

GARNish

December 2012 Edition 18



1001 Genomes Project

GARNish

Editorial and contents

Welcome to the December 2012 issue of GARNish

It's a great pleasure to write the Editorial for this edition of GARNish. I've been a member of the GARNet committee for just over a year now and it's great to see a number of issues that have been discussed at our meetings starting to deliver benefits to members of the community. This includes the 'hot topic' Next Generation Sequencing (NGS) that is impacting (and in numerous cases revolutionizing) many of our research projects. Gaining access to an NGS service is becoming increasingly important to Arabidopsis (and other plant) researchers in order to perform whole genome sequencing to identify nucleotide changes causing a mutant phenotype, for example. Ian Moore and Smita Kurup's article in this edition (pg. 10) covers potential services at TGAC for the Arabidopsis community and we encourage you to take a look. It also reveals that a surprising number of University, Institute and commercial NGS services are available to UK researchers. Until very recently researchers submitting BBSRC grants requesting funding for NGS services had to exclusively employ TGAC, the new BBSRC Genome Institute in Norwich. For many reasons, Arabidopsis researchers would prefer to have the choice to employ a wide range of NGS service providers. Thankfully, BBSRC have recently agreed that researchers are now free to employ any NGS service provider.

Research funding remains the single greatest area of concern for almost every UK group working on Arabidopsis or any other plant or crop species. The effective loss of Defra as a source of large scale research funding has resulted in BBSRC becoming the primary source of support to the UK plant community. In this issue of GARNish Charis Cook (GARNet) describes exactly how much funding is going to UK Arabidopsis and plant research groups (pg. 7). For example, in 2010/11, more than half of the total BBSRC responsive mode grant funding (£31M) to committee B went to plant science research, half of which went to Arabidopsis research. Over the whole of the BBSRC budget, this translates to 48 plant science research projects (plus 24 non-responsive mode grants to plant researchers in 2010/11; data not shown in article). Given that there are 350 plant research groups in the UK

based in 42 institutions, grant success would average to just over one BBSRC award per institution. I am sure that, like me, you will be shocked to learn about these figures. They are a serious cause for concern for many reasons. Arguably the most damaging effect in the long term will be its impact on plant science research and teaching in university departments due to the increased difficulty of convincing our Heads of Schools to recruit academic staff in this area, and our ability to attract and/or retain the next generation of plant researchers to a UK institute.

You are probably asking, why has plant science research funding become so limited when the Government and the current UK Chief Scientist are pushing the area of Global Food Security so hard? Part of the reason for the squeeze on UK plant research funding in recent years has been the negative effect of reducing the number of responsive mode committees our community are able to apply to; in the majority of cases plant scientists are restricted to committee B. Thankfully, help is at hand. BBSRC has recently made the decision to open up Committee C (Genes, Development and STEM approaches to biology) to plant applications (effectively recreating the Plant-Microbial Science [PMS] and Genes and Developmental Biology [GDB] themed committees successfully employed over from the last several decades). By effectively doubling the number of committees we are all able to apply to, BBSRC has (in the short term) thrown a lifeline to many UK plant research groups and may (in the longer term) ensure many of our Universities continue to appoint academic staff and teach in this area. Whilst a very welcome decision by BBSRC, we must not forget that this remains an administrative fix; ultimately the only way to increase the number of grants available to plant researchers is to increase the number of grants submitted. Given the impact of global food shortages, energy costs and climate change in the coming decades, significant increases in plant, crop and soil science research funding are required to help mitigate their effects. Increased Government investment into UK Ag R&D staff, facilities and breeding programmes needs to happen now since the lead-time to develop new, better adapted crop varieties will take at least 15 years. The clock is ticking.....

Malcolm Bennet

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Many thanks to all who contributed to this issue, especially Arthur Korte, Paula Kover, Claire Grierson, Antony Dodd, Kerry Franklin, Heather Whitney, Ian Moore, Smita Kurup, Mimi Tanimoto, Paul Wiley, Malcolm Bennet, and Mary Williams.

Cover image credit: Envel Kerdaffrec, Gregor Mendel Institute.

UK Plant Science Federation Update

Mimi Tanimoto

UK Plant Sciences Federation

Registration and abstract submission are now open for UK PlantSci 2013, which will be held in Dundee from 16th-17th April 2013. We are pleased to announce that the keynote speakers will be Professor Sir David Baulcombe (University of Cambridge) and Professor Charles Godfray (University of Oxford).

