffield, UK
Roland Pieruschka Forschungszentrum Jülich, Germany
Silke Robatzek Sainsbury Laboratory, Norwich, UK
Julian Schroeder UC San Diego, CA, USA
Kenichiro Shimazaki Kyushu University, Tokyo, Japan
Chun-Peng Song Henan University, Kaifeng, China
Keiko Torii University of Washington, WA, USA
Alain Vavasseur CEA-Cadarache, France
Ian Woodward University of Sheffield, UK
Jianhua Zhang Hong Kong Baptist University, China

Organisation

Alistair Hetherington (University of Bristol, UK),
Ian Woodward (University of Sheffield, UK)

Contact

Jill Brooke
np-symposia@lancaster.ac.uk
New Phytologist Central Office, Bailrigg House,
Lancaster University, Lancaster, LA1 4YE, UK.

New Phytologist Trust

The New Phytologist Trust is a non-profit-making organisation dedicated to the promotion of plant science.

Further details and registration at

www.newphytologist.org



New
Phytologist

ICAR

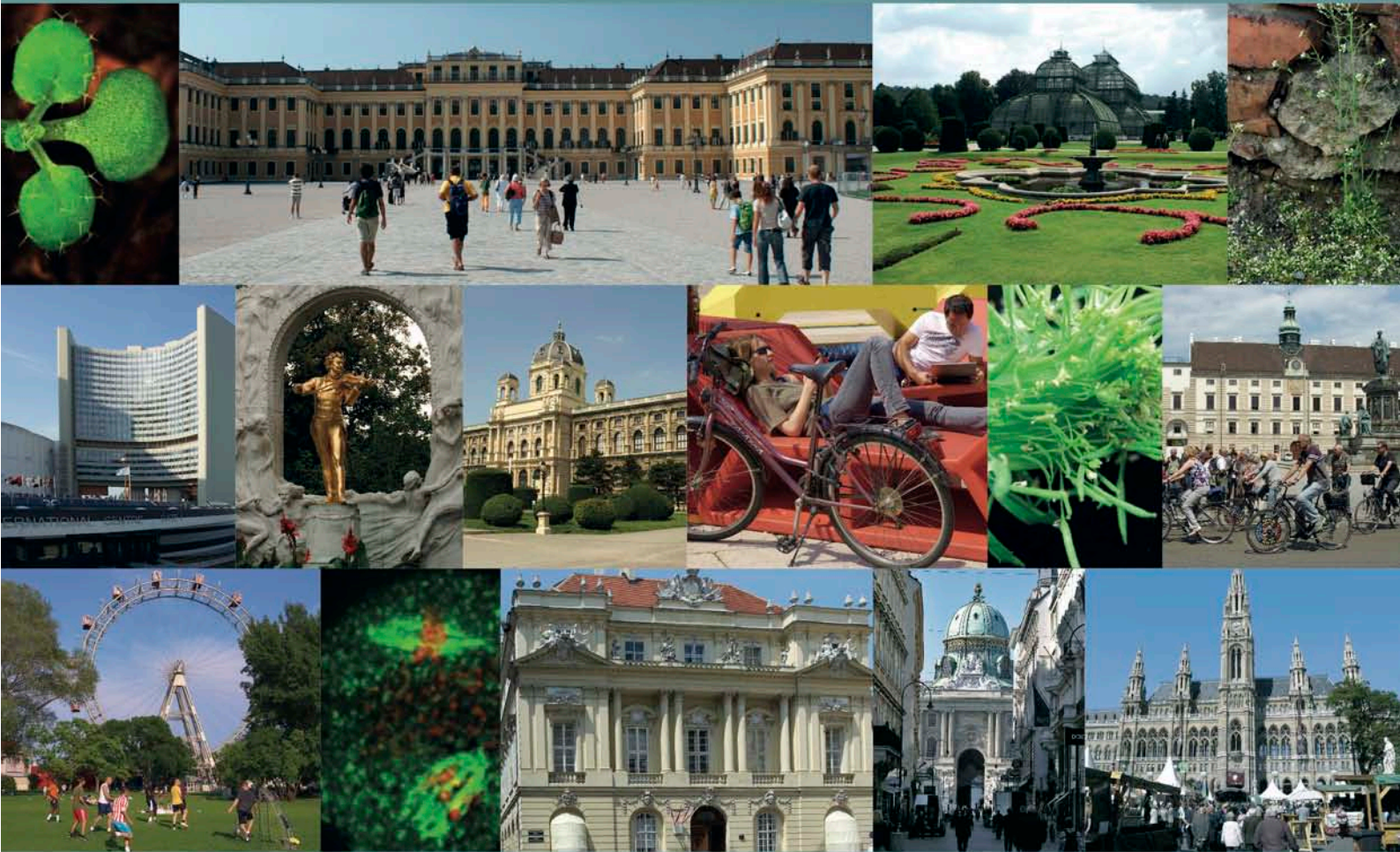
Vienna, Austria
July 3rd-7th 2012

Join us in one of Europe's
most beautiful cities
for the 23rd International
Conference on Arabidopsis
Research

Hofburg Imperial Palace,
Vienna Austria

Over 70 international speakers
and more than 500 posters covering
the following topics:

- Epigenetics
- Plant Defense
- Responses to the Abiotic Environment
- Cell Biology
- Natural Variation
- Other Species
- Systems Biology & Metabolism
- Development
- RNA Mediated Regulation
- Interactions with the Biotic Environment
- Bioenergy
- Novel Tools/Bioinformatics
- Plant Hormones
- Hot Topics
- Lifting Yield Barriers in Breeding
- Systems Biology of Development



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 University of Birmingham and University of Essex.

Spotlight on the University of Birmingham

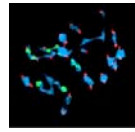


The School of Biosciences at the University of Birmingham is part of the University's College of Life and Environmental Sciences and is situated on the picturesque Edgbaston campus close to the city centre. Research in the School of Biosciences at the University of Birmingham falls into 3 overarching themes: Molecular and Cell

