June 2010. Edition 13

GARNish

The official GARNet Newsletter

a perspective on

Plant science Funding

Also in this issue; Decline in Plant Biology, Alternative Splicing and Tablet

Editorial

Welcome to the Summer 2010 issue of GARNish, the GARNet newsletter. This season we have articles on “hot topics” in plant science along with new technologies that the plant science community will be using more and more routinely as time marches on.

In this issue we have an article on alternative splicing in plants (yes, contrary to popular belief of a few years ago, plants do alternatively splice!). With increasing application of next-generation sequencing technology to investigate plant alternative splicing, we can anticipate a huge increase in our knowledge relatively quickly.

Of course, next-generation sequencing has huge potential in many other fields besides alternative splicing: I would wager that most of us are already using it, or are planning to use it as soon as we get the money… To this end, we have an article introducing you to Tablet, a user-friendly visualisation software package for next-generation sequencing data that is freely available at SCRI.

Funding is on all our minds, and in this issue we have an article "straight from the horse's mouth" on plant science funding from Alf Game at the BBSRC, who met with the GARNet committee back in February. Hopefully this will allay some fears, and importantly encourage plant scientists to join committees and pools of experts to make sure we are represented.

In case you are not sure what GARNet actually is (and what it does, and what it can do for you), we have an article from Irene Lavagi introducing GARNet. She also introduces us to MASC (not NASC, but MASC, the Multinational Arabidopsis Steering Committee).

As in every newsletter, we continue finding out what our Arabidopsis -researcher contemporaries across the UK are doing. This edition of GARNish is brought to you by the letter E (encompassing a large geographical spread!), with synopses of the world-class research being performed by groups based in Edinburgh, Exeter and East Anglia.

As ever, GARNet continues to promote outreach activities. In this issue of GARNish we have a piece by Jerry Pritchard (Birmingham), a long-standing outreach champion, outlining some of his successful activities over the past year.

Don’t forget – you can come and join us at the GARNet meeting, “Cells and Systems” at the University of Durham on 6th and 7th of September. The program is really wide-ranging and exciting and we hope to see you there. GARNet will have an active presence: if you have questions, come to our stand during the poster sessions!

We need to thank departing GARNet committee members Miltos Tsiantis (Oxford) and PhilipWhite (SCRI) and introduce the new ones, Ian Moore (Oxford), Nicholas Smirnoff (Exeter) and Juliet Coates (Birmingham), as well as welcoming Alex Webb (Cambridge) as chair.

Thanks as always go to Ruth Bastow for her efficient coordination of GARNet’s many activities.

Happy summer, with time to do some research once students have left and exams are over….

Juliet Coates.

Contents

Front cover image kindly supplied by Jim Haseloff.
Many thanks to all who contributed to this issue, particularly John Brown, Juliet Coates, Tamas Dalmay, Alf Game, Murray Grant, Irene Lavagi, David Marshall, Karl Oparka and Jeremy Pritchard
If you have any comments about GARNish or if you would like to contribute an article to the next issue please e-mail ruth@arabidopsis.org.uk

GARNet 2010 Meeting - Cells and Systems

The 2010 GARNet Meeting will take place on the 6-7th September 2010 at Durham University and is entitled ‘Cells and Systems’ http://www.garnetmeeting.org

We have an excellent line up of speakers including
Liam Dolan (University of Oxford), Jose Feijo (Gulbenkian Institute Lisbon), Karen Halliday (University of Edinburgh), Nicholas Harberd (University of Oxford), Chris Hawes (Oxford Brookes), Martin Huselkamp (University of Cologne), Jim Murray (University of Cardiff), Francois Tardieu (INRA Montpellier), Ulrich Schurr (Forschungszentrum Jülich) and Marc Vidal (Dana-Farber Cancer Institute, Boston). For a full programme visit http://www.garnetmeeting.org

There are plenty of opportunities for you to share your latest research discoveries with the UK community either via a poster or a short talk. Please submit your abstract via the online registration form. Registration costs for this two-day meeting are modest, £75 for Students, £120 for Post-Docs and £150 for Academics before the 3rd July. With all this on offer don’t miss your opportunity to attend the 2010 GARNet Meeting, register now at http://www.garnetmeeting.org to avoid disappointment!

News and Views

Arabidopsis Scientist Appointed to BBSRC Council

Professor Keith Lindsey from Durham University has been recently appointed to the Council of BBSRC. Within BBSRC, the Council is the highest decision-making body. Indeed, it determines policy, priorities and strategy. BBSRC's Council comprises the Chair, the Chief executive and fourteen other members. At least seven of these fourteen members are appointed for their qualifications and credentials. Last March Lord Drayson, Minister for Science and Innovation, appointed two new members to the Council, including Professor Lindsey, whose appointment is for a period of four years. Professor Lindsey is Professor of Plant Molecular Biology, Director of Research at Durham University's School of Biological and Biomedical Sciences. He is also a co-founder and Scientific Director of Creative Gene Technology Ltd. Current research in the Lindsey laboratory focuses on seed function and plant growth regions using an integrated approach that exploits genetics, genomics, proteomics and physiology with potential application to increase the yield of crops.
In the light of the recent BBSRC's 5-year strategic plan (http://www.bbsrc.ac.uk/publications/policy/strategy/strategic-plan-index.aspx) that includes Plant Science in two out of the three strategic research priorities (i.e. Food Security; Bioenergy and industrial biotechnology), Professor Lindsey's appointment is extermely timely to help meet the challenges of the coming years.

1001 Genomes - A Catalog of *Arabidopsis thaliana* Genetic Variation

Natural *Arabidopsis thaliana* accessions (strains) are found throughout most of the northern hemisphere and show great phenotypic variation, including physiological, and morphological traits at the level of their metabolite content. Flowering and germination behaviour, light and stress response, and importantly disease resistance traits are also very diverse. In the wild, *Arabidopsis thaliana* is available as inbred strains, lending itself to repeated phenotyping of the same, adapted genotype under diverse controlled conditions.
A consortium of scientists advocated the need to sequence 1001 accessions of Arabidopsis (Weigel and Mott, 2009) and launched 1001 Genomes Project for Arabidopsis thaliana in 2008 (http://1001genomes.org/). Collaborating institutions in the UK include the Sainsbury Laboratory (Jonathan Jones), the Wellcome Trust Center for Human Genetics (Richard Mott) University of Bath (Paula Kover), and Warwick University (Eric Holub, Robin Allaby, Jim Beynon and Murray Grant from Exeter University).
The project aims to discover the whole-genome sequence variation in 1001 accessions of *Arabidopsis thaliana* to enable researchers to link phenotypic differences with genotypic variation in plant. Information obtained from sequencing 1001 *Arabidopsis thaliana* accessions will represent the beginning of a new era of genetics, where large-scale association studies in wild type strains are combined with genetic analyses in experimental crosses to identify at a whole-genome and entire species scale the alleles responsible for phenotypic diversity. The broader impacts of the 1001 Genomes project for *Arabidopsis thaliana* include plant breeding, human genetics and evolution.
The current technological sequencing revolution allows the resequencing of large number of genomes at relatively low costs. Although the human 1000 Genomes project was launched in the same year the two projects differ in several aspects, the most important being the fact that each of the accessions in the Arabidopsis 1001 Genomes project is an inbred line with seeds that will be deposited with stock centres, and therefore publically available to all scientists. In addition, the ease of manipulation of Arabidopsis makes it feasible for each accession to be phenotyped in different environments, so that the collected sequence information can be used in association studies.
In February 2010, the complete genome sequence of over 80 accessions sequenced using the Illumina platform by the Weigel's laboratory, were released by the Max Planck Institute for Developmental Biology (Germany). At the end of April 2010 the accessions were made available at ABRC and NASC. Each of the accessions is an inbred line that can be ordered individually or as part of a set. Further sequenced accessions will be made available soon and completion of the 1001 Genomes project for *Arabidopsis thaliana* is scheduled for mid 2011.

Future of Arabidopsis Informatics

As a result of the growing data mountain that researchers have to deal with on a regular basis and the evolving needs of the community as it adopts systems approaches the Multinational Arabidopsis Steering Committee (MASC) and the North American Arabidopsis Steering Committee (NAASC) held two workshops in Nottingham, UK (15-16 April) and Washington DC, USA (10-11 May) respectively, to consider the future bioinformatics needs of the Arabidopsis science community. The outcomes of these workshops will be presented at the International Conference on Arabidopsis Research (ICAR) in Yokohama and a final report summarising the workshops will be published online on the MASC website later this year and sent to policy makers and funding agencies.

Challenges in Alternative Splicing in Plants

*John WS Brown[1,2], Craig G, Simpson[2] and Andrea Barta[3]

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Alternative splicing (AS) generates more than one mRNA from a gene. This greatly increases the protein complement of complex organisms and regulates gene expression post-transcriptionally. Bioinformatic and experimental approaches including next generation sequencing (NGS) now illustrate the scale of alternative splicing in plants. In animal systems, the concept of transcriptional networks inter-linked with networks of alternative splicing to control and fine-tune gene expression is widely accepted. Add to this recent findings that small RNA-targeted chromatin modification affects AS and that alternative splicing and processing of non-coding RNAs in plants affects expression of genes in the flowering pathway, and a clear picture emerges of AS as a major post-transcriptional regulator of gene expression which is fully integrated with other control pathways. As plant scientists, we have major challenges ahead to fully appreciate the importance of AS in regulating plant growth, development and responses to environmental conditions. We must learn to incorporate AS into our thinking.

The selection of alternative splice sites generates different mRNAs from the precursor mRNAs of a gene. The consequences of AS are two-fold. Firstly, different mRNAs can be translated into different proteins, which differ by the addition or exclusion of specific domains or regions. The resultant proteins can have subtle or major differences in function or activity affecting sub-cellular localisation, protein-protein interactions, ligand or substrate binding and modification (e.g. phosphorylation). Secondly, AS can generate mRNAs that contain premature termination codons and these transcripts are usually recognised by the nonsense-mediated decay (NMD) pathway and degraded. Therefore, AS has the potential to increase proteome complexity and to regulate mRNA levels post-transcriptionally.

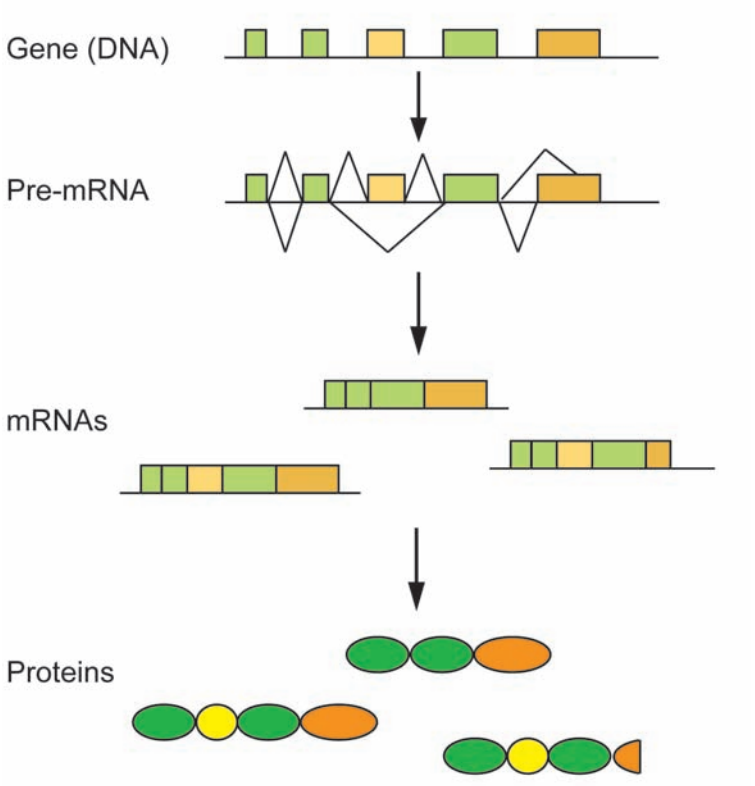


Figure 1
Precursor transcripts are alternatively spliced (diagonal lines) to join different combinations of exons or parts of exons (rectangles) to give different mRNAs which are translated into proteins

A common question is “how much alternative splicing is really functional and how much is noise?” This question usually begs the answer “Not much, so don’t worry about it!” However, the reality is that awareness of the importance of AS is growing rapidly and many plant scientists are beginning to appreciate that AS modulates and fine-tunes transcript levels of genes which are involved in numerous process, for example the regulation of developmental, signaling and metabolic pathways and biotic and abiotic stress responses. Over the last 10 years, the reported number of plant (Arabidopsis and rice) genes that undergo AS has risen from 7% to around 35%. A recent NGS study to discover AS events in Arabidopsis concluded that 43% of Arabidopsis genes are alternatively spliced[1]. Our unpublished work from characterizing AS in individual genes and by NGS suggests that this is still an underestimate and, not surprisingly, in parallel, the number of genes which are alternatively spliced in humans has recently risen to >95%!!

The relative lack of information on AS in plants is due to the lower number of expressed sequence tags (ESTs) compared to human and mouse and the lower depth of sequencing of full-length cDNAs in Arabidopsis on which gene models are based. In addition, many AS events are under-represented in EST databases because they often occur only in specific cells and tissues, at specific stages of development and/or under certain physiological conditions. Another reason is that only a handful of research groups worldwide focus on plant splicing/alternative splicing per se in contrast to the many human/animal groups who in addition to studying mechanisms of alternative splicing have the major driver of human health and disease. Over 15% of all human diseases involve splicing defects including muscular dystrophy, neurodegenerative diseases, cystic fibrosis and cancer (http://www.eurasnet.info).