For the full programme, to submit an abstract, and to register, go to <http://www.plantsci2013.org.uk/>. For students, there will be a poster competition with an iPod Nano as the first prize.

The 2nd International Fascination of Plants Day will be on 18th May 2013. Botanic gardens, research labs, schools and farmers will open their doors to provide engaging activities for the public. We encourage anyone who works with or is interested in plants, to get involved and inspire others by organising an event for Fascination of Plants Day. For further details please contact mimitanimoto@societyofbiology.org

The GARNet Committee

Malcolm Bennett

University of Nottingham
Term on committee Jan 2010 - Dec 2013

Jim Beynon

University of Warwick
GARNet PI

Juliet Coates

University of Birmingham
Term on committee Jan 2010 - Dec 2012

John Doonan

University of Aberystwyth
Term on Committee Jan 2012 - Dec 2014

Anthony Hall

University of Liverpool
Term on committee Jan 2012 - Dec 2014

Smita Kurup

Rothamsted Research
Term on committee Jan 2010 - Dec 2013

Sabina Leonelli

University of Exeter
Ex-Officio Member

Sean May

NASC
Ex-Officio Member

Ian Moore

University of Oxford
Term on committee Jan 2010 - Dec 2012

Jim Murray

University of Cardiff
GARNet Chair Jan 2011 - Dec 2013

Heather Knight

Durham University
Term on committee Jan 2012 - Dec 2014

Nick Smirnoff

University of Exeter
Term on committee Jan 2010 - Dec 2012

Cyril Zipfel

The Sainsbury Laboratory Norwich
Term on committee Jan 2012 - Dec 2014

✿ Tweets and blog from GARNet

GARNet has entered the world of social media. Our major new venture is the GARNet blog, which is updated regularly with posts on new methods, spotlighted journal articles, key highlights from workshops and conferences, advice on specific grant calls, and round-ups of events and funding opportunities. The most well received posts this year have been a piece on the β -carotene rich orange sweet potato project; a collection of key resources for sharing and accessing large-scale data; and funding updates. Where possible, posts include links to relevant teaching resources translating the cutting edge plant research highlighted on the blog to the classroom or lecture-theatre.

Follow Ruth and Charis on Twitter on **@GARNetweets** and **@weedinggems** for updates on research papers, funding, jobs, plant science in the media, and live updates from conferences. You can also find GARNet on Google+.

GARNet: www.garnetcommunity.org.uk
 Blog: <http://blog.garnetcommunity.org.uk>

✿ Crop Plant Trait Ontology Workshop, Oregon State University



Plant breeders, biologists and bioinformatics specialists from ten countries, seven US states, and two plant agribusinesses gathered in Corvallis, Oregon on September 13th-15th

2012 for a Crop Plant Trait Ontology Workshop. The workshop was hosted by the Plant Ontology and the Trait Ontology, and co-organised by TransPlant, European Bioinformatics Institute, GARNet, Generation Challenge Program, Sol Genomics Network, and SoyBase.

The goal of the workshop was to engage researchers associated with major cultivated crops worldwide, widen their awareness and showcase the latest developments in ontologies for plants. In addition to hearing presentations, participants engaged in hands-on activities, learning to use the ontology editor OBO-Edit and working in small groups to classify plant trait terms which had been submitted in advance.

The delegates concluded that there is a need for a broad, coordinated effort to create a semantic framework for meaningful cross-species queries using a Common Reference Ontology for Plants. This Reference Ontology will encompass all green plants and will facilitate queries for related gene expression and phenotype data from plant genomics, genetics experiments from the various species- and clade-specific databases, and describe accessions in the various international crop germplasm collections. By creating a Common Reference Trait Ontology for Plants, we can achieve the goal of facilitating plant genetic and phenotypic data discovery and exchange.

For further information, list of participants and sponsors, links to presentations and more details, please visit the workshop wiki page at: <http://tinyurl.com/Trait-Ontology>.

✿ Science and Plants for Schools

Science and Plants for Schools (SAPS) is a Gatsby Foundation-sponsored initiative that aims to get plant science into classrooms. The SAPS website features many practical plant science experiments for teachers to run in their classes, and the team want help from the research community to develop more.