Biology (headed by Prof. Noni Franklin-Tong), Molecular Microbiology and Organisms and the Environment. Within these themes research is carried out in a wide range of disciplines, including plant- and animal science, systems biology, structural biology and ecology. Birmingham has high-tech facilities for genomics, proteomics, metabolomics, structural biology, horticulture and optical imaging, making it well-equipped for modern plant science research. 90% of Biosciences research was rated as of international quality in the 2008 RAE.

The School of Biosciences has around 60 academic staff, 70 postdoctoral researchers, 50 support staff, 25 administrative staff, 170 PhD students, 75 Postgraduate Masters students and 800 undergraduates. The School offers several flexible undergraduate degree programmes (including a 4-year MSci degree), which include Plant Science modules at all levels. Undergraduate and postgraduate students carry out lab-based research projects across disciplines. Many of those who work in Birmingham Plant Science research labs go on to further plant science research in other UK and international universities.

The School of Biosciences is keen to support independent research fellows and the University of Birmingham is currently investing in recruiting to high-quality post-doctoral fellowships: www.birmingham.ac.uk/staff/excellence/fellows/index.aspx



Sue Armstrong

s.j.armstrong@bham.ac.uk

www.birmingham.ac.uk/staff/profiles/bio-sciences/armstrong-sue.aspx

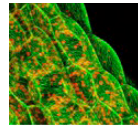
Organisation and behaviour of chromosomes in plant meiosis

Sue Armstrong's research interests are concerned with meiosis, a highly conserved pathway, by which haploid gametes are formed following a double cell-division process. Her laboratory is interested in chromosome behaviour during pairing, recombination and synapsis in plant meiosis. She uses molecular cytogenetic and immunolocalisation techniques combined with the molecular resources available for *Arabidopsis* molecular biology, to investigate aspects of this complex process that continues to be poorly understood. Sue Armstrong and Chris Franklin have been awarded a BBSRC Lola grant (2008) to transfer *Arabidopsis* knowledge to barley and to find ways to manipulate crossover frequency and distribution in this cereal. She is also the co-ordinator for a large FP7 collaborative award (www.meiosys.org). Current research falls into 3 areas:

1. Telomere biology in *Arabidopsis*. Investigating how homologous telomeres pair during early meiotic prophase. Recent attention has been paid to the bouquet, a nearly universal event during which telomeres move and cluster on the nuclear envelope in early prophase. The lab is looking at pairing in telomere deficient plants in order to understand the significance of this early step in the meiotic pathway.
2. Genetic and cytogenetic investigation of homoeologous pairing and recombination in *B. napus* (AACC). Breeders wishing to introduce new characteristics into the *B. napus* (oil seed rape) crop are creating synthetic lines by crossing *B. oleracea* with *B. rapa*. In natural *B. napus* plants pairing control is strict; (A/A and C/C) whereas in synthetics pairing control is less strict (A/C) and can lead to unstable progeny and loss of fertility. The lab is investigating the nature of this problem.
3. Evolution of sex chromosomes in the plant genus *Silene* in collaboration with Dmitry Filatov (Oxford). Research is concerned with evolution and chromosome behaviour in meiosis in the genus *Silene*. This plant genus provides an opportunity to conduct a comparative cytogenetical study of the relatively early stages of sex chromosome evolution because it contains cytologically distinguishable heteromorphic sex chromosomes that have evolved relatively recently, 10-20 million years ago. The research uses the cytogenetics tools developed for *Arabidopsis* to analyse the changes in sex chromosome structure and meiotic behaviour during sex chromosome evolution in *Silene*. The lab is carrying out a high resolution comparative

Spotlight on the University of Birmingham

cytogenetic analysis of the X and Y chromosomes in dioecious *Silene*, in particular, (i) how the structure of chromosomes have evolved to form clearly distinguishable heteromorphic X and Y chromosomes, (ii) how these plants cope with heterologous sex chromosomes during meiosis; specifically do they restrict pairing to the pseudoautosomal region (PAR) of the X and Y in plants? (iii) what mechanisms are involved in suppressing recombination in the non-recombining regions (NRY) of the *Silene* Y chromosome? Overall, the research will show if these mechanisms are similar to those arrived at in mammalian systems or whether novel approaches achieve the same outcome.



Juliet Coates

j.c.coates@bham.ac.uk

www.birmingham.ac.uk/staff/profiles/biosciences/coates-juliet.aspx

Plant development and evolution

Juliet is interested in how the huge diversity of complex multicellular plants evolved from aquatic algal ancestors. The transition of plants from water to land was a giant evolutionary leap that enabled plants to colonise a wide range of ecological niches. Algae and plants are integral to the atmosphere, ecosystems and society. Understanding how modern land plants evolved is one of the most under-investigated areas of biology. Tracing the evolutionary history of plants and algae enables humans to use them productively. By understanding how land plants evolved, we can identify their drought- and stress-resistance strategies and apply this knowledge to crop plants. Algae can also live in inhospitable environments and they provide a relatively untapped resource of fuel, food and novel biochemicals. Research areas:

1. Conserved molecular and cellular developmental mechanisms. Investigation of evolutionarily ancient proteins required for development in animals, amoebae, parasites and plants. Functional genomics in plant model systems including *Physcomitrella*, *Arabidopsis*, and *Selaginella*. Current collaborators: Rita Tewari (Nottingham), Peter Winn, Mike Tomlinson (Birmingham). Current funding: Leverhulme Trust research grant.
2. Regulation of plant root architecture. What are the signals and proteins that control how roots branch to form a network? This is a developmental process of huge agricultural importance, and is critical for plant growth and responses to changing environments. Current collaborator: Malcolm Bennett (Nottingham).
3. Biology and development of complex green algae. Green macroalgae (seaweeds) share multicellular complexity and environmental challenges with land plants. The lab is developing green macroalgae as model systems for molecular genetics and investigating the conservation of plant- and macroalgal developmental processes. Current collaborators: Jim Callow (Birmingham), John Bothwell (Belfast), Thomas Wichard (Jena), Benedicte Charrier (Roscoff), Rafael Robaina Romero (Gran Canaria). Current funding: NERC PhD studentship.