Challenges in Alternative Splicing in Plants

There are many challenges ahead for plant AS research. At the core is the discovery and annotation of most, if not all, AS events, which will be achieved by NGS (see accompanying article by David Marshall on page). This information will allow the development of genome-wide systems to measure dynamic changes in AS in plants - incorporating AS data is vital if changes in gene expression are to be understood on a quantitative level. Secondly, the consequences of AS have to be elucidated for genes and pathways in terms of the functions of different proteins generated by AS and the regulation of expression by AS and NMD. Thirdly, we know little about the mechanisms by which AS is regulated in plants. The factors influencing AS have to be identified, their binding sequences and target mRNAs defined and the mechanisms by which they cause AS determined. Most progress has been made on the serine-arginine-rich (SR) protein family[2] but many other proteins and factors will influence splice site selection[3,4]. Finally, perhaps the greatest challenge is to understand how regulation of expression by AS is co-ordinated and integrated with chromatin modification, transcription and RNA export?

Addressing these questions is daunting but essential to understanding how plants function.We are actively involved in research in many of the above areas and are members of the European Alternative Splicing Network of Excellence (EURASNET). Along with Robert Fluhr (Rehovot, Israel) and Artur Jarmolowski (Poznan, Poland) our groups in Dundee and Vienna have an ERA-PG grant on Plant Alternative Splicing and Abiotic Stress (PASAS) to address quantification of AS and the influence of AS in abiotic stress responses.

Figure 2
Research groups members involved in the PASAS ERA-PG project.

As more and more landmark examples of alternative splicing emerge[5] we can look forward to exciting developments and insights. So..... “how much alternative splicing is really functional and how much is noise?” – there will be noise but there will be some great music!

1 Filichkin SA, Priest HD, Givan SA, Shen R, Bryant DW, Fox SE, Wong WK, Mockler TC (2010) Genome-wide mapping of alternative splicing in *Arabidopsis thaliana*. *Genome Research* **(20)** 45-58

2 Barta A, Kalyna M, Lorković ZJ. (2008) Plant SR proteins and their functions. *Current Topics in Microbiology Immunolgy* **(326)** 83-102

3 Simpson CG, Manthri S, Raczynska KD, Kalyna M, Lewandowska D, Kusenda B, Maronova M, Szweykowska-Kulinsk a Z, Jarmolowski A, Barta A, Brown JW. (2010) Regulation of plant gene expression by alternative splicing. *Biochemic al Society Transactions* **(38)** 667-671;

4 Raczynska KD, Simpson CG, Ciesiolka A, Szewc L, Lewandowska D, McNicol J, Szweykowska-Kulinska Z, Brown JW, Jarmolowski A. (2010) Involvement of the nuclear cap-binding protein complex in alternative splicing in *Arabidopsis thaliana*. *Nucleic Acids Research* **(38)** 265-278

5 Zhang XN and Mount SM (2009) Two alternatively spliced isoforms of the Arabidopsis SR45 protein have distinct roles during normal plant development. *Plant Physiology* **(150)** 1450-1458

Getting the money: A perspective on peer-reviewed funding in the plant and crop sciences

Alf Game, Deputy Director Research, Innovation & Skills and Head of Delivery Group, BBSRC

BBSRC is the principal funder of plant and crop sciences research in the UK. Since BBSRC was set up in 1994 there have been many changes in the scientific world in the UK, and in the way BBSRC works. A few months ago I met with members of the GARNet Steering Committee to discuss some of the more recent trends and changes and the way these appear to be affecting the plant and crop science research community. This is a summary of some of the issues raised.

I look after the Delivery Group, which runs the peer review system at BBSRC. This article isn't meant to present a thorough statistical analysis of trends, but some impressions and observations in the light of the experience of my colleagues and I have had of working with funding and with the plant and crop science community. Table 1 shows the proportion of the BBSRC grants budget spent on crop and plant sciences over recent years: broadly speaking, crop science has remained level, plant sciences has declined slightly. About 50% of the crop and plant science spend is in responsive mode, the remainder is about 25% BBSRC Institute budget and 25% initiatives. The budget itself has increased, so funding for crops as a proportion of the BBSRC research spend has risen very slightly and plant science has fallen a little. The success rate of plant science grant applications is usually above the average – currently, the overall success rate currently hovers between 20% and 25%, and plant sciences usually has a slightly better success rate than that.

	Annual Spend (£M)				
	2004/05	2005/06	2006/07	2007/08	2008/09
Crop science	30.3	32.7	33.7	38.6	44.3
Other plant science	26.1	26	26	27.3	27.1
Total research spend	222.1	244.1	268.3	290.7	309.8
% of overall BBSRC total: crop science	13.60%	13.40%	12.60%	13.30%	14.30%
% of overall BBSRC total: other plant science	11.80%	10.70%	9.70%	9.40%	8.70%

Table 1 Crop and plant science Summary of annual spend and percentage share of BBSRC total annual spend

The relative increase of spend on crop research relative to plants is in line with the general strategic direction in BBSRC following the BBSRC Review of Crop Sciences (the Gilligan Report). However, anyone who has spent time speaking to the plant sciences community recently will be aware that this rather simple picture does not reflect the general perception in the greenhouse and at the bench.

In recent years there have been a number of trends in BBSRC funding generally e.g:

- The number of grants to non-biological departments has risen from about 3% in 1994 to over 15%
- The number of grants involving more than one department or institution has risen on a similar trajectory
- There is a steady trend to concentration of a greater proportion of funding into fewer institutions
- There are more bigger, longer or multiple post-doc grants

This is a reflection of a changing scientific landscape in which interdisciplinary, integrative and post-genomic quantitative science have risen in importance, bringing new communities into the BBSRC tent and favouring larger-scale or problem-led approaches that require strength across a breadth of science. This shift has to be at the expense of a reduced proportion for something else, and although we have not seriously crunched any numbers, the obvious thing is that there are fewer three-year one-postdoc standard grants of the type that was the bread-and-butter of bioscience funding in 1994. However, this trend is common across bioscience, so is there something different going on in plant sciences?

If the success rate is higher than average, but the proportion of the funds won is not rising, one conclusion might be that fewer applications are coming in. BBSRC, in common with other research councils, has been putting pressure on institutions to reduce the demand on the peer review system. Whilst it would be nice to imagine that the plant sciences community has an elevated sense of duty and compliance (and there are indeed some examples of groups greatly improving their own success rate) it seems more likely that other factors are also at work.

For some time, both prior to the restructuring of BBSRC's grant committees and since, the committees responsible for plant and crop science have seen some decline in grant application numbers in that area. This could be because scientists are making fewer applications than they did, or it could be because there are fewer individuals out there to make them. It could also have been due to the appearance of a number of initiatives in the area drawing applicants away from responsive mode. Most likely it is a mix of all three.

For much of plant and crop science BBSRC is the sole or main UK public sector funding source. DEFRA, the main departmental funder, has seen significant policy redirection in recent years. The charity sector is very small and the industrial user base, although an enthusiastic advocate of research, is – with a couple of big exceptions – not a large-scale funder. This is in marked contrast to other communities in the life sciences base which have access to a plurality of public and private sector funding sources.

Getting the money: A perspective on peer-reviewed funding in the plant and crop sciences

What this means is that changes in the direction and volume of funding from the funders have a more direct influence on this community. That can be good news both for the funders and for those in the right place to respond to change – witness the way the plant sciences community, latterly assisted by GARNet, has responded spectacularly to the successive opportunities in molecular biology, genomics and systems biology over the last 15 years. But these developments, when coupled with the general trends in funding discussed above, are presumably not without consequence for those who do not benefit. It is difficult to know what to advise, beyond the observation that partnership with others and a more integrated approach to research appear to have proven a successful way forward for many.

There is concern about what is happening in some HEIs, but very little hard evidence. Chatter in the margins of meetings about vacant posts not being filled, or being replaced with more biomed-oriented appointees, is frequent – usually attributed to either a decline in interest from students or a perceived inability to raise grant funding. Success in the RAE has not always, it seems, translated into support institutionally. But equally, there are examples of expansion and growth. In truth, we know very little about the health of the discipline, beyond a growing awareness that despite its international competitiveness, it is quite fragile and vulnerable. It is unlikely that BBSRC is going to be able to devote significant effort to looking more closely at this in the near future – it might be helpful if the plant science community and relevant learned societies could undertake a study in this area.

The restructuring of the BBSRC Committees from seven to four has been seen by some as restricting opportunity by reducing the number of committees to which plant scientists can apply. That certainly was not the intention, and one would expect appropriate applications to find their way to Committees C and D as well as Committee B. We would certainly like to see more scientists with a plant research background on those Committees, but that relies on us getting applications to join the pool/core from people demonstrating the right expertise. We need people able and willing to apply their knowledge of e.g. cell biology, biochemistry, genetics or informatics, across a broad(ish) range of relevant bio-science. Applicants who have not had previous experience of committee work tend to describe their expertise too narrowly – perhaps from a concern that they might end up being asked to do things beyond their competence. That shouldn't happen and if it does, you discuss it with the secretariat and they find another way forwardBut no one will put you on a Committee if you insist that the only things you can review are applications to apply swamp-throbble reciprocation theory to models of self-incompatibility in sukebind. And we won't appoint you to anything if you are a BBSRC grantholder but have not responded to requests to referee grant applications. There is a call for applications to join the pool, focusing on a number of areas where we have expertise shortages, out at the moment – please consider whether you can help. See the BBSRC website: http://www.bbsrc.ac.uk/media/news/2010/100430-appointments-panels-committees.aspx The closing date for applications this year is 11 June 2010

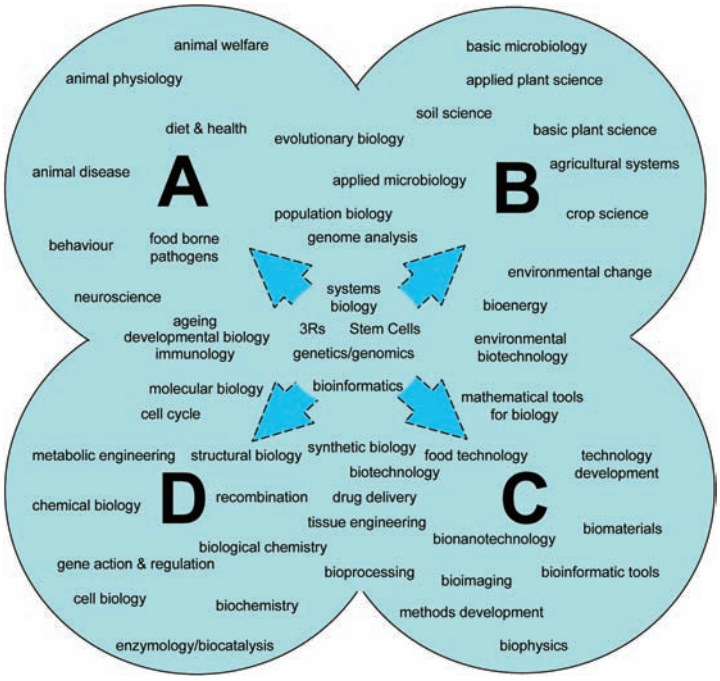
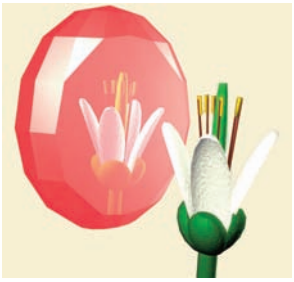


Figure 1 Diagram showing exemplar science areas and where they fit under the new committee structure. This is not an exhaustive list of science areas nor is a list of current priorities

BBSRC has just published its new Strategic Plan 2010-2015. Plant science is central to two of the three strategic priority areas: Food security and Bioenergy; and industrial biotechnology. Overall the plan shows ongoing commitment to sustaining a world class bioscience base and realising the benefits of that for society and the economy. We are now waiting anxiously to discover from Government what funding we will have to enable you, the scientists to deliver that promise.

GARNet and MASC Uncovered

written by Irene Lavagi, University of Warwick, UK



What is GARNet?
GARNet supports Arabidopsis researchers and the wider plant community in the UK.
GARNet aims to ensure that the full impact of the excellent UK plant science base is realised by:

- Acting as an information hub
- Providing a point of contact for researchers and funding agencies
- Promoting interactions between fundamental and applied plant science
- Increasing opportunities for UK plant science at the international level.

GARNet's activities currently focus on 4 key areas:

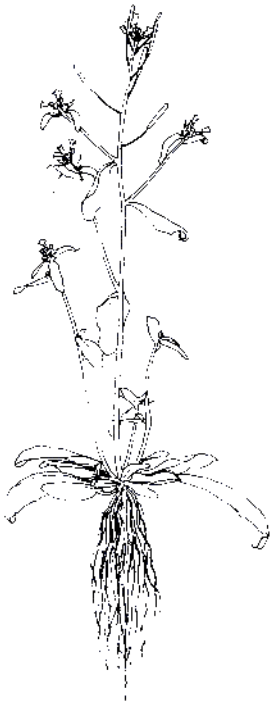
- Community liaison and information flow to continue the core activities of GARNet and provide outreach to the wider scientific community
- Strengthening the UK Arabidopsis research base, including predictive biology research
- Translation: generating new links and promoting existing links between UK plant and crop communities and helping researchers to capitalise on their strengths by promoting interactions and information exchange
- Promoting international activities including coordination of MASC (Multinational Arabidopsis Steering Committee, see below for details).

Who is on the GARNet committee
GARNet represents UK Arabidopsis scientists via a committee of 12 elected members. GARNet is coordinated by Ruth Bastow and the current GARNet chair is Alex Webb (University of Cambridge). Each year, new members are elected to the GARNet committee as others rotate off. Juliet Coates (University of Birmingham) Ian Moore (University of Oxford) and Nicholas Smirnoff (University of Exeter) were elected in December 2009 for a 3-year term to join the current committee of Anna Amtmann (University of Glasgow), Jim Beynon (University of Warwick), Alessandra Devoto (Royal Holloway University of London), Claire Halpin (Scottish Crop Research Institute), Patrick Hussey (Durham University) Stefan Kepinski (University of Leeds), Andrew Millar (University of Edinburgh) and Robert Sablowski (University of Oxford). The committee also has two *ex officio* members, Sean May (Director of NASC, the Nottingham Arabidopsis Stock Centre) and Sabina Leonelli (University of Exeter), a social scientist whose research interests incude Arabidopsis, genomics and bioinformatics.