If you have run an undergraduate practical or outreach event that you think would translate well to a classroom, please get in touch. SAPS are particularly interested in practical ways of teaching photosynthesis, systems biology, and in fast 10-minute demonstrations that grab attention. They work with students from primary school up to when they leave school at 18.



SAPS: www.saps.org.uk

✿ Plant Pathology Audit

The British Society of Plant Pathology (BSPP) Audit of Plant Pathology Training and Education in the UK was published in November. It reports a major decline in teaching and research on plant diseases in British Universities. Fewer than half the institutions that teach biology, agri-

culture, or forestry offer plant pathology courses. President of the BSPP Professor James Brown said, "These job losses are severe. Britain is not producing graduates with the expertise needed to identify and control plant diseases in our farms and woodlands. One of the most worrying findings is the decline in practical training in plant pathology."

ERA-CAPS: First Joint Call

Paul Wiley
BBSRC

The ERA-Net for Coordinating Action in Plant Sciences (ERA-CAPS) launched its first joint call for proposals on November 19th. The call, "Expanding the European Research Area in Molecular Plant Sciences", covers all areas of molecular plant science. Four themes have been highlighted as areas of particular interest: Food Security, Non-Food Crops, Adaptation to a Changing Climate, and Biotic/Abiotic Stress. Applications outside of these themes are also welcomed.

Fifteen countries are contributing funds to the call: Austria, Belgium, Denmark, France, Germany, Ireland, Israel, Latvia, The Netherlands, New Zealand, Norway, Poland, Portugal, Serbia, and the UK. The NSF in the USA is running a parallel call through their Plant Genome Research Program that will allow US researchers to join consortia.

The call has a one-stage application process, and consortia must comprise research groups from a minimum of three different countries. The closing date is February 15th 2013, and the total budget is around €20M.

Full details of the application process, funding organisations and contacts are available on the ERA-CAPS website (www.era-caps.org).

Contact: Paul Wiley (eracaps@bbsrc.ac.uk)



Diary

UK PlantSci 2013: 16–17 April,
Dundee, Scotland



GARNet Synthetic Biology workshop: 21-22
May, Nottingham, England


31st New Phytologist Symposium (Orchid sym-
bioses: models for evolutionary ecology): 14-16
May, Calabria, Italy.

International Symposium on Plant Photobiology:
3-6 June, Edinburgh, Scotland.

ICAR 2013: 24 – 28 June, Sydney, Australia

SEB Annual Main Meeting 2013: 3–6 July,
Valencia, Spain

ASPB Plant Biology 2013: 20–24 July,
Providence RI, USA

 7thEPSO Conference: 1–4 September,
Peloponnese, Greece

Plant Genome Evolution: 8-10 September,
Amsterdam, The Netherlands.

32nd New Phytologist Symposium (Plant inter-
actions with other organisms): 20-23 November,
Buenos Aires, Argentina.

Funding deadlines in 2013

BBSRC: 9 January; 21-22 May; June (TBC).

EPSRC: Outline proposal batch meetings 11
February; 15 April; 16 June.

FP7 KBBE theme: 5 February

Marie Curie Actions: Researchers' Night, IAPP,
IRSES, all in January; CIG, 18 September.

NERC Standard Research and New Investiga-
tor Grants: 1 July; 1 December.

For regular updates about open calls for re-
search grant and fellowship applications, out-
reach grants, and other opportunities, see the
GARNet blog.



✿ Expanding plant science expertise at a new facility in Bristol

Gary Foster, Claire Grierson, Antony Dodd, Kerry Franklin, and Heather Whitney

The University of Bristol, Woodland Road, Bristol BS8 1UG. For email addresses, see pg. 22.

Biological Sciences at the University of Bristol will be moving into a new iconic £54 million state-of-the-art Life Sciences Building in 2013. Clustered around a central atrium will be teaching and research laboratories, seminar rooms, computer facilities, staff offices and a café. The building will be fully equipped to become one of the UK's leading facilities for the advancement of Biological Sciences and a range of related disciplines.

Gary Foster, Professor of Molecular Plant Pathology, said: "This investment in Life Sciences is a major move by the University of Bristol, showing strength and ambition, with Bristol being an exciting and ideal place to carry out research over the coming years.

"The new building will also provide outstanding laboratories for science teaching and will enhance the undergraduate experience by facilitating research-led study and staff-student interaction, making Bristol University the first choice for research and teaching.



An artist's impression of the new Life Sciences building, which will open in 2013.