Jim Callow

j.a.callow@bham.ac.uk

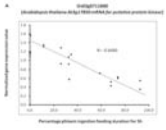
www.birmingham.ac.uk/schools/biosciences/staff/profile.aspx?ReferenceId=4314

Marine bioadhesion and biofouling

The fouling of ship hulls and other underwater structures is a significant economic and environmental problem*. The Bioadhesion and Biofouling Research Group, led by Professor JA Callow and Dr Maureen E Callow, has worked in this area for the past 15 years, the focus being on marine algae (*Ulva*, *Ectocarpus*, various species of diatom). Fundamental work is currently directed towards understanding how the physico-chemical and biological properties of surfaces influence bioadhesion and how fouling organisms respond to signals, including those emanating from microbial biofilms. In other studies the cellular and physiological basis of surface selection is being explored. For example it was recently established that the NO-signalling cascade is involved in perception and response of algal cells to surfaces of different wettability. In more applied work the current emphasis is on interdisciplinary, collaborative investigations into the interactions between algal cells and micro/nanostructured materials, including those with 'biomimetic' implications. The work has impact in the knowledge-driven development of prototypes for novel, environmentally-benign, antifouling coatings*. Work is funded by the US Office of Naval Research, the European Commission (SEACOAT, a Marie-Curie ITN), and industry.

*CallowJA, CallowME. (2011). Trends in the development of environmentally friendly fouling-resistant marine coatings. *Nature Communications* 2: 10.1038/ncomms1251.

Spotlight on the University of Birmingham

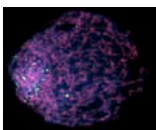


Brian Ford-Lloyd

b.ford-lloyd@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/ford-lloyd-brian.aspx

Plant genetics and genomics of biotic and abiotic stress

The world's plant genetic resources hold much value for world food security, but they are under considerable threat. Crop improvement particularly under climate change depends on the genetic diversity existing in our plant genetic resources, which are arguably inadequately conserved and used. Biodiversity is at risk from multiple threats including climate change, and the genetic diversity contained within plant genetic resources, particularly of species that are wild relatives of our crops face similar threats but are essential to our ability to respond to the new stresses in the agricultural environment inherent in climate change. It is important to consider the genetic value of these crop wild relatives, how they may be conserved, and what new technologies can be implemented to enhance their use. It is important therefore to focus the new molecular technologies, genomics, transcriptomics and metabolomics, onto finding solutions to the problems of ensuring effective conservation of these resources and their enhanced use. In Birmingham using these technologies it has been possible to identify genes conferring resistance to brown planthopper from rice genetic resources. This will not only help in the improvement of new rice varieties but has also identified ways to make conservation of genetic resources more effective.



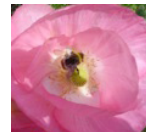
Chris Franklin

f.c.h.franklin@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/franklin-chris.aspx

Control of meiotic recombination

Chris Franklin is Professor of Plant Molecular Biology and Director of Research in the School of Biosciences. Chris's research is focussed on the control of meiotic recombination in *Arabidopsis* and crops. Molecular cytogenetics is being used in conjunction with meiotic mutants to understand how recombination is coordinated with extensive remodelling of the chromosomes that occurs during prophase I of meiosis. This has established the important role played by the proteins that form the chromosome axes in the regulation of genetic crossover formation. He is also involved in an EU FP7 project, MEIOsys, which is using systems biology to identify the protein-protein interaction networks that regulate the frequency and distribution

of meiotic crossovers. These fundamental studies are being used to underpin a translational programme of research funded by BBSRC (Lola) aimed at manipulating meiotic recombination in cereals using barley as an experimental system. Crossover formation in the cereals and forage grasses is highly skewed towards the distal regions of the chromosomes near the telomeres. Estimates suggest that as a consequence 30-50% of genes are located in areas of low recombination. This is a barrier for breeding mapping programmes. The group have now established that this skewed recombination is associated with the spatio-temporal characteristics of recombination initiation and are now developing experimental strategies to overcome this problem. The group is also studying the effect of environment on meiotic recombination. Evidence indicates that even modest increases in temperature of just a few degrees have a significant impact on recombination leading to reduced fertility. They are currently studying which aspects of meiotic recombination are most susceptible.