Currently GARNet is supported by a 5 year BBSRC grant with Jim Beynon as the GARNet PI. The GARNet grant also provides funding for the coordination of MASC for 3 years.
If you would like to learn more about GARNet and meet some of the current committee members then come along to our stand at the GARNet Meeting, 6-7th September at Durham University.

What does GARNet do?

- The role of GARNet is to facilitate information flow both within the Arabid opsis reserach community, and to and from other plant science communities and funding agencies. Information generated by GARNet is placed in the public domain.
- The GARNet Committee meets 4 times a year to discuss current and future community needs and respond to community requests.
- GARNet promotes information flow through the GARNet website http://garnet.arabidopsis.org.uk/) and via the biannual newsletter GARNish (http://garnet.arabidopsis.org.uk/garnish.html)
- GARNet organises an annual meeting for the UK plant science community. This year the meeting is entitled "Cells and Systems" and will be held in Durham on 6-7 September http://www.garnetmeeting.org.
- GARNet organises workshops and discussion meetings to promote new areas of interest, inform people of funding opportunities and bring communities together
- GARNet runs the very popular arab-uk BBSRC mailing list.
- GARNet, through its coordinator, Ruth Bastow, attends meetings and worshops in the UK, in the rest of Europe, and the rest of the world.



GARNet and MASC Uncovered

What can GARNet do for me?

- GARNet, through its committee of elected members (advisory committee), represents the UK Arabidopsis community to funders and other plant science communities both nationally and internationally. If you have an issue that you would like to raise that affects the Arabidopsis community in some way then please contact the GARNet Coordinator Ruth Bastow (ruth@arabidopsis.info), the GARNet Liasion Officer Irene Lavagi (i.lavagi@warwick.ac.uk) or any committee member.
- GARNet promotes interaction with other plant communities. Through the activities of the GARNet Coordinator (Ruth Bastow), members of the GARNet advisory committee are informed of the developments across the UK. If there is something going on your community that you would like to make us aware of, please contact Ruth Bastow (ruth@arabidopsis.info), Irene Lavagi (i.lavagi@warwick.ac.uk) or a committee member.

What is MASC?

MASC is the Multinational Arabidopsis Steering Committee. MASC has been key to the success of the international Arabidopsis community and instrumental in making Arabidopsis into a successful model organism.

MASC was originally set up in 1990 to coordinate the sequencing of the Arabidopsis genome and to implement overall research coordination. MASC was charged with annually reviewing scientific progress and identifying needs and new opportunities for the global Arabidopsis research community.

Since 2002, there has been a MASC coordinator. Today the MASC coordinates global genomic research activities and promotes international cooperation.

The MASC coordinator helps MASC to function as an information hub via its web pages at TAIR, generates annual reports, assists in organising the annual International Conference on Arabidopsis Research (ICAR) and acts as a contact point for researchers and funding agencies.

Where is MASC?

- MASC offices are currently at the University of Warwick, UK, where the PI (Jim Beynon) of the BBSRC grant that funds the coordination of MASC and the MASC coordinator (Irene Lavagi) are based. Keith Lindsey (Durham University) is the MASC Chair for 2009-2010.
- MASC offices will be at Warwick University until 2012, when another country will hopefully take on the coordination of MASC with the support from its funding agency.

What does MASC do?

With the help of the coordinator, Irene Lavagi, MASC produces an annual report and holds an annual committee meeting that typically takes place at the International Conference on Arabidopsis Research (ICAR). MASC liaises and interacts with various national funding agencies (including BBSRC in the UK, NSF in the US, DFG in Germany). MASC also liaises with national networks (including GARNet in the UK and NAASC, the North American Arabidopsis Steering Committee in the US) and with the Arabidopsis community resources providers, including the stock centres (NASC in the UK and ABRC in the US) and TAIR (US).

MASC Report - The annual MASC report includes advances in Arabidopsis research made by the international community in the year prior to its publication. Scientific highlights of Arabidopsis research articles, and examples of translational research highlighting the broader impacts of Arabidopsis research are presented. MASC Country representatives, Subcommittee Chairs and Directors of community resources each produce a report that is included in the annual report. Graphic representations and tables of the advances made towards the production of community resources (e.g. T-DNA lines, cDNAs, ORFs, RNAi lines and expression data) for the entire Arabidopsis genome are also presented. In addition, each year the MASC report contains a section entitled Analysis and Recommendations, that reflects the success of the community, looks sforward to the challenges and opportunities of the future and provide a set of recommendations for the year head. As the NSF-funded programme “Arabidopsis 2010” draws to its end, an article on the last 10 years in Arabidopsis research encompassing the views of funding officials and researchers was included in this year’s report. The MASC report is distributed at ICAR to the conference delegates (over 1,200 for 2010) and is made publically available through the NASC website (http://arabidopsis.info/progreports.html) and through the MASC pages at TAIR (http://www.arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp).

GARNet and MASC Uncovered

MASC recommendations from coming year are summarised below:

- To work towards homozygous mutant lines for all genes; a detailed analysis of their expression patterns and epigenetic control the large scale analysis of proteins and metabolites and their functions; the genomic analysis of wild accessions of Arabidopsis for a better understanding of genome evolution and adaptation; and the development of modelling tools.
- The continued elaboration of a systems approach to plant biology, incorporating diverse data sets and using computational techniques to integrate data and predict plant function.
- The development of resouces for i) association mapping, ii) ecological genetics and iii) field experiments. Such resources include plant populations, appropriate and accessible statistical methods, good field sites, and sharing of knowledge.
- The development of an international policy to maintain bioinformatics and biological material resource centres, through sustainable funding models.
- The development of strategies to store, maintain, distribute and interpret the very large amounts of data that will be generated experimentally in the coming years.
- The effective translation of basic plant knowledge and tools, generated in Arabidopsis research, to crops in order to address the major global challenges of food and energy security in the face of climate change.

What did MASC do in the past 12 months?

Over the past 12 months MASC has greatly contributed to the assessment of the current Bioinformatics resources and the identification of the immediate and future needs of the international Arabidopsis community. Nicholas Provart (Chair of the MASC Bioinformatics Subcommittee) conducted a survey that was sent worldwide to Arabidopsis researchers via mailing lists (arab-uk, arab-gen) to explore the community needs. A summary of the Survey can be found at http://www.arabidopsis.org/portals/masc/Bioinformatics_Survey_18Mar2010.pdf

Following the announcement of the NSF cuts to the funding of TAIR and in the light of the recent exponential explosion in data, the international Arabidopsis community decided to reassess its informatics needs via two workshops, one in the UK (15-16 April 2010, Nottingham) sponsored by BBSRC, and one in the US (10-11 May 2010, Washington DC) sponsored by NSF. The outcomes of these workshops are summarised in a report that will be made publically available at (http://www.arabidopsis.org/portals/masc/masc_docs/masc_wk_rep.jsp). A cohesive international community provides a unified voice to inform funding agencies on the short and long-term bioinformatics needs of the community.

How and where can I read more about MASC and its activities?

MASC does not have a website *per se*, its webpages are hosted at TAIR. MASC is one of the Portals of TAIR (from the TAIR homepage choose the 'Portals' tab, 'MASC/Functional Genomics') or visit http://www.arabidopsis.org/portals/masc/index.jsp. The MASC webpages can be navigated using the links on the left. These include the Coordinator's Journal and MASC related documents such as workshop reports, MASC annual reports, country reports and subcommittee reports.

Who is on the MASC committee?

The MASC committee is composed of:

- Chair- Keith Lindsey 2009-2010, Co-chair - Kazuo Shinozaki (RIKEN, Japan) and Coordinator - Irene Lavagi (University of Warwick)
- Country representatives - Ruth Bastow, Jim Beynon and Irene Lavagi for the UK (University of Warwick). To view other country representatives http://www.arabidopsis.org/portals/masc/MASC_members.jsp
- Subcommittee Chairs - Bioinformatics (Nicholas Provart, Canada); Clone-based Functional Genomics Resources (ORFeomics - Joe Ecker, US); Metabolomics (Kazuki Saito, Japan); Natural Variation and Comparative genomics (Chris Pires and Brian Dilkes, US); Phenomics (Eva Huala, US and Sean May, UK); Proteomics (Wolfram Weckwerth, Austria; Sacha Baginsky, Switzerland; Harvey Millar, Australia; Klaas van Wijk, US); Systems Biology (Andrew Millar, UK and Rodrigo Gutierrez, Chile)
- Subcommittee Members - can be viewed at http://www.arabidopsis.org/portals/masc/Subcommittees.jsp
- Resources Directors - Eva Huala (TAIR), Erich Grotewold (ABRC), Sean May (NASC)

BBSRC request for Appointments to BBSRC Strategy Panels and Pool of Experts

BBSRC are looking to appoint high calibre experts from academia and industry on their Strategy Panels and Pool of experts. BBSRC Panels play a leading role in developing and implementing the Council's policies and priorities, whereas the Pool of Experts, Peer Review and Training Awards Committee, play key roles in delivering the Council's Mission, by peer reviewing research grant proposals, awarding studentships and fellowships and assessing final reports on funded grant proposals. This is an outstanding opportunity for plant scientists to get involved and promote excellent plant science by directly implementing the priorities of BBSRC's Strategy.

5th Conference

epso

Plants for life

Olos (Lapland), Finland

29 August - 1 September 2010

Achieving sustainability

Crop genomes for sustainable agriculture
Breeding tools and strategies

Strengthening the functioning of ecosystems

Improvements in plant health
Climate change impact on plant production
Climate, ecosystems and genomics
Biodiversity

Science policy

Plant science in Europe and beyond

Achieving Quality

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

Confirmed speakers

Wout Boerjan, Thomas Boller, Hely Haeggman, Jean-Christophe Glazmann, Wilhelm Gruissem, Ruben Gutzat, Heribert Hirt, Stefan Jansson, Jonathan Jones, Maarten Koornneef, Jane Langdale, Leena Mannonen, Jenny McElwain, Karin Metzlaff, Maurice Moloney, Kirsi-Marja Oksman-Caldentey, Bruce Osbourne, Shivaji Pandey, Riitta Puupponen-Pimiä, Alexander Platt, Hugh W Pritchard, Werner Roos, Bill Rutherford, Kazuki Saito, Dirk Scheel, Bernhard Schmid, Alan Schulman, Ulrich Schurr, Eva Stoger, Kazimierz Strzalka, Gale Taylor, Richard Thompson, Chiara Tonelli, Arjen van Tunen, Tomas Vanek, Olivier Vionnet, Eero Vuorio, Tim Willis, Ian Woodward, Dani Zamir

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

Information and registration at www.epsoweb.org

What You See is What You Get: Visualizing Next Generation Sequence Assembly and Alignment data in Tablet

David Marshall*, Iain Milne, Gordon Stephen, Linda Cardle, Micha Bayer and Paul Shaw.
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The development and commercialisation of new sequencing technologies (Next Generation Sequencing, NGS or Second Generation Sequencing, 2GS) generating high-volume, short-read sequence data is having a dramatic impact on many aspects of plant genetics and cell biology. However, the sheer volume of data generated by these new sequencing technologies together with their shorter reads and different error models have presented a major set of bioinformatics challenges. Not only do we need new robust software tools: the sheer scale of the results means that it has been extremely challenging to even explore the resulting analysis.

Here at SCRI, the Plant Bioinformatics Group is being increasingly challenged by scientists coming with requests such as *"I have just had 60 million Illumina sequence reads or 2 x Roche 454 Titanium runs done by one of the UK sequencing centres what can I do with the data?"* We have addressed this in two main ways. One is to keep a watching brief on the development of software tools for 2GS assembly and/or alignment and develop our expertise, and the other is to try and develop an approach that gives the laboratory scientists easy access to the results of the analysis that we undertake.
In both cases a key component of our approach has been to use data visualization. Visualization has proved to be of major value both in understanding how well available software tools for assembly and alignment are dealing with particular data sets and in tuning the available parameters. In addition, returning the resulting analyses to laboratory scientists in a form that they can readily explore visually has proved extremely valuable. However, when we first started this work we found most of the existing visualization tools for 2GS alignments and assemblies were clumsy to use, performed badly with large data sets, only accepted a very limited range of input formats, and often had extremely tedious installation routines with complex dependencies on various combinations of software libraries. Our solution to overcoming these limitations has been to develop our own visualization tool, Tablet[1]. The role that Tablet plays in our work can best be appreciated by looking at a couple of applications.

The majority of the work we are currently undertaking involves the analysis of 2GS transcriptome or "RNA_seq" data from a range of species including barley, soft fruit and Arabidopsis - though genomic applications are increasing. The major focus has been SNP discovery either directly e.g. for 2GS resequencing of amplicons or alternatively to design Illumina Golden Gate genotyping assays[2]. The actual pipeline we use for analysis is in a constant state of flux either as a result of new tools becoming available or as we find new bugs or problems in existing software. Currently, for Illumina data, after initial QC screening, we use Mosaik[3] for alignment (where we have a suitable sequence template) or Velvet/Oases[4,5] for assembly. For Roche 454 data we are using both the Roche tools and a range of other packages for alignment and assembly. For both technologies alignment or assembly is followed by SNP discovery using tools such as Gigabayes[6]. At this stage we now have either an alignment or assembly with potential SNPs marked up that we can view in Tablet, which we can pass back to the laboratory scientists to visually explore their own data, for example, to judge the supporting evidence for a given SNP or to decide whether there is too much local polymorphism to design a robust assay (See Figure 1).