The Life Sciences building will be split into three zones, including a five-storey laboratory wing complete with acoustic chambers, spectroscopy and microscope rooms, clean rooms, and a double height plant room. The new building provides expanded state of the art laboratories for Bristol plant science research as well as extensive plant growth facilities through suites of controlled en-

vironment rooms, and new greenhouses on the roof. The growing strength and size of the plant science base in Bristol is recognised through these new facilities and provides significant new opportunities not only in science but also in recruitment. The School has a strong track-record of developing and supporting independently-funded Research Fellows, recently appointing three (Dr Kerry Franklin, Dr Antony Dodd and Dr Heather Whitney) to permanent academic positions.

In addition to completing the new building, there will also be a new public realm works and extensive landscaping which will link St Michael's Hill and Tyndall Avenue to Royal Fort House and its adjoining gardens. The building and surrounding area has been rated BREEAM Excellent, being highly sustainable and environmental friendly. The building will incorporate Green Living Walls and areas to contain plants which will promote wildlife within the area.

✿ GARNet Advisory Committee elections 2013: Voting now open

The GARNet Advisory Committee is the link between GARNet and the Arabidopsis research community, steering GARNet's activities to ensure we best support UK plant scientists. Committee members are volunteers elected from and by the research community. They serve three year terms. At the end of 2012, three committee members are stepping down, and the process of electing three new members is in progress.

There are eight candidates for three vacancies on the committee: Dr Antony Dodd (University of Bristol); Prof. Nicholas Harberd (University of Oxford); Dr Paula Kover (University of Bath); Dr Vinod Kumar (John Innes Centre); Dr Sarah McKim (University of Dundee); Dr Steve Penfield (University of Exeter); Prof. David Salt (University of Aberdeen); and Dr Carol Wagstaff (University of Reading).

If you want to vote, please email charis@garnet-community.org.uk with the names of your **three preferred candidates**, in order of preference.

For the names of current committee members and their terms, see page 2.

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Funding

Both BBSRC responsive mode Committees B and C are now available for plant science proposals

Charis Cook

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Plant scientists largely depend upon the BBSRC for funding, and the bulk of that funding is from responsive mode funding calls. An analysis of grants awarded in BBSRC responsive mode showed that plant science does very well from Committee B, the only avenue obviously available to plant science grant proposals. A good proportion of the plant science funded was Arabidopsis research: in both 2009/10 and 2010/11, more than half of the total money (£25M and £31M respectively) allocated by Committee B went to plant science research, of which roughly half was for work on Arabidopsis (Figure 1).

When looking at Committee B alone, plant scientists appear to be good at winning responsive mode grants. However, in the two academic years looked at only 11% of total committee-based responsive mode funding was allocated to plant research. Committees A and D both dispensed roughly 15% more money in responsive mode than Committee B. This is because the same percentage of grants from each committee are funded, so Committees A and D, which receive more grant proposals, award more grants than the other committees.

In 2010/11, the total number of grants awarded by the committees in responsive mode was 386, of which 48 were to plant science research projects. Plant scientists won 24 non-respon-

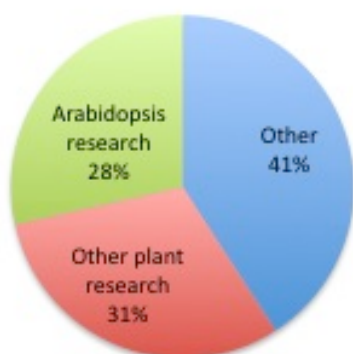
sive mode grants in that year. This means that research funding from the BBSRC for plants was roughly £30M, out of a £387M budget for research and capital grants. An additional £51M was allocated to maintenance of BBSRC research institutes. What can realistically be done to improve the number of grants being awarded to plant science? At the September GARNet advisory committee meeting, two conclusions were drawn:

1. As the age-old adage goes, 'You have to be in it to win it!' More proposals from the plant science community will lead to more grants awarded to the plant science community, because that is how responsive mode works. If the community maintains a high level of grant applications, if you are unlucky in one round you may have a good chance in the next.

2. Put yourself forward for appointment to a BBSRC Committee, and be supportive of good plant science grants. If there are no plant science experts on the Committees, plant research is likely to get passed over as a matter of course.