Noni Franklin-Tong

v.e.franklin-tong@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/franklin-tong-noni.aspx

Plant cell biology

Noni Franklin-Tong is Professor of Plant Cell Biology. Her research focuses on the cellular mechanisms involved in the model cell-cell recognition system of self-incompatibility (SI) in *Papaver rhoeas* (the Field Poppy). This has high importance in relation to the future focus on food security, and Noni's research has world-wide impact in the broader fields of plant cell signalling, the plant cytoskeleton and programmed cell death in plants. Sexual reproduction in higher plants involves pollination, involving specific interactions between pollen and pistil. A key mechanism to prevent inbreeding is self-incompatibility (SI). Incompatible ("self") pollen is rejected and compatible ("non-self") pollen is allowed to fertilize the plant. Noni's lab is investigating the signalling cascades, targets and mechanisms regulating pollen tube growth inhibition and subsequent programmed cell death in *Papaver*. Their long-term goal is to establish how the different components integrate and interact in what has turned out to be a complex signalling network. Currently research falls into several areas:

1. Investigations into programmed cell death, reactive oxygen species and nitric oxide signalling in the SI response.
2. Alterations in the cytoskeleton in response to SI signaling; role of the cytoskel-

Spotlight on the University of Birmingham

eton in inducing programmed cell death.
 3. Cytosolic soluble inorganic pyrophosphatases as novel targets for SI signals (In collaboration with Dr Scott White)
 4. Investigating novel receptor-ligand interactions and downstream signaling events during the SI response (In collaboration with Christoph Baumann (York), Dale Sanders (JIC), Josh Rappoport and Steve Publicover (University of Birmingham))
 5. Pursuing possible commercial aspects of using SI, by investigating whether poppy SI can be transferred to other species, including Arabidopsis and crops (In collaboration with PBL and Chris Franklin).



Nigel Maxted

n.maxted@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/maxted-nigel.aspx

Plant genetic conservation

Nigel Maxted is a Senior Lecturer and Consultant in Plant Genetic Conservation. His research group's focus is on the conservation of genetic diversity in plants, largely on species of socio-economic value, working primarily in Northern Asia, Middle East, Africa and Europe, as well as the UK. The research has often involved the development of novel approaches to conservation, particularly in the management of *in situ* crop wild relative (CWR) and landrace (LR) diversity. Recent activities have focused on research methodologies for the production of inventories and conservation of CWR and LR in Europe and the UK. Several projects are jointly managed with Professor Brian Ford-Lloyd also from the School of Biosciences. Current active research projects include: (a) EC FP7 Research funding of Novel characterization of crop wild relatives and landraces resources as a basis for improved crop breeding (PGR Secure), (b) Defra (SAIN) funding of Conservation for enhanced utilization of crop wild relative diversity for sustainable development and climate change mitigation (CWR China), (c) IUCN funding of IUCN red listing of European crop wild relative diversity, (d) Garden Organic funding of Characterisation of UK vegetable landrace diversity, (e) Norwegian Government funding for Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives for Exploitation, and (f) EU ERA funding of Cooperation between the Royal Botanic Garden of Jordan and the European Research Area in the area of plants and seed conservation, genetic resource diversity and biotechnology, and utilisation and access benefit sharing.

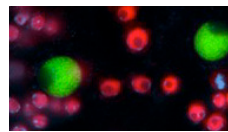


Jeremy Pritchard

j.pritchard@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/pritchard-jeremy.aspx

Plant stress physiology

Research in the Pritchard group is centered on plant response to biotic and abiotic stress, using genomics, proteomics, transcriptomics and metabolomics. Focus at the level of the single cell has enabled demonstration that plant responses to stresses, including drought, salt, pollution and pest attack are highly heterogeneous. The single cell approach has been extended to sampling the long distance transport pathways of the phloem and xylem by exploiting sap-feeding insects and has uncovered the new aspects of the regulation of these compartments, including the central role of xylem composition in salt tolerance and the highly homeostatic nature of the phloem sieve element. Determination of phloem specific gene expression is beginning to uncover the molecular mechanisms that underlie these physiological observations. Ability to sample from the precise feeding location of insects allows components of their performance to be dissected. Current work is linking physiological data at the cellular level with the emerging genomic resources (including transcriptomics) in model organisms such as Arabidopsis and extending to crops such as barley and rice even herb crops such as coriander and thyme.