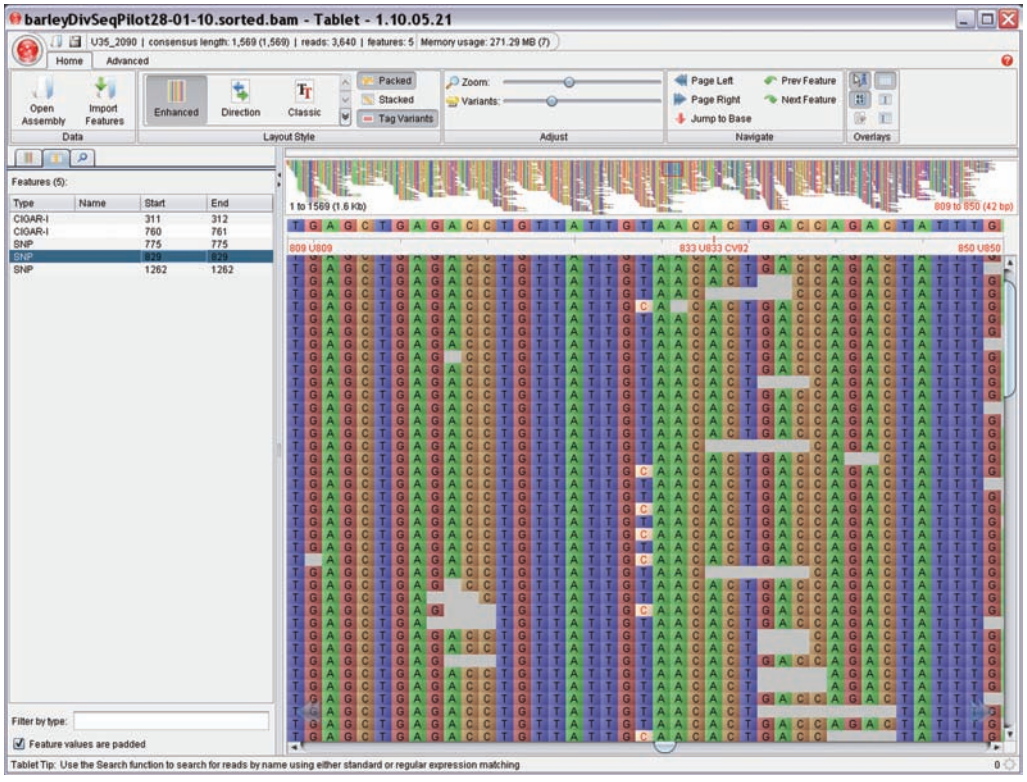


Figure 1 Tablet display showing the highlighted visualization of SNPs in a barley Illumina data set with RNA_seq reads from 7 different varieties aligned with Mosaik to contig consensus sequences from the Harvest 35# transcript assembly. Data courtesy of Joanne Russell and Pete Hedley (SCRI).

What You See is What You Get: Visualizing Next Generation Sequence Assembly and Alignment data in Tablet.

We also have developed at SCRI a comparable application “Flapjack” which is designed to display “graphical genotype” data from large SNP data sets such as the 250 K Arabidopsis data set, the NAM Maize SNP data or our own barley SNP data. We are working closely with Ed Buckler and the Gramene diversity group who have adopted Flapjack as their graphical genotyping tool of choice to ensure that high-density SNP data sets from rice, maize and Arabidopsis can be readily viewed in Flapjack.

One exciting application of RNA_seq data has been in the use of Illumina or comparable short reads aligned to genomic sequence to define introns/exons and splice junctions. This approach is both providing valuable evidence to support and develop computationally derived gene models from genomic sequence and is leading to a major upward revision in our appreciation of the extent of alternative splicing and transcript diversity in plants. Currently, we are working with John Brown and colleagues in the University of Dundee/SCRI to develop an analysis pipeline based on the use of the Bowtie[7] and Tophat[8] programmes to align reads to genomics sequence and to split reads across splice junctions followed by visual inspection of identified splice junctions in Tablet (see Figure 2).

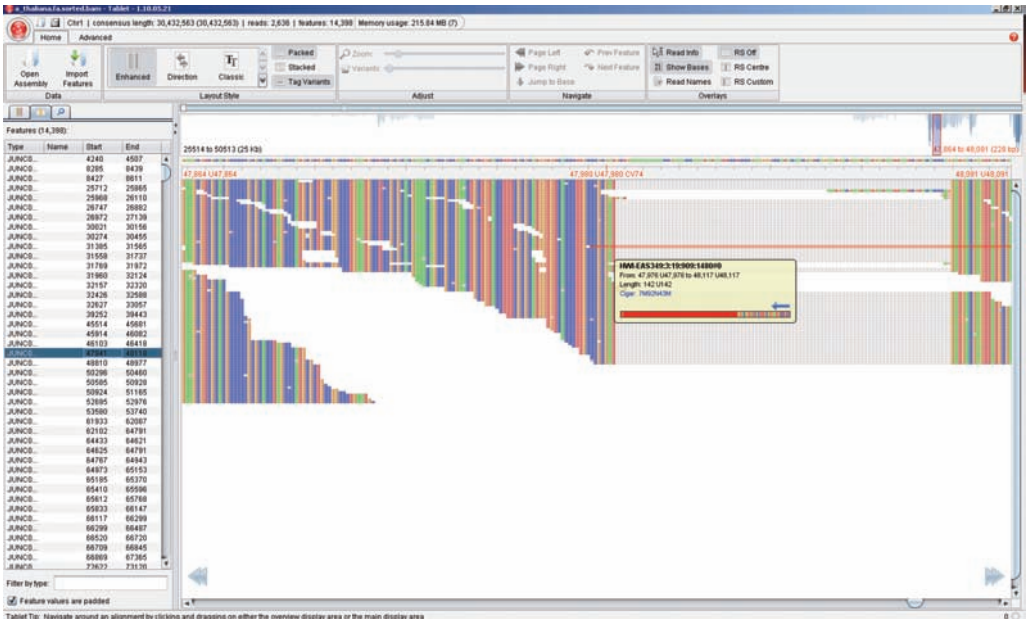


Figure 2 Visualization in Tablet of Illumina RNA_seq reads aligned to the entire Arabidopsis genome with splice junctions identified and junction spanning reads padded using the Bowtie/Tophat analysis pipeline. Data courtesy of John Brown and Craig Simpson (SCRI/University of Dundee)

Tablet is written in Java and is designed to be cross platform and run across PC, Mac or Linux operating systems. It is easily installed from our website and works directly “out of the box” with no complex dependencies on preinstalled packages. Once installed, Tablet will check back to our website each time it runs for new updates or bug-fixes. A particular feature of Tablet is the range of input formats which it will support, including ACE, AFG, SOAP, MAQ and SAM/BAM. Although Tablet was originally developed to meet our own internal plant 2GS applications, over the last 12 months it has been increasingly used by university and institute laboratories, sequencing centres and companies around the world. Tablet and Flapjack together with online help are freely available from: http://bioinf.scri.ac.uk/tablet/ and http://bioinf.scri.ac.uk/flapjack/. We welcome comments and suggestions with regard to any of our software packages.

References

1 Milne, I, Bayer, M, Cardle, L, Shaw, P, Stephen, G, Wright, F, and Marshall, D (2010) Tablet – Next Generation Sequence Assembly Visualization. *Bioinformatics* **26**, 401-402

2 Hansen HM, Wiemels JL, Wrensch M, Wiencke JK. (2007) DNA quantification of whole genome amplified samples for genotyping on a multiplexed bead array platform. *Cancer Epidemiol Biomarkers Prev* **16** (8), 686-90.

3 http://bioinformatics.bc.edu/marthlab/Mosaik

4 http://www.ebi.ac.uk/~zerbino/velvet/

5 http://www.ebi.ac.uk/~zerbino/oases/

6 http://bioinformatics.bc.edu/marthlab/GigaBayes

7 http://bowtie-bio.sourceforge.net/index.shtml

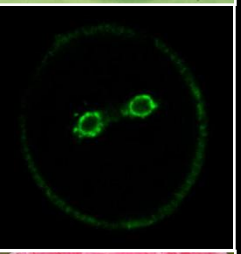
8 http://tophat.cbcb.umd.edu/manual.html

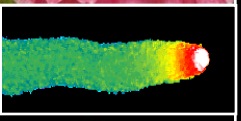
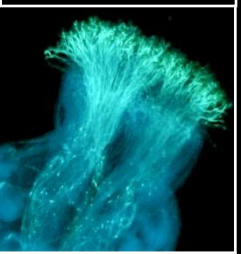
XXI International Congress on Sexual Plant Reproduction

Bristol, UK — 2-6 Aug 2010

http://www.sebiology.org/management/meetings/ICSPR/SexualPlantReproduction.html






Sessions include: Evolution of plant reproductive development, Meiosis, Gametophyte development, Flowers: form and function, Pollen-pistil interactions, Seed development, Apomixis

Confirmed speakers include:

Spencer Barrett (Canada)
Philip Becraft (USA)
Jorge Becker (Portugal)
Fred Berger (Singapore)
Zac Cande (USA)
Peter Crane (USA)
Hugh Dickinson (UK)
Pam Diggle (USA)
Thomas Dresselhaus (Germany)
James Doughty (UK)
José Feijó (Portugal)
Chris Franklin (UK)
Noni Franklin-Tong (UK)
Ned Friedman (USA)
Ueli Grossniklaus (Switzerland)
Phil Gilmartin (UK)
José Gutierrez-Marcos (UK)
Beverley Glover (UK)
Pat Heslop-Harrison (UK)
Tetsuya Higashiyama (Japan)
Simon Hiscock (UK)
Teh-hui Kao (USA)
Anna Koltunow (Australia)
Betty Lord (USA)
Bruce McClure (USA)
Christine Mezard (France)
Holger Puchta (Germany)
Tim Robbins (UK)
Paula Rudall (UK)
Scott Russell (USA)
Peter Schlögelhofer (Austria)
Rod Scott (UK)
Charlie Scutt (France)
Seiji Takayama (Japan)
Dave Twell (UK)
Peter van Dijk (Netherlands)
Zoe Wison (UK)
Weicai Yang (China)

Registration: from Aug 2009 (includes tea, coffee, lunches, receptions)
Early bird (before April 5th 2010): £220
Late (by 15th July 2010): £300
Student bursaries will be available
Places are limited so please register early

Call for Papers
We welcome offered oral talks (20 min), as well as poster presentations. Please submit your **abstract** and register early if you wish to be considered.

http://www.sebiology.org/management/meetings/ICSPR/SexualPlantReproduction.html

Organising committee: Simon Hiscock, Noni Franklin Tong, Hugh Dickinson, James Doughty, Chris Franklin, Pat Heslop-Harrison, Rod Scott, Tim Robbins, Dave Twell

25th New Phytologist/ Colston Research Society Symposium

Colonization of the terrestrial environment

University of Bristol, UK
21–22 September 2010

www.newphytologist.org

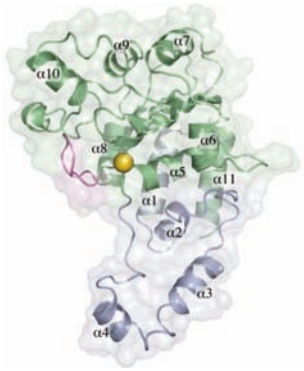
New Phytologist

UK Plant Science

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

Spotlight on the University of East Anglia

Plant research at the University of East Anglia is carried out on the university campus and at The Sainsbury Laboratory (TSL). The three groups at the UEA campus work on plant metabolism/hormones and gene silencing. One group addresses metabolic biochemistry and signalling function of inositol phosphates in plants with a special focus on the regulation of inositol hexakisphosphate (phytic acid) synthesis in model and crop plants. Another important area is the role of jasmonates in plant defence and growth and the third group works on many different aspects of gene silencing mediated by short RNAs. TSL was founded in 1989 as a joint venture between the Gatsby Charitable Foundation, the University of East Anglia, the BBSRC and the John Innes Foundation. TSL is dedicated to making fundamental discoveries about plants and how they interact with microbes and viruses. The laboratory has a worldwide reputation for its research in molecular plant pathology and genetics. With the formation of the TSL+ research group, the mission of the laboratory has expanded to encompass projects with a more direct applied aspect, in many cases building on discoveries that have arisen from the fundamental work in the lab.



Name Mark Banfield
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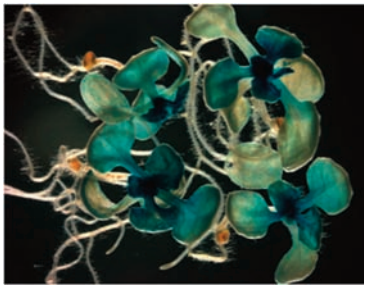
Research Area Molecular plant defence

Research Activities

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



Name Charles Brearley
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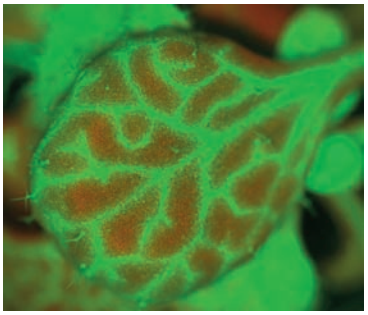
Research Area Plant metabolism of inositol phosphates and phytate

Research Activities

Research in the Brearley laboratory focuses on the metabolism of inositol phosphates and phytate. The world faces a phosphate crisis: the phosphate resources that Western agriculture applies to soil as fertilizer are running out. Most of the phosphate applied to soil is not available to crops. The small proportion of phosphate available to crops ends up in a chemically stable and enduring form, phytate. Each year more than 50 million metric tonnes of phytate are accumulated by plants globally, representing more than 60% of the elemental P sold world wide for use in mineral fertilizers. Phytate, mixed salts of inositol hexakisphosphate (InsP6), is the most abundant organic phosphate in the terrestrial environment and is derived from plants. The laboratory at UEA has long standing interest in the metabolic biochemistry of inositol phosphate metabolism in plants, with a special interest in phytic acid. The Brearley group, with collaborators, has solved the conundrum of how phytate accumulates in membrane-bound storage bodies of plants: it is deposited there by an ABC transporter protein. The group is also interested in the structural biology of inositol phosphate metabolism and how it informs understanding of the processes by which plants accumulate significant quantities of a compound that is a potent antinutrient, likely contributing to mineral deficiencies that affect millions of people worldwide. The research also addresses the signaling role of higher inositol phosphates in plants.