There was good news for the 2011/12 calls and beyond. It is now much easier for plant scientists to apply to Committee C, which is taking over primary responsibility for genetics and development instead of dealing only with development and methodologies, which had previously often been re-assigned, according to their context, to other committees. There is a plant scientist on Committee C, so be sure to consider sending a proposal through it because if this year goes by with very few plant proposals, the next Committee C may not be so plant-friendly.

Committee B responsive mode 2009/10



Committee B responsive mode 2010/11

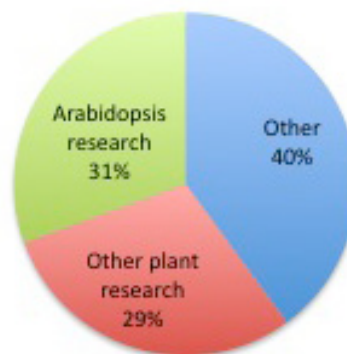


Figure 1: BBSRC Committee B responsive mode funding breakdown in 2009/10 and 2010/11

GARNet workshop: Making Data Accessible to All

Charis Cook and Ruth Bastow

In July 2012, GARNet held a workshop entitled 'Making Data Accessible to All'. Together, workshop speakers and delegates discussed the current challenges in data storage, which data are 'valuable' and which may reasonably be left behind, and who should have the responsibility of sharing, storing, and curating data.

The challenges of data sharing are more significant than ever due to the demand from UK funding bodies for open access to the results of research they fund, and the rise of data driven science such as systems biology which depends upon well curated and publicly available data. Although most journals require that large-scale data sets are deposited in the appropriate repository, the extent to which these requirements are enforced appears to be unclear. In some cases, for example for high throughput plant phenotype data, depositing data is not possible as appropriate central repositories do not currently exist. In addition to these problems the workshop also highlighted that there is no requirement for researchers to make the data underlying a table or graph in a publication publicly available. This makes it very difficult for those wishing to combine or reuse data sets.

Not all data are created equal. Certain data types (often based on DNA/RNA sequence) can be easily stored in well-established online central repositories. They are clear guidelines on the minimal information that a researcher is required to collect and deposit data. For example GEO and Array express are well-utilised repositories and the MIAME guidelines for transcriptomics are used by a number of funders and journals. Sharing and re-use of sequence-based data is equally well supported via user-friendly web based interfaces and associated analysis tools such as Genevestigator and NASC arrays. However this is not the case for all data types.

The dominance of high-throughput data generation methods for datasets as varied as protein interactions and phenotypic information means there are many datasets for which current data sharing platforms are not appropriate. Some ex-

perimental techniques are simply too modern for suitable data sharing outlets to have been established. Other datasets present the problem of simply being too large to currently store and share, e.g. imaging data. Researchers, publishers and funding bodies all have a responsibility and a role to play in finding effective solutions to make such data accessible.

In many cases the solutions will be driven by the user/researcher who, in the absence of a useful database, tool or resource will create their own. In fact a number of researchers utilise purpose built in house repositories to store their research data and share it with colleagues and collaborators in advance of publication. Such activities are beneficial to building a culture of data sharing, and generally result in producing data that is carefully annotated and curated.

In order for data sharing to take hold and bear fruit in plant science and biology as a whole, the workshop concluded that incentives for researchers to store and share data, effective policing measures, and shifts in attitudes towards an open access philosophy at all levels are urgently needed. Funding bodies, universities, and publishers and journals can provide important 'sticks and carrots' by shifting priorities and attitudes to support the practice of data sharing, with all its demands. At the same time, researchers need to seriously commit to data sharing by making it part of their principal aims and outputs. In most cases, community involvement matters much more than the availability of technology. Recent initiatives to encourage data publication such as data only journals and data sharing platforms, principally Dryad and Figshare, are acknowledged as important drivers of the shift toward an ethos of data sharing.

Workshop presentations can be found online at <http://www.plantsci.org.uk/news/workshop-talks-now-available-making-data-accessible-all>. The full list of speakers at the workshop was: Sabina Leonelli (Exeter), Andrew Millar (Edinburgh), Nick Smirnoff (Exeter), Jay Moore (Warwick), Jacob Newman (UEA), Mary Traynor (J. Ex. Bot.), Giles Jonker (Elsevier), Ruth Wilson (Nature Publishing Group), Mark Hahnel (Figshare), Claire Bird (Oxford University Press), Sean May (NASC), David Swarbreck (TGAC), and Paul Burlinson (BBSRC).