Eugenio Sanchez-Moran

e.sanchezmoran@bham.ac.uk
www.birmingham.ac.uk/staff/profiles/biosciences/sanchez-moran-eugenio.aspx

Chromatin structure and chromosome dynamics

Eugenio is a David Phillips Fellow at the University of Birmingham. Eugenio started to be interested in genetics and especially chromosomes as an undergraduate in Madrid (Spain) where he obtained a degree and a PhD. Subsequently, he was awarded with a Marie Curie Individual Fellowship at the laboratory of Prof. Chris Franklin (University of Birmingham) to carry out the first analysis of the meiotic proteome in Arabidopsis. This resulted in the identification of a number of very important meiotic proteins. Since then, Eugenio has been supported by a couple of BBSRC grants for a postdoctoral position at Birmingham. Currently, he is a David Phillips Fellow at the University of Birmingham and his research aims to unravel the biological significance that the different levels of DNA compaction structures and

Spotlight on the University of Essex

components have on chromosome condensation and DNA processes in the nucleus. He believes that this research will contribute to the understanding of different important themes like cell division, cancer, stem cells, chromosome alterations, fertility and plant breeding.

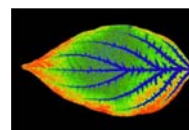
 Spotlight on the University of Essex


The Department of Biological Sciences in the University of Essex has some 52 teaching and academic staff, 45 administrative and technical staff, 35 research staff, over 680 under-

graduates and about 165 postgraduates, half of whom are from outside the UK. The structure of the Department provides a strong base in both teaching and research. The Department comprises four research groups: Molecular Medicine, Molecular Biophysics, Sports and Exercise Science, and Environmental Biology. Group boundaries are not rigid and many projects involve collaboration between members of two or even three groups. More details about the Department, its activities and staff can be obtained from www.essex.ac.uk/bs/. The Department has undergone a recent expansion built upon a successful outcome in the RAE2008 where we doubled our QR income and in which the University of Essex was ranked 9th overall.

All the academic plant science researchers are members of the Environmental Biology group and are united around the theme of Plant Productivity. We have always emphasised the combining of plant physiology (especially photosynthetic physiology) with molecular genetics as a means of identifying novel genes and processes that are determinants of yield under benign and stressful conditions. Increasingly this strategy is being augmented and informed by computational biology, with current funded research deploying a strong Systems Biology and Bioinformatics component. The strong co-operation within the Plant Sciences team is reflected in the various permutations of members who contribute to BBSRC, EU and privately sponsored research, which raised £1.2 million in 2010-11 alone. We are well supported by state-of-the-art equipment for measuring and imaging plants' responses to their environment (managed by Dr Phillip Davey), a new confocal microscopy suite (managed by Dr Philippe Laissue), a dedicated Unix cluster for plant bioinformatics (supervised by Dr Igor Chernukhin) and a well-equipped plant molecular genetics laboratory (managed by Dr Ruben Alvarez). In 2012, these facilities will be augmented by an auto-

mated controlled environment phenotyping facility and a series of "roof top" gardens which are currently being constructed. It is intended that the combined use of these facilities will allow us to prioritise our efforts on genes that have effects on yield both inside and outside the laboratory. Finally, we have an ever growing number of global partnerships in Europe, USA and India that allow us to trial our most promising genes in crop plant species allowing this small group of researchers to extend from model-to-crop and from laboratory-to-field.