Spotlight on the University of East Anglia



Name Tamas Dalmay
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Research Area Short RNA mediated gene silencing

Research Activities

One of the most recently discovered layers of gene expression regulation involves very short (20-24 nucleotides) RNA molecules (sRNAs). The sRNA content of plants is very complex but the diverse types of sRNAs can be organised into two main groups: small interfering RNAs (siRNAs) and microRNAs (miRNAs). siRNAs are further grouped into several classes based on their biogenesis and mode of action. The Dalmay group investigates the role of different classes of sRNAs in several plant species, with a particular interest in tomato and fleshy fruit development. The group has employed high throughput sequencing to discover many new miRNAs and trans-acting siRNAs and is using transgenic approaches to explore the function of these. The group also investigates the formation of viral siRNAs during virus infection and the role of sRNAs in abiotic stresses.

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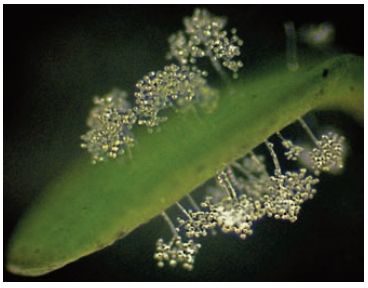
Research Area Plant defence

Research Activities

Pathogen effector molecules, that can either suppress host defences, or activate them if recognized by a Resistance (R) protein, provide profound insights into plant/pathogen interactions. The identification and analysis of bacterial effectors (and avirulence proteins) has led to major advances in understanding how phytopathogenic bacteria cause disease (or fail to do so). With advances in DNA sequencing and other genomics methods, potentially devastating crop pathogens such as rusts, powdery mildews and downy mildews are now “within range” for genomics-based approaches. This provides opportunities to reveal new biological mechanisms and to accelerate recruitment of new sources of host resistance variation for crop improvement.

The main goals of the Jones group are to investigate the effector complements of Arabidopsis downy mildew (*Hyaloperonospora arabidopsidis, [Hpa]*) and various races of white rust (*Albugo*) species that infect Arabidopsis, Brassica and other brassicaceae. This approach takes advantage of genomics and other tools for investigating Arabidopsis biology, of recent advances in Oomycete genomics, and an ERA-PG project coordinated by Jim Beynon. In January 2009 the laboratory was awarded European Research Council funding to expand the *Albugo* project. This funding will allow researchers to gain insight into the extent to which “non-host resistance” (NHR) in Arabidopsis to Brassica strains of *Albugo* is explained by effector-triggered immunity, or by failure of the effector complement to suppress disease. In addition, the group continue with studies on various aspects of plant/bacteria interaction, particularly the recognition of AvrRps4 by RPS4, and have identified a putative “guardee” that appears to be required for RPS4 function. Researchers are also investigating the roles of auxin and DELLA proteins in resistance and susceptibility. Jonathan recently obtained a BBSRC grant to use new genomics tools to accelerate cloning resistance genes from wild potato relatives for potato blight resistance.



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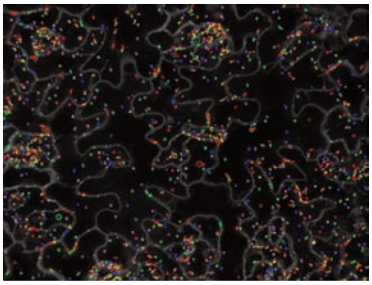
Research Area Plant defence

Research Activities

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

Spotlight on the University of East Anglia



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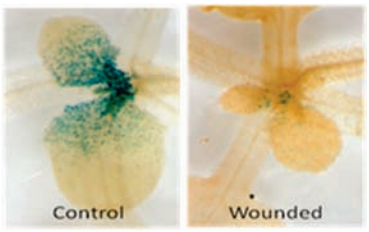
Research Area Plant immunity

Research Activities

Membrane compartmentalization and trafficking are pivotal for eukaryotic life. The group aims to better understand plant-microbe interactions at the cellular and subcellular level. Plant defence in response to pathogen infection is tightly associated with a global reprogramming of membrane trafficking pathways. For example, accommodation of haustoria, a globular feeding structure of fungi and oomycetes, requires substantial subcellular rearrangements. Although this hallmark of microbial attack has been described for many years, we are only now beginning to identify the molecular components involved in microbe-induced membrane trafficking. The Arabidopsis receptor FLS2 is responsible for the perception of bacterial flagellin (flg22), a so-called pathogen-associated molecular pattern (PAMP), which triggers a first line of active plant defences. In non-challenged plants, FLS2 localizes to the plasma membrane, but upon flg22 activation it is internalized. The Robatzek laboratory studies the components of FLS2 endocytosis to shed light on the mechanisms of PAMP-triggered immunity. A combination of genetic screening, high throughput confocal laser microscopy and custom automated image processing are applied to identify mutants that display altered endosomal trafficking. Designated *fel* mutants, they provide a unique tool to determine the genetic principles of endocytic trafficking and to zoom into pathogen-induced dynamic changes of membrane compartmentalization.



Name John Turner
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Website http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=306
Research Area Plant hormones

Research Activities

Research in the Turner laboratory focuses on the mechanisms used by plants to reduce the effects of environmental stress, in particular on the broad-spectrum defences used by plants to deter pests and pathogens. Current work in the group builds on research performed by the Turner group over many years, including the discovery of the key regulators of jasmonate-induced defences. Plant jasmonates were identified in the 1960s as the compounds responsible for the fragrant smell of flowers. The discovery in the Turner laboratory that *COI1* an Arabidopsis gene required for response to the growth inhibitory phytotoxin, coronatine, was also required for growth inhibition by jasmonate, initiated the laboratory's interest in jasmonates. The very same gene was later identified as the jasmonate receptor. Members of the Turner laboratory have worked on the characterization of the functions of endogenous jasmonates in plants, revealing a range of other essential functions for jasmonate in plant including defence and gametophyte development. Recently, they have shown that jasmonate signaling is also recruited for the control of elongation growth in plants growing in the shade of neighbours, a response involving phytochrome signalling. Current work in the Turner laboratory is examining the phytochrome- and jasmonate-regulated trade-off between commitment for defence and commitment for growth. The Turner group endeavour to use the knowledge gained from this work to enhance crop productivity.

Spotlight on the University of East Anglia

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Research Area Crop disease resistance

Research Activities

The group results from cooperation between the Two Blades Foundation and the Sainsbury Laboratory, and aims to solve crop disease problems using state-of-the-art technologies. The initial focus of the group is on generating resistance to wheat stem rust caused by newly appearing super-virulent strains of the pathogen *Puccinia graminis f. sp. tritici*. The group's current focus is on identifying major disease resistance (R) genes from wild species related to important crops. They isolate many R genes, which is now possible using a combination of classical genetics and next-generation sequencing methods, and deploy them in combinations at single transgenic loci. Such multiple R gene cassettes should provide a superior solution for breeding durable disease resistance.

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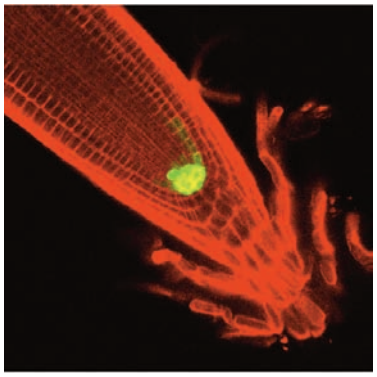
Research Area Receptor kinase-mediated innate immunity

Research Activities

Higher eukaryotes can recognize invading microorganisms by detecting conserved molecules referred to as PAMPs (pathogen-associated molecular patterns) by pattern recognition receptors (PRRs). The mechanisms underlying this innate immune recognition and subsequent signalling have been extensively studied over the last decade in insects and mammals, but much remains to be discovered in plants. Arabidopsis thaliana provides an excellent model system to study PAMP-triggered immunity (PTI), and detects a variety of PAMPs, including conserved domains of bacterial flagellin and EF-Tu, or their peptide surrogates, flg22 and elf18, respectively. The significance of PAMP-triggered immunity (PTI) against bacteria is demonstrated by the fact that successful bacterial pathogens have evolved to avoid PAMP recognition or to suppress PTI-signalling by secreting effectors into the host cells. Although many resistance (R) proteins have been identified and many genetic or biochemical approaches to dissecting effector-triggered immunity (ETI) initiated, there is only limited knowledge about plant PRRs and PRR signal transduction. Indeed, in-depth understanding of PTI is required, not only because of its intrinsic interest, but because many of the pathogen effector targets will be PTI components. Furthermore, there are more PRRs to discover in order to fully understand the molecular interplay between host and pathogen that directs the outcome of infection. The Zipfel laboratory is using a combination of forward- and reverse-genetics, as well as biochemical and proteomic approaches to understand how PAMP is perceived, what signalling events it triggers, and what contribution PAMP perception makes to plant immunity.

Spotlight on the University of Edinburgh

The Institute of Molecular Plant Sciences (IMPS) houses several principal investigators (PIs), post-doctoral researchers and PhD students, and provides a stimulating environment for studies on a broad range of plant-based topics. IMPS is one of few plant-based research and teaching institutes within the UK and continues to offer a dedicated undergraduate honours programme in the Plant Sciences. Postgraduate research is supported by state-of-the-art facilities, and an IMPS research forum facilitates inter-laboratory collaborations. IMPS has close links with the Centre for Systems Biology at Edinburgh (CSBE http://csbe.bio.ed.ac.uk/) and the Royal Botanic Gardens, Edinburgh (RBGE http://www.rbge.org.uk/), providing further breadth to our research base. In addition, researchers within IMPS have strong links with the Scottish Crop Research Institute (SCRI http://www.scri.ac.uk/) and the newly formed Scottish Universities Life Sciences Alliance (SULSA http://www.sulsa.ac.uk/). Research within IMPS covers a broad range of interests, including: developmental biology, molecular plant pathology, speciation, circadian clocks, bioimaging, biochemistry and cell biology.



Name Peter Doerner
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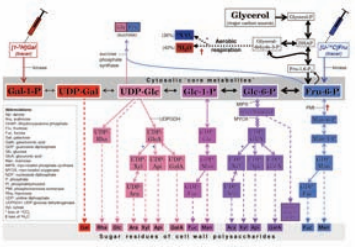
Research Area Plant growth control and abiotic stress tolerance

Research Activities

To ensure global food security, it will be critical to improve the performance of crops when they are exposed to abiotic stress. The team in Peter Doerner's lab is focusing on two key aspects: (i) the mechanisms controlling cell growth and division in 'normal' and stress conditions; and (ii) the signalling pathways and growth responses involved in controlling cellular and whole plant responses (e.g. root system architecture) during phosphate limitation. Recent work on cell division control during abiotic stress has identified a novel mechanism for growth arrest in Arabidopsis, involving a protein kinase cascade. Work is underway to establish the molecular details of this pathway, such that this knowledge can be used to improve abiotic stress tolerance in crop plants in the future. Work is also underway to identify the proteins involved in perceiving phosphate and orchestrating cellular responses to perceived levels of this critical nutrient. A rough framework of biochemical functions involved in phosphate sensing and signalling has been established, and is now being followed up by targeted efforts to identify key regulators. In a separate approach, forward genetics has been successful to identify genes involved in controlling root growth patterns at different levels of phosphate abundance, opening up opportunities to fine-tune growth responses to levels of phosphate availability.



Name Stephen Fry
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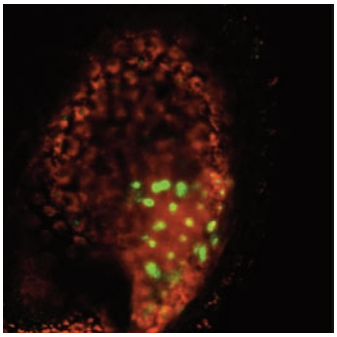
Research Area Biochemistry and physiology of plant cell walls

Research Activities

The Edinburgh Cell Wall Group led by Stephen Fry studies the primary cell wall and apoplast in plants. The main goal is to track the behaviour of cell wall components in living cells. The work emphasises the distinction between enzyme activity (measurable *in vitro*) and the more biologically relevant enzyme action (observed *in vivo*). Work carried out by Stephen Fry's laboratory shows that cell walls are a rich source of novel enzymatic activities and organic structures. Specific areas of interest currently include: 1. Wall loosening during cell expansion and fruit softening. The team discovered xyloglucan endotransglucosylase (XET), which breaks and reforms glycosidic bonds in the backbone of xyloglucan, and is studying XET's role in wall-restructuring. The group is also very interested in non-enzymatic scission of polysaccharides in the walls of living cells by naturally produced hydroxyl radicals. 2. Wall assembly and cross-linking. Studies related to XET recently led to the discovery of novel wall-assembling endotransglycosylases, for example mixed-linkage-glucan:xyloglucan endotransglucosylase (MXE; a novel 'heterotransglycosylase' apparently confined to Equisetum), whose reaction-products are being traced *in vivo*. The lab is also documenting the cross-linking role of oxidative phenolic coupling (ferulate in polysaccharides and tyrosine in glycoproteins) i*n vivo*. 3. Vitamin C metabolism in plants, including the discovery of novel ascorbate metabolites (e.g. 4-O-oxalyl-threonate). 4. Sugar-nucleotide metabolism involved in wall polysaccharide biosynthesis. The lab devised a valuable dual-radiolabelling ($^{3}H/^{14}C$) protocol to determine which of several competing pathways predominate *in vivo*. It was shown that the UDP-glucose oxidation pathway greatly exceeds any contribution of the inositol pathway. 5. Documenting the evolution of primary cell walls in land plants and their charophytic algal relatives.

Spotlight on the University of Edinburgh



Name Justin Goodrich
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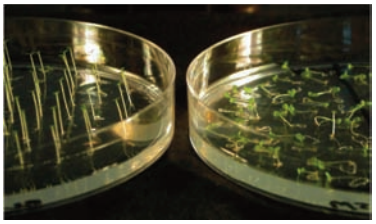
Research Area Epigenetic control of seed and flower development

Research Activities

The Polycomb-group (Pc-G) genes are key regulators of cell fate decisions in plants and animals. In plants, they control many agronomically important traits including flowering time, the response to vernalization, and the proliferation of the endosperm tissue in seed. They act by modifying chromatin so that their target genes become transcriptionally inactivated. A major advance in unravelling their mechanism has been the demonstration that transcriptional inactivation by Polycomb gene products is achieved in part through the methylation of specific residues of histone proteins, the proteins that package DNA. The Goodrich group are profiling where these modifications occur in the genome as a way of identifying Polycomb target genes, many of which are developmentally important. In collaboration with the Jacobsen group (USA), the Goodrich group have produced the first of such profiles for Arabidopsis seedlings. They are currently profiling the changes that occur during the switch to flowering, as a way to identify genes controlling the commitment to flowering. A genetic screen to identify modifiers of *polycomb* mutant phenotypes has also been undertaken to help identify novel Polycomb genes and targets.

One gene identified in this screen is a novel transcription factor that is expressed in endosperm but acts non-autonomously to control development of the epidermal layer of the embryo. The Goodrich group is collaborating with Gwyneth Ingram's laboratory to characterise the targets of this gene and their role in endosperm and embryo development.



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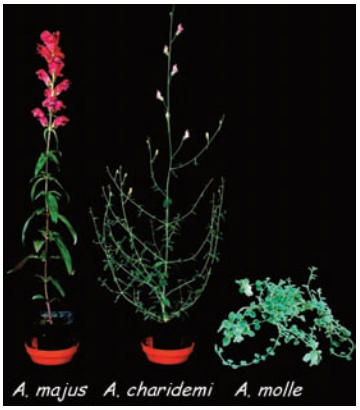
Research Area Light and temperature signal transduction

Research Activities

In spite of the predicted global changes in climate, very little is known of how physiological temperature changes influence any complex molecular signalling network. The Halliday laboratory is combining molecular, genetic and theoretical approaches to address this knowledge deficit aiming to: 1. Establish how temperature alters the molecular circuitry of the light and circadian network in the model plant *Arabidopsis thaliana.* 2. Understand how environmental light and temperature signals control growth, carbon assimilation and photosynthetic rate.

Temperature changes affect the rate of almost all biochemical processes, yet some biological functions are maintained robustly across a wide range of physiological temperatures, while others sensitively respond to temperature. Using computational modelling and mathematical analysis, the group seek to understand the principles and molecular mechanisms that underlie temperature buffering or sensitivity in biological networks.



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Research Area Control of organ growth, size and shape, and evolution of plant form

Research Activities

Research in Andrew Hudson's laboratory examines the genetic basis for natural variation in plant form and how it relates to fitness. Part of the work uses a selection of Antirrhinum (snapdragon) species, which are morphologically diverse and adapted to different, often extreme environments. Their ability to form fertile hybrids with the genetic model species *A. majus* has allowed the identification of the genes that underlie their differences in characters, including leaf and petal sizes and shapes, and suggests how these characters might evolve. The team is also investigating the genetic and ecological basis for high levels of phenotypic diversity in local populations of *Arabidopsis thaliana*, which maintain high levels of phenotypic diversity, and the evolution of a regulatory mechanism that controls both leaf development and defence.

Spotlight on the University of Edinburgh

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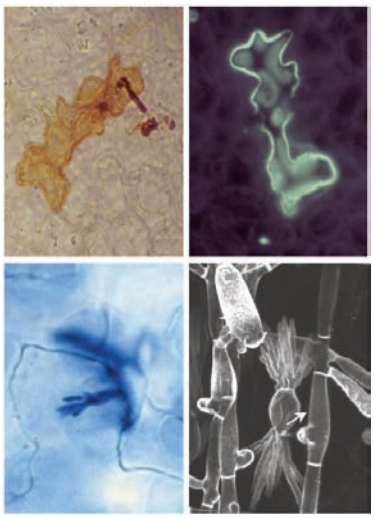
Research Area Evolutionary development and speciation

Research Activities

Catherine's group investigates the genetic basis of diversity in plant form. They use Begonia as a model system to understand how tropical diversity has evolved and is maintained. Begonia is one of the ten largest genera of angiosperms with at least 1,500 species found throughout the wet tropics. Vegetatively the species vary considerably, but reproductive barriers are weak allowing genetic analysis of species-level differences. A genetic map is being produced to allow QTL analysis of morphology, ecophysiology and reproductive traits. This will identify how many genes control the traits that differentiate species, giving an indication of how easily change can occur. It will also allow Kidner's team to test whether key developmental genes are involved in dramatic changes of form and whether parallel morphological changes involve the same genes. The transcriptomes of two closely related species have been sequenced and soon a third, more distantly related species will be added to the dataset. This will identify diversifying and conserved gene families as well as providing genetic markers for the map and for population biology. Sequencing of the complete chloroplast genomes of 16 species provided a robust phylogenetic backbone and will identify variable regions to allow construction of phylogentic trees for very closely related species, enabling characterisation of recent radiations. Fieldwork conducted in Mexico has increased the Royal Botanic Garden Edinburgh's collections of rare, endemic species and allowed study of hybrid zones where new roads bring previously isolated species into contact.



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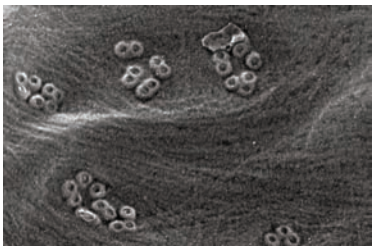
Research Area Plant disease and resistance

Research Activities

Plant diseases are a significant constraint on agricultural production. Consequently, effective disease resistance is an extremely desirable crop input trait. Plants have evolved a plethora of sophisticated defence mechanisms to protect themselves against attempted pathogen ingress. The synthesis of nitric oxide (NO) and reactive oxygen intermediates (ROIs) is a conspicuous feature of this complex defence response. These key small molecules orchestrate immune signalling networks and gene expression cascades and drive the programmed "execution" of plant cells at sites of attempted pathogen infection. Work in the Loake laboratory has introduced a new level of understanding to these processes by showing that S-nitrosylation, the addition of a NO moiety to a reactive cysteine thiol to form an S-nitrosothiol, is a central regulator of multiple modes of plant disease resistance. Building on these findings, the Loake laboratory is now employing a variety of complementary strategies to further explore the pivotal role of S-nitrosylation in disease resistance. Other post-translational modifications of interest include SUMOylation and ubiquitination, processes where peptide modifiers are added to target proteins to either modulate their cellular function(s) or mark them for degradation, respectively. In collaboration with industry, the Loake group is also exploring the regulation of defence-related biochemical pathways that synthesise clinically important plant natural products.

Spotlight on the University of Edinburgh



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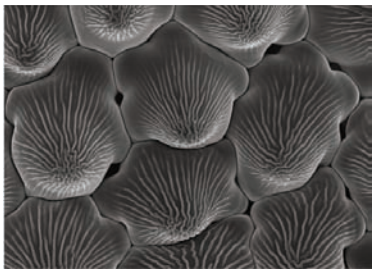
Research Area Plant cell biology

Research Activities

Research in the Oparka laboratory examines the structure/function relationships of plasmodesmata (PD) and the basic mechanisms by which macromolecules pass between higher plant cells. Recent work has focussed on the formation of primary and secondary PD, and in the development of novel approaches for studying PD dynamics non-invasively.

The group also researches the mechanisms by which plant-viral genomes pass between cells, with emphasis on the movement of the filamentous viruses potato virus X (PVX) and tobacco mosaic virus (TMV). Specific emphasis is placed on the role of viral movement proteins in facilitating the passage of viral genomes through PD. Additional interests include studies of the movement of non-cell autonomous plant proteins, and the isolation of novel protein components from PD using proteomics and viral-vector based technologies. The group also studies the long-distance movement of macromolecules in plants with emphasis on the nature and regulation of phloem unloading in sink organs such as developing roots and storage organs. The Oparka group is also interested in the biotechnological uses of viral vectors as protein delivery vehicles in plants. Recently they have explored a wide range of novel imaging approaches, based on fluorescent reporter technologies, to track RNA and protein movement within living plant cells. These include the development of an *in vivo* reporter of viral RNA based on the RNA-binding protein Pumilio, and the use of novel 'super-resolution' microscopy approaches for imaging viral movement complexes.



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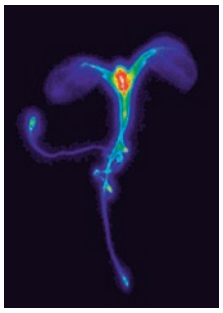
Research Area Plant epidermis specification and development

Research Activities

The plant epidermis is a highly specialized, multifunctional sheet of cells that covers all aerial plant surfaces. It fulfils critical physiological and protective roles as well as conferring mechanical strength to non-lignified plant tissues by harnessing turgor pressure. The epidermis may also play key roles in the developmental regulation of plant growth. Part of the research in Gwyneth Ingram's group aims to understand how epidermal identity is acquired during early embryogenesis, by dissecting the genetic and biochemical links between transcription factors necessary for epidermal specification, and signalling molecules capable of perceiving extracellular signals and/or positional information. The potential role of the endosperm (the zygotic tissue which surrounds the developing embryo during seed development) in providing developmental signals is also being investigated. Interestingly, epidermal specification in the embryo is thought to be a one-off event. Subsequent maintenance of epidermal identity, which is another focus of the laboratory, necessitates continuous cell-cell signalling within the epidermal cell layer; implying a dependence upon epidermal continuity/cell adhesion. Thus, in addition to identifying some of the factors involved in intra-epidermal signalling pathways, recent research from the group has also concentrated on understanding how epidermal integrity is maintained during development, and in particular whether mechanical signals could play a role in this process.

Spotlight on the University of Edinburgh



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Research Area Systems biology and the circadian clock

Research Activities

The circadian clock generates 24-hour rhythms in many biological processes, including auxin and ethylene synthesis, photosynthetic capacity, organ elongation rates, and responses to abiotic factors such as day length and temperature. The Millar group takes a multi-disciplinary approach to understand the clock and its importance in timing plant biology. Group members have a broad range of backgrounds, from high-performance computing to experimental biology. The combination of mathematical modelling and experimental approaches has been fruitful in understanding the gene network that generates the rhythms, centred on transcription factors LHY and CCA, and the Pseudo-Response Regulator TOC1 and its homologues in the PRR family. Real-time imaging systems are used to monitor rhythmic LUC reporter gene expression in plants, together with genetic, pharmacological and environmental manipulations. The impact of clock regulation upon downstream pathways is of growing interest, following transcriptomic and proteomic studies. Rhythmic control of flowering pathways via CO has been modelled. Metabolic functions including starch metabolism are of growing interest. The clock gene networks of all organisms include interlocking negative feedback loops, so comparative experiments are currently underway in Arabidopsis and the unicellular alga *Ostreococcus tauri*, which might reveal the common (even ancestral) clock components. Andrew directs the Centre for Systems Biology at Edinburgh (CSBE), which uses this work as one of its test projects to develop informatics infrastructure that will help to streamline systems approaches. Andrew has also been engaged with research community organisations, including GARNet and SULSA.

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Research Area Plant evolution

Research Activities

Richard Milne's interests lie in various areas of plant evolution, with particular focuses on hybridisation and biogeography. His main study group is *Rhododendron*, but he has dabbled across a wide taxonomic range, from liverworts to ferns and gymnosperms, and from Arctic-alpines to pantropical rainforest tree families. He is particularly interested in the population structure of plant hybrid zones, particularly situations where large numbers of fertile first generation (F1) hybrids are present but little or no backcrossing to the parent species occurs. Although not the first to detect this pattern in hybrid zones, he was first to realise its significance in maintaining species barriers, and has detected this pattern several times in *Rhododendron*.

Regarding plant biogeography, Richard recently led research showing that the 200 Chinese and Himalayan large-leaved Rhododendrons (members of subgenus *Hymenanthes*) are a recent offshoot from an older group spread across the northern Hemisphere, and that hybridisation might have been involved in their evolution. Much of his recent work has been through collaborations with research groups in Kunming and Lanzhou (China), and one such collaboration has examined the movement of Junipers between continents over the past 80 million years. It was found that the genus had reached America during distinct periods, and was much more dispersable than the related *Cupressus*, probably because *Juniperus* has edible berry-like fruits. Other collaborative work has examined the distribution of various taxa across western China, and the effect that the uplift of the Qinghai-Tibet plateau and subsequent glacial maxima have had upon biogeography, diversification and ploidy levels.

Spotlight on the University of Exeter

The Plant Science group at Exeter University is based at the Streatham Campus in Exeter. The group benefits from a new glasshouse complex, completed in early 2010, and extensive controlled environment rooms and chambers. Recent University investment has provided confocal, transmission and scanning electron microscopes, next generation sequencing and mass spectrometry facilities which are extensively used by the plant science group. Research projects based on *Arabidopsis thaliana* encompass plant-microorganism interactions, responses to oxidative and other abiotic stresses, calcium signalling and metabolism. A number of these projects are concerned with natural variation and performance under field conditions. Other plant-microoganism interaction research includes the pathogenicity mechanisms of rice blast fungus (*Magnaporthe grisea*) and plant growth promotion by rhizosphere fungi. Members of the group collaborate with mathematicians within the Exeter Systems Biology Centre (http://www.exeter.ac.uk/research/excellence/keythemes/systemsbiology/) and with the nearby Plymouth Marine Laboratory and Marine Biological Association on algal metabolism and molecular biology. A new BBSRC-funded Food Security and Sustainable Agriculture MSc course will include input from the nearby Rothamsted Research North Wyke site and plant scientists at Exter are actively involved in a new MSc in Systems Biology.