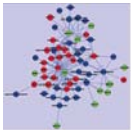
Neil Baker

baken@essex.ac.uk
www.essex.ac.uk/bs/staff/profile.aspx?ID=1105

Plant physiology and biophysics

Neil's primary interests are the intrinsic and environmental factors that determine the efficiency of light utilisation in photosynthesis by higher plants and algae. Recently a particular focus has been the onset of photo-oxidative stress and the mechanisms by which plants can alleviate such stress. An important aspect of his research has been the development of novel, non-invasive spectroscopic techniques to investigate the development and functioning of the photosynthetic membranes in intact leaves under natural environmental conditions. Of particular importance has been his demonstration of how chlorophyll fluorescence measurements from leaves can provide accurate estimates of the quantum efficiency of photosynthetic electron transport and the application of chlorophyll fluorescence imaging to investigate heterogeneity of photosynthetic function both in leaves and individual cells. These fluorescence techniques have been coupled with measurements of infrared gas exchange, on-line mass spectrometry and thermal imaging to provide a powerful suite of non-invasive tools for the study of photosynthetic performance *in vivo*. Recently, these measurements have been used to study the rate of reduction of oxygen by photosystem I via the Mehler reaction and the operation of the water-water cycle in plants. Although algae can use these reactions to dissipate excess excitation energy, the rate of these reactions in leaves of higher plants is not sufficient to serve as a major mechanism protecting against photo-oxidative stress. There are currently collaborative projects running with Phil Mullineaux on the signalling responses of leaves in response to perturbations of photosynthesis by environmental stress and with Tracy Lawson on the relationships between leaf photosynthesis and stomatal function.

Spotlight on the University of Essex



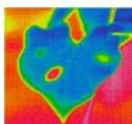
Uli Bechtold

ubech@essex.ac.uk

www.essex.ac.uk/bs/staff/profile.aspx?ID=1197

Plant molecular physiology and biotechnology plant cytoskeleton

Uli's research focuses on identifying genes underlying drought tolerance and water productivity (water used per unit of yield) using a systems biology approach involving transcriptomics and modelling of whole plant adaptations, as well as studying natural variation of drought tolerance and water productivity. Current research focuses on drought signalling networks, using a modelling approach to identify novel regulatory genes. This work is carried out in collaboration with Jim Beynon, Vicky Buchanan-Wollaston, Katherine Denby (University of Warwick), Nick Smirnov and Murray Grant (University of Exeter). In collaboration with Christine Raines and Tracy Lawson a similar approach is taken to identify key regulatory genes affecting photosynthesis under environmental stress conditions with the aim to improve photosynthetic performance in water limiting environments. Recent work published in *Plant Cell & Environment* has also shown considerable variation in water productivity amongst *Arabidopsis* genotypes and efforts to map water productivity loci using QTL analysis and genome wide association mapping is a major research focus. This work takes advantage of the different growth and phenotyping facilities available at Essex, translating traits identified in the lab directly to the field environment. Another line of research comes from a longstanding collaboration with Phil Mullineaux, which has identified a clade A1 heat shock transcription factor to improve productivity in *Arabidopsis* and oilseed rape. This transcription factor also confers drought tolerance and a broad range of biotic stress tolerances in *Arabidopsis* and work to test multiple stress phenotypes in transgenic oilseed rape is currently being carried out.



Tracy Lawson

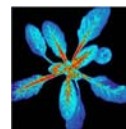
tlawson@essex.ac.uk

www.essex.ac.uk/bs/staff/profile.aspx?ID=1206

Plant photosynthetic physiology & water relations

Tracy's research focuses on stomata, their function, the central role they play in plant water use efficiency (WUE) and the implications for crop yields. Currently, this research concentrates on the temporal responses of stomata to the rapidly fluctuating natural light envi-

ronments that plants experience and the impact the speed of stomatal response has on both photosynthetic processes and water loss. Stomata and photosynthesis respond to a number of environmental cues; however responses are not synchronized, with stomatal adjustments generally an order of magnitude slower than mesophyll responses. The resulting disconnection between stomatal conductance and photosynthetic rate means that under fluctuating conditions, WUE is most likely far from optimal. Tracy is interested in spatial and temporal patterns of stomatal behaviour and the impact restricted CO₂ diffusion has on photosynthetic carbon gain and the potential long term influence on photosynthetic processes via photoinhibition. As part of this research Tracy uses modern imaging techniques (chlorophyll fluorescence and thermography) to study lateral gas diffusion within leaves and the impact of CO₂ consumption and stomatal behaviour on photosynthesis. Her research also involves understanding the underlying mechanisms and signals that promote the relationship between mesophyll photosynthetic carbon fixation in relation to stomatal conductance. Her research (with Neil Baker) also examines the role of guard cell chloroplasts in stomatal function and how guard cell photosynthesis may provide a functional link between mesophyll photosynthesis and guard cell aperture. Tracy works with Christine Raines and Uli Bechtold exploring avenues to increase photosynthesis and yield through manipulating expression of key Calvin cycle enzyme genes, whilst transcriptional network analysis is being used to identify novel Calvin cycle gene 'hubs' that may confer an advantage under conditions of environmental stress. Collaboration with Phil Mullineaux has facilitated a holistic approach to Tracy's research, through the use of molecular genetic techniques to address these fundamental physiological issues.