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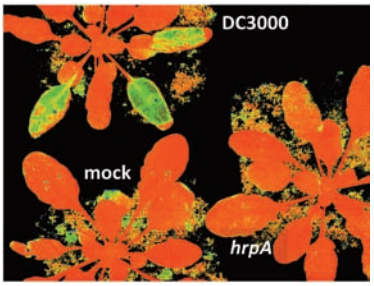
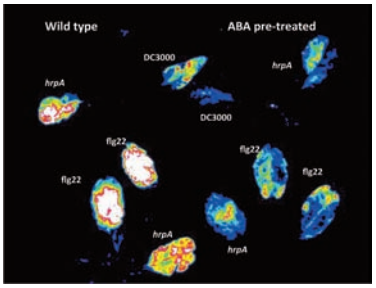
Research Area Pollination systems

Research Activities

Pollination systems provide important ecosystem services that support crop yield and sustain the biodiversity of wild plants by ensuring fertilization of seeds. James Cresswell's research programme aims to contribute to the general theory of pollination systems to provide a framework for explanation and prediction from a mechanistic basis. The Cresswell group studies pollination at several scales from the individual flower to the whole landscape scale, with a focus on modelling of gene flow. In addition to its fundamental value, this theory can be applied to confinement problems in GM crops and to the conservation of rare plant species. The Cresswell laboratory studies insect-pollinated (e.g. oilseed rape), wind-pollinated (conifers and grasses) and largely selfing systems (Arabidopsis). Current interests include the impacts of agrochemicals on pollination through unintended effects on pollinating insects. Besides using the conventional tools of pollination biology, the group develops interdisciplinary collaborations with specialists in animal behaviour, engineering, computer science and mathematics.





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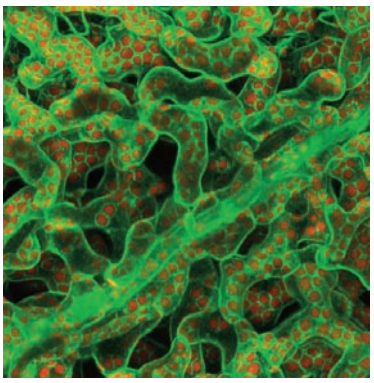
Research Area Molecular plant pathology

Research Activities

Pre- and post-harvest crop losses continue to have profound consequences economically and environmentally. Any integrated plan to improve food security needs to address novel approaches to crop protection. Research in the Grant laboratory uses multidisciplinary approaches to understand the dynamics and molecular mechanisms underpinning plant defence responses. The Grant group uses the pathosystem *Arabidopsis-Pseudomonas* to examine the three core, inter-dependent, host defense responses: plant innate immunity, suppression of plant defences and signalling events underpinning systemic immunity. The group utilises a combination of real time imaging, unbiased transcriptomics and metabolomics approaches to infer and model signalling networks involved in plant defence. To date these approaches have identified unexpected roles for phytohormones in elaborating defence responses. Work conducted by the Grant group has identified jasmonate and auxin signalling pathways as central to establishment of systemic immunity and they have shown that virulent bacteria hijack the host's abscisic acid signalling networks to antagonise salicylic acid-based defence responses. The group are currently studying the molecular basis of these responses. In the longer term they will use this knowledge to develop biotechnological approaches to (i) attenuate pathogen virulence strategies and (ii) establish robust combinations of natural products that can provide broad spectrum cross-protection to the agricultural sector. In collaboration with the Universities of Warwick and Essex, the laboratory is part of the BBSRC SABR funded PRESTA project that investigates how plants integrate environmental stress responses. This research aims to develop validated network models that predict the plants response to multiple stresses. The ultimate objective of this research is to translate these findings to inform on crop evaluation and trait association studies.

Spotlight on the University of Exeter



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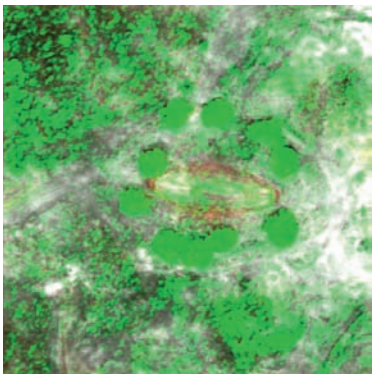
Research Area Plant cell signalling and algal biofuels

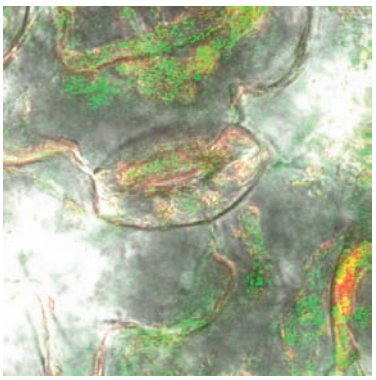
Research Activities

Work in John Love's group employs a multidisciplinary combination of molecular biology, cellular imaging, biochemistry and bioinformatics to investigate two main themes: the functional integration of molecular and cellular signalling pathways during photoperiodism in *A. thaliana* and the production of biofuels in planktonic algae and microbes.

Research carried out in the Love laboratory utilizes Arabidopsis plants that are impaired in circadian Ca^{2+} signalling as well as mutant plants to investigate the role of Ca^{2+}-mediated signal transduction. The role of calmodulin in the photoperiodic control of flowering is also currently being investigated. In addition, the laboratory is involved in several cross-disciplinary collaborations, including with Nicholas Smirnoff (metabolic signalling) and with other academics to develop and apply recombinant technologies to image and quantify metabolites and cellular signaling components (in particular ascorbate and Ca^{2+}). In collaboration with Shell Global Solutions, the group investigates the molecular and cell biology of hydrocarbon production in algae.

Understanding the seasonality of flowering is critical for sustainable agriculture in a changing climate. Likewise, the generation of new biofuels is essential to the future energy security of the UK. The laboratory's innovative approach to these problems is a prime example of fundamental science that has the potential to impact practical applications, helping to improve crop management practices and energy production to the benefit of UK agriculture, industry, the consumer and the environment.





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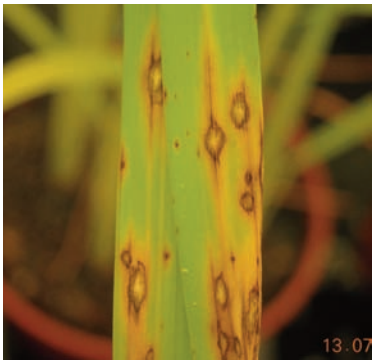
Research Area Plant and algal metabolism. Plant stress responses

Research Activities

The focus of Nick Smirnoff's laboratory is on the functions of ascorbate (vitamin C), plant stress responses and algal metabolism. Ascorbate is an antioxidant with a role in photoprotection of photosynthesis. It is also a cofactor for 2-oxoglutarate-dependent dioxygenases. Previously, the Smirnoff group has identified the biosynthetic pathway of ascorbate and demonstrated it to be essential for growth. Currently, research using *Arabidopsis thaliana* is focused on determining how ascorbate synthesis is linked to light intensity and on the function of the cell wall enzyme ascorbate oxidase. In the area of stress responses, transcriptional networks involved in the response of Arabidopsis to biotic and abiotic stresses are being investigated in a consortium with Murray Grant at Exeter and colleagues at Warwick and Essex Universities. Metabolite profiling and proteomics are being used as tools to unravel the metabolic functions of ascorbate and to link transcriptional responses to stress with metabolic responses. Research on algal metabolism currently includes calcification in the coccolithophore *Emiliania huxleyi* and lipid metabolism in cyanobacteria. *E. huxleyi* is a marine bloom-forming microalga that is covered with calcium carbonate plates (coccoliths). In a collaborative project with the Marine Biological Association at Plymouth, the function and metabolic consequences of calcification are being investigated by comparing strains with and without coccoliths. The pathways and control of fatty acid metabolism are being investigated in cyanobacteria.

Spotlight on the University of Exeter



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Research Area Molecular basis of plant disease

Research Activities

Professor Nick Talbot is leading a research team attempting to conquer the rice blast disease, which each year kills enough rice to feed 60 million people. Research at Exeter is focused on investigating the biology of the rice blast fungus *Magnaporthe oryzae* and understanding how it uses specialised infection structures called appressoria to breach the tough outer cuticle of rice leaves to gain entry to rice tissue. The research group uses a combination of reverse genetics, cell biology, biochemistry and next generation sequencing approaches to define the genetic control points regulating appressorium-mediated plant infection and the underlying mechanism by which appressoria function. They are also studying how the fungus invades living rice cells and suppresses plant defence. Knowledge gained about this fungus can then be applied to controlling a disease of critical importance to the global food supply.

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Research Area Plant-fungal interactions

Research Activities

Novel approaches geared towards simultaneously increasing plant growth and enhancing host defences against a range of plant parasites provide enormous potential to enhance global food security in an environmentally sustainable way. Research in the Thornton group is focussed on the growth promotion and protection of plants by the soil dwelling biocontrol fungus *Trichoderma hamatum*. Work in the lab is specifically aimed at determining the molecular basis of the growth promotion phenomenon. Research conducted by the Thornton group has shown that by genetically manipulating the fungus to alter hyphal cell wall permeability, further significant improvements in plant growth promotion can be achieved. A mutation in the *T. hamatum* hexosaminidase (exo-chitinase) gene results in incorrect chitin deposition at the hyphal tip and an increase in secretory potential of the fungus. This mutant displays enhanced plant growth promotion activity that is linked to its ability to hyper-secrete water-soluble plant growth stimulants. A combination of NMR and ESI-MS approaches has revealed a profound change in the metabolite profile of the mutant compared to the wild-type strain. Complementary DIGE studies have identified a number of enzymes involved in secondary metabolite biosynthesis, which have altered expression in the mutant strain, and mutants in these can markedly alter growth promotion activities. Current work aims to identify the bioactives that stimulate plant growth. The ability to identify plant growth stimulants derived from a ubiquitous group of beneficial soil fungi could have important implications for the development of natural products that enhance crop productivity. Importantly, *T. hamatum* stimulates growth on a wide range of crop plants and the model plant *Arabidopsis thaliana* displays natural variation in growth promotion. Thus current research in the Thornton laboratory is using this model organism to unravel the genetic basis of the host response to *Trichoderma*.

A Decline in Plant Biology?

written by Jeremy Prichard, University of Birmingham, UK

As plant biologists we are arguably victims of our own success; the model plant Arabidopsis is sequenced and increasing numbers of crop plants have similar rapidly developing resources. There is an expectation that, with a burgeoning global population, food supply will require plants more than ever before, governments argue for sustainability and security of our agriculture[1]. The BBSRC strategic plan for 2010-15 has food security as research priority one[2]. Yet despite this clear evidence of the importance of plants, our green friends are not receiving their rightful recognition from the public and within the education system, particularly in schools. Within a strong University department or research institute the poor perception of plants might not be seen as a problem. Yet arguably a negative or passive view of plant science in the wider community is a ticking time bomb under our discipline. The negative aspects can work at a number of levels; while some labs may still able to attract sufficient high quality PhD students to maintain a momentum, this is not true everywhere. A shortage of personnel will inevitably have a knock-on effect on post-doctoral research and therefore the whole plant research agenda. Outside the ivory towers of the research community a lack of appreciation of the diversity of the plant science agenda will negatively affect public perception, science policy and ultimately research funding. In this belt tightening time if the public do not value plant science, then neither will the politicians and so there will be a negative effect on research resources.

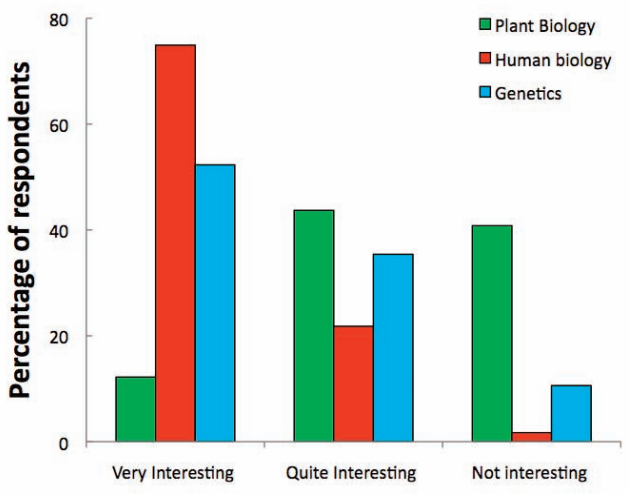

Figure 1: Perception of different subject areas in the Biology 'A' level curriculum by participating students. Data is recalculated from the 2003 CEI report for the Wellcome trust report on 'A Level Biology, Higher Education and Research in the Biological Sciences'

Is it such a difficult problem to present plants as interesting? Think of the physicists. They have spent millions of tax payers' money on the Hadron collider, a machine that does not have a direct effect on the day to day lives of the general public, yet they are able to project their ideas so well that the public and the international media are interested and tune in to a range of science communication events. Why then can we not generate the same enthusiasm for the things that we eat, wear, give us air to breathe, clean the environment, produce new drugs, grow in the deserts and give us day to day pleasure?

Is Plant Science really declining? Perception in schools

The poor perception of plants is a deeply engrained problem. Once it is in the general consciousness that plants are not as interesting as (say) animals the situation becomes reinforced by the education system. If teachers do not think plants are interesting then why should their pupils? The 2003 Wellcome trust report on 'A Level Biology, Higher Education and Research in the Biological Sciences' [3] provides some clear and depressing evidence of the school system as one of the causal factors. In a survey of student perception of their different subject areas within biology Plant Biology was seen as largely 'quite interesting' or 'not interesting' with only 12.2% of pupils saying they thought that plant biology was 'very interesting' (Figure 1). In a qualitatively different pattern human biology and to a lesser extent genetics were seen as 'very interesting' – for example a massive 74.9% thought that human biology was 'very interesting'.

So if pupils don't like plant sciences why is this? The obvious candidates are teachers and there is also evidence for this in the Wellcome trust report. If teachers present plants as mundane then there is little pressure for the curriculum to adapt and incorporate the increasingly exciting plant science. When analysing pupils and teachers interest in the component subject areas of biology there is a clear correlation between the teacher's interest and that of the pupils (figure 2).