Phil Mullineaux

mullin@essex.ac.uk

www.essex.ac.uk/bs/staff/profile.aspx?ID=1239

Plant molecular physiology and biotechnology

Phil's research focuses on understanding the temporal and spatial signalling responses of the *Arabidopsis* leaf to high light and low humidity and linking this to their photosynthetic responses. Originally, his research studied the role of reactive oxygen species (ROS) to regulate genes coding for key enzymes of the foliar antioxidant network such as ASCORBATE PEROXIDASE2. This led to his more recently published work on the involvement of chloroplast-to-nucleus signalling and abscisic acid in driving the rapid changes in

Spotlight on the University of Essex

high light inducible gene expression in bundle sheath cells. Strong collaborations with Tracy Lawson and Neil Baker have allowed a multidisciplinary approach to his research. Ongoing research now considers how the leaf responds to varying degrees of high light intensity by initiating either acclimation or cell death and how this impacts on plant immunity to infection. He is also developing GFP-based probes for the real time spatial determination of ROS accumulation (with Nick Smirnoff at Exeter University) and has funding to determine how far these responses occur in arid zone plants under high light, water deficit and herbivore pressure. Phil has a second line of research, in collaboration with Uli Bechtold, which seeks to identify and study genes that strongly influence the yield of plants under multiple abiotic and biotic stress conditions. This has led to the identification of clade A1 heat shock transcription factors as key determinants of productivity in both *Arabidopsis* and oil seed rape. Both the research on signalling in response to abiotic stress involves BBSRC-supported collaborations with University of Warwick Centre for Systems Biology, the University of Exeter, new support from the EU to transfer his research to legumes as part of a consortium called ABSTRESS.

tosynthesis, with Tracy Lawson and Uli Bechtold, Essex aimed at increasing crop yield. Together these two projects will produce plants with altered complements of enzymes of carbon fixation to improve photosynthesis based on empirical studies and in silico modelling.



Christine Raines

rainc@essex.ac.uk

www.essex.ac.uk/bs/staff/profile.aspx?ID=1243

Plant molecular physiology

Christine is Head of Department of Biological Sciences, Chair of the SEB Plant Section and the incoming Editor in Chief of the *Journal of Experimental Botany* (JXB). Over the past 20 years Christine's research has focussed on the regulation and limitations to photosynthetic carbon assimilation taking a molecular physiological approach. Work in Christine's lab showed that the enzyme SBPase exercises strong control over CO₂ assimilation in tobacco plants and that photosynthetic capacity and yield are increased in transgenic tobacco plants with elevated SBPase. Work on the regulation of the Calvin cycle showed that activity of this cycle is modulated via the dynamic formation and dissociation of the PRK/GAPDH/CP12 complex. This mechanism enables plants to respond to rapidly to changing light levels that occur in the natural environment by balancing the action of the Calvin cycle with availability of ATP and NADPH. Recent funding in the Raines lab is from two BBSRC initiatives Crop Improvement Research Club, CIRC, in collaboration with Professor Martin Parry, Rothamsted Research and Approaches to bring about a step change in pho-



UK PlantSci 2012

18-19th April

Inaugural Research Conference of the
UK Plant Sciences Federation

Speakers to include;

Ian Bancroft (John Innes Centre)

Bill Davies (University of Lancaster)

Iain Donnison (University of Aberystwyth)

Ian Graham (CNAP)

Julian Hibberd (University of Cambridge)

Sandy Knapp (Natural History Museum)

Giles Oldroyd (John Innes Centre)

Graham Moore (John Innes Centre)

Richard Mott (Wellcome Trust)

Alison Smith (University of Cambridge)

Richard Summers (RAGT)

John Innes Centre

Norwich

www.plantsci2012.org.uk

Sponsored by;



SEB

Society for Experimental Biology