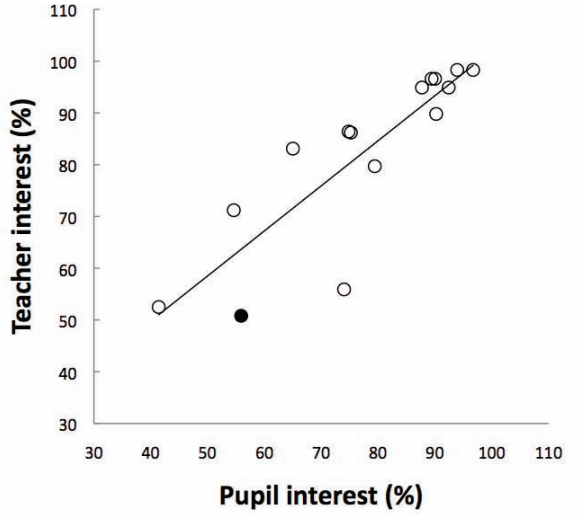

Figure 2: A direct relationship between teacher interest in A level subjects biology and that of the pupils. The filled circle is Plant Biology. Data is recalculated from the 2003 CEI report for the Wellcome trust report on 'A Level Biology, Higher Education and Research in the Biological Sciences'

Thus the teacher has a massive influence – why then are the teachers not engaged? It is a difficult issue to untangle cause and effect but a contributing factor is the vicious circle of the teacher's own education – if they are not engaged in plants during their studies then how

A Decline in Plant Biology?

can they be expected to enthuse the students? It could be argued that it is a failing of the plant community – but that would be unfair. In enthusing anyone about anything context is central (this is why the success of the Hadron Collider publicity is so amazing!). Human biology is easy to enthuse students about since they are (usually!) human. In the 'A' level curriculum and beyond their own experience of disease and the vocational career paths to medicine strongly and implicitly justify these areas of Biology. Media such as TV largely focus on medicine and health as these can immediately be seen to have a clear purpose. While there are countless gardening and farming programmes these do not seem to link clearly to the hard science that underpins the plant theme, indeed for areas such as plant molecular biology there may be hard opposition. Animal programmes are immediately attractive as the animals can be seen to do something; even the great David Attenbourgh will present plants with an animal close by! This disconnection between plants and the underlying science has probably contributed to the development of an 'A' level curriculum in which plant biology is reduced to measuring the weight change in plant tissue immersed in different sucrose solutions while animal biology gets disease, health, the circulation systems and exciting molecular biology.

Is there a wider need for Plant Biology?

Is it a problem that Plant Biology is not recognised as relevant and important? Probably yes it is. While a recent report from the Food Research Partnership Skills Sub-Group (2010)[4] specifically focussing on the agri food sector concluded that; 'The supply of high level skills in the sector is at least sufficient to satisfy current demand, other surveys highlight a decline in plant and agricultural biology skills. The report from the BBSRC Bioscience Skills and Careers Strategy Panel (2009)[5] identified a shortage of skills in Plant Physiology, Plant Breeding and Plant Pathology. Reasons cited for these lack of skills included poor training, poor perception in schools and absence of a clear career pathway in these areas.

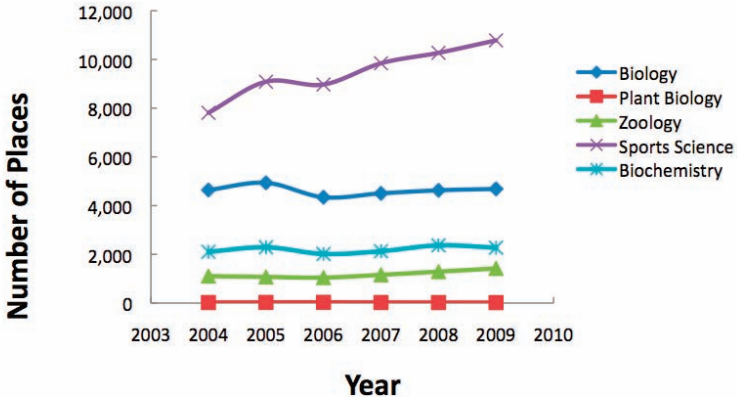

Figure 3: Number of university places by subject highlighting the small number of places available to study Plant Biology. These figures are almost exactly paralleled by the relative numbers of applicants. Data is from the UCAS web site[6].

Universities now offer fewer explicitly plant-based courses than a decade ago. This is not surprising given the negative perception of plant science in schools and the reduction in the recruiting base, all of which has resulted in a relatively small number of places now on offer to study plants in the UK (Figure 3).

At the university level the problem is not perhaps as severe as the data in Figure 3 might suggest. While many plant biology degrees have gone, the biology degrees will incorporate plant biology as a major part of the syllabus. This may be to 'hide' the potential negative recruiting effect of Plant Biology, but on the positive side it is also because biology itself has changed and is now an interdisciplinary and integrated subject. Plant Biology takes a central place here for many of the political and strategic reasons outlined earlier. Presenting Plant Sciences as part of the new modern cannon of the Biosciences is one approach to rectifying the perception of plant science outside the research community. Given the rapid advances in plant biology research areas and approaches it is not surprising that the first taste of modern plant biology is at University and not at school. Despite the lack of explicit plant biology many student are pleasantly surprised by plant biology and what it can offer as evidenced by the high take up and reception of plant biology in second and final year optional modules. First year tutors now make great efforts to enthuse students about plant biology, effectively ignoring the dearth of Plant Biology at A level and starting again. While such approaches may currently maintain a supply of appropriately trained and informed graduates there is no guarantee that this back door approach will continue. In addition such a strategy does not address the lack of enthusiasm for our subject in schools and the resulting sustained decrease in the positive perception of plants in the wider community and potential negative effects on science policy.

How can we promote Plant Science?

Active knowledge impact programmes are needed to promote plant science, that is to say communicating our discipline to a wider audience. While such activity has not been a major part of research programmes in the UK (although it has been important in some US research funding schemes) recent discussions about the nature of funding have pushed knowledge impact further up the agenda. Thus, some research applications now require a much more explicit plan of how the impact of a research programme will be disseminated. With this impetus, now is a good time to think about public events and schools activities. These can have multiple benefits in addition to meeting funding requirements, perhaps by increasing visibility of a University department and therefore contributing to student recruitment. Well-designed impact activities can also be combined with graduate school activities enhancing the training and broadening the skills of postgraduate students and even postdoctoral researchers.

A Decline in Plant Biology?

Ultimately any good publicity for maintaining the wide diversity of subject areas that make up plant science must be a good thing and will directly or indirectly have a positive impact on the research itself. Post graduate training with University Graduate schools is adapting to deliver transferable skills such as organisation, communication, networking, team-working and careers through knowledge impact activities.

If you are not already creating some impact there is likely to be someone in your department who is who could advise/assist you. If there is not there are a number of other avenues; learned societies such as the Society for Experimental Biology (SEB)[7], the Biochemical Society (BS)[8] and the British Ecological Society (BES)[9] have established Education and Public affairs programmes that can offer support. Similarly the major research funders such as the BBSRC, NERC and the Wellcome Trust have public outreach sections. In addition, the Science Learning Centres and science centres such as Techniquest and the Glasgow Science Centre can offer voluntary opportunities and even bursaries to attend science communication courses. A major set of resources is delivered by Science and Plants for Schools (SAPS)[10] which aims to 'help young people to become more aware of the importance of plants in the global economy, and to encourage more of them to follow careers in plant science and molecular biology'. The December 2009 issue of GARNish promoted a number of Gatsby funded Plant Educational resources[11].

Dr Jeremy Pritchard is a Plant Physiologist at the University of Birmingham. He is an admissions tutor, chairs the Society of Experimental Biology (SEB) Education and Public Affairs Committee (EPA) and is a BBSRC Local Outreach Co-ordinator.

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1 http://www.defra.gov.uk/foodfarm/food/pdf/food-assess-approach-0908.pdf

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3 http://www.wellcome.ac.uk/stellent/groups/corporatesite/@msh_peda/documents/web_document/wtd003436.pdf

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6 http://www.ucas.ac.uk/

7 http://www.sebiology.org/

8 http://www.biochemistry.org/

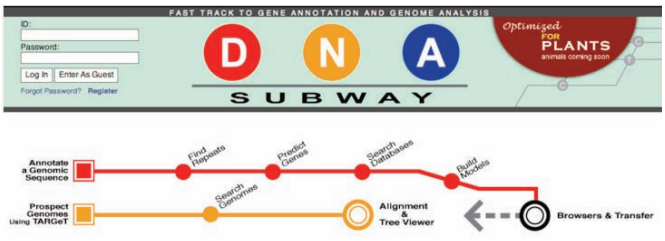
9 http://www.britishecologicalsociety.org/

10 http://www-saps.plantsci.cam.ac.uk/

11 http://garnet.arabidopsis.org.uk/garnish.html

A DNA Subway from the iPLANT Collaborative

provided by Irene Lavagi



DNA Subway is a new bioinformatics tool developed by the iPlant Collaborative that makes high-level genome analysis available for teaching purposes. DNA Subway meets iPlant's challenge, to develop a cyber infrastructure that provides access to large-scale datasets and high-powered informatics tools to plant researchers and educators. DNA Subway was developed at the Cold Spring Harbour Laboratory's Dolan DNA Learning Center (DNALC) and presents complex bioinformatics and visualization tools in a user friendly, intuitive and appealing interface. Depending on the itinerary, an underground passenger will use different Lines. Similarly, depending on the type of genome analysis that one wants to perform, different DNA Subway lines should be chosen. For example, the Red Line allows to predict and annotate genes in up to 100,000 base pairs, whereas the Yellow Line can prospect entire plant genomes for specific genes. As new lines are being developed it will be possible to analyse transcriptome data obtained from next generation sequencing, and even to construct and work with phylogenetic trees. Although the number of lines and stations providing services for multiple lines is limited in comparison with a typical underground system, this transport service is free of charge! You can "ride" DNA Subway at http://dnasubway.iplantcollaborative.org/

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- Ron Milo (Rehovot, Israel)
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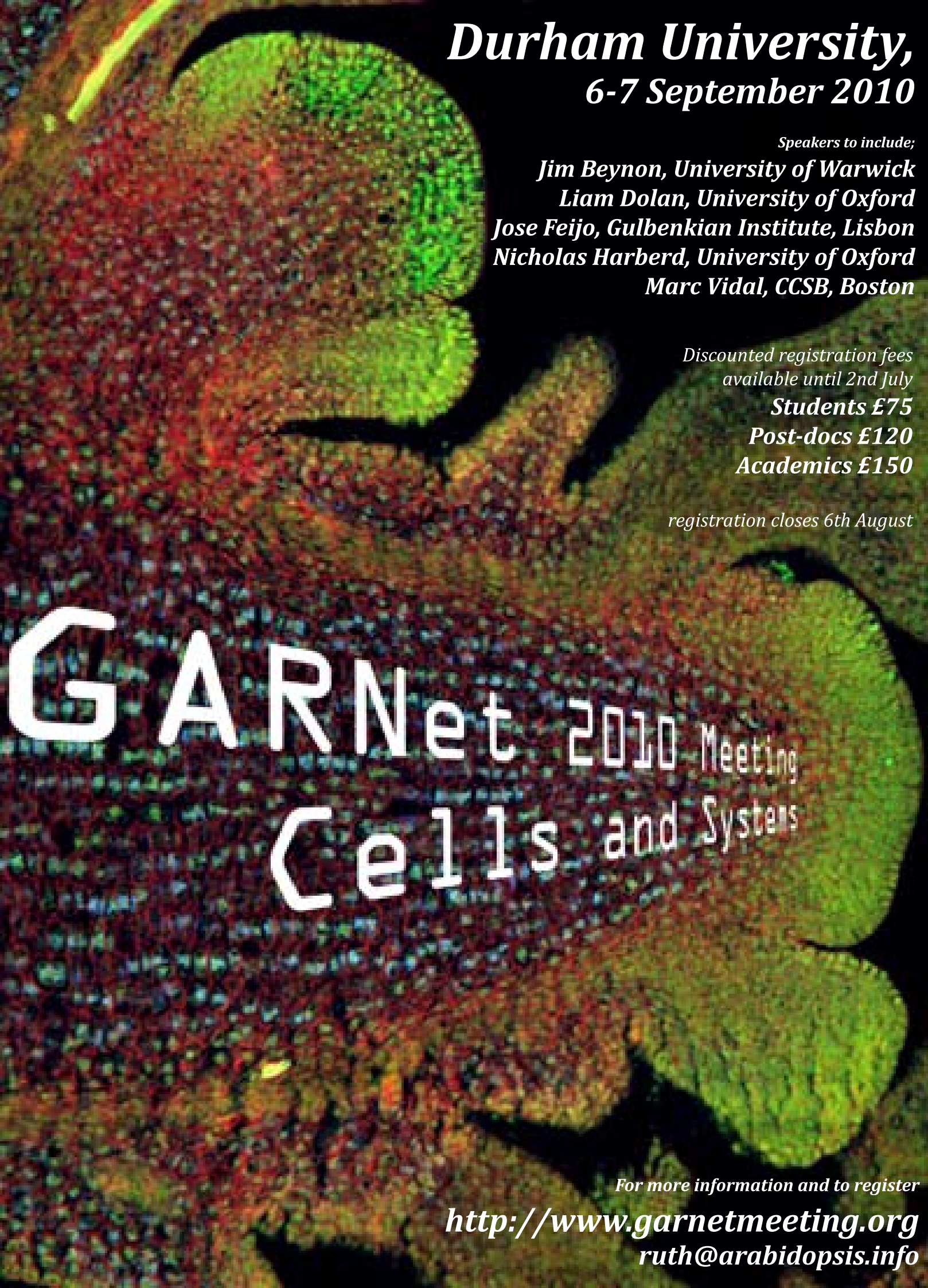

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