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Making Data Accessible

A collection of standard repositories to share and access data

One of the outcomes of GARNet's July *Making Data Accessible* workshop was the recognition of a need for standard practices in data generation, sharing, and usage. To encourage this, GARNet put together a list of important data repositories

for various large-scale datasets, including 'main' repositories and plant-specific resources. As data sharing is dependant on consistent methods, format and quality, the table also includes minimum information guidelines where available.

For a version including links to the online resources, go to the GARNet blog.

Data type	Main repository	Plant repository	Minimum information guidelines	General journal requirement	Other repositories
Genes and gene nomenclature	Genbank	TAIR	Genbank, TAIR	Submission to Genbank or TAIR	
Genome sequence	Genbank	TAIR			
MIGS (Field et al., 2008)	Submission to Genbank	EMBL			
DNA barcodes	EMBL		Barcode of Life standards		BOLD Systems
RNA sequences	EMBL		BCB RNA-seq		RefSeq
Chip sequencing	GEO		Minseq (draft), GEO guidelines	Submission to GEO	NCBI Sequence read archive, International Regulome Consortium
Transcriptomics	GEO, ArrayExpress	NASC	MIAME from NCBI	Submission to GEO or Array Express	Array Express, PLEXdb, EFP Browser
Protein structure and sequence	Protein Data Bank	Plant PDB		Submission to PDB, PIR	NCBI Protein, PIR
Proteomics	GEO	MASCP-Gator	MIAPE (Taylor et al., 2007)	Submission to GEO, Swiss-Prot	EBI PRIDE, NCBI Protein, Plant PDB, EMBL
Metabolomics	BMRB iHub (Ionomics)	Plant Metabolomic Network	Metabolomics Standards Initiative	Submission to BMRB	Metabolome Express
Epigenomics	NCBI Epigenomics		FGED Society MINSEQ		Chromatin.csl
Interactions	IMEX	TAIR nbrowse	IntAct guidelines	Submission to IMEX	IntAct
Mathematical models	Biomodels.net	PLASMO	MIRIAM from Biomodels.net		Biomodels
Pathway information	BioCyc	AraCyc			
Synthetic biology	Parts registry		Parts registry		SBOL Standard

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Next Generation Sequencing

The Genome Analysis Centre and the Arabidopsis Community

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The power and scope of genetic research is being rapidly expanded by Next-Generation Sequencing (NGS). The speed of this change is matched by the rate of change in sequencing technologies, services, and costs. Many procedures that were specialist applications only a few years ago, such as mutant identification, are now essentially routine contract services. In 2009, BBSRC established TGAC, The Genome Analysis Centre, in the Norwich Research Park to provide a commercial contract NGS service as well as a collaborative partner for innovative *de novo* sequencing and bioinformatics. TGAC augments other academic and commercial service providers in the UK and internationally, and here we set out the facilities and services that it provides to the Arabidopsis community.

Sequencing Technologies and Indicative Pricing

TGAC has Illumina, Roche 454, and SOLiD sequencing technologies (<http://www.tgac.ac.uk/about/technology/>). Arabidopsis genome re-sequencing is currently offered on the Illumina HiSeq 2000 platform. A single lane on this platform will generate enough data from nuclear DNA samples to yield over 150-fold coverage of the Arabidopsis genome. This is far greater than is required for simple re-sequencing, SNP detection, or mutant mapping (10-20x). By bar-coding individual samples, several can be run at once to reduce costs for each sequencing project. Prices are liable to change (usually downwards) and need to be discussed with TGAC project managers so the costs supplied below should be considered indicative at the time of going to press. These costs are based on multiplexing specified numbers of samples per lane and on 100 base paired-end sequencing (100 nucleotides from each end of each sequenced library fragment).

Multiplexing will most probably come at the cost of delayed delivery as samples will wait until Illumina flow cells can be filled, which will depend on demand. Recent quotes have specified delivery within 6-8 weeks of receiving DNA samples. More rapid turn-around can be offered through use of the Illumina MiSeq (10x, £805 +VAT based on pooling with up to 1 other sample; 30x, £1500 +VAT based on running a single sample). TGAC has a budget to replace and upgrade facilities and will shortly be able to offer faster sequencing of lower numbers of samples on the Illumina HiSeq 2500 platform.

Sequence depth per sample	Samples per HiSeq lane	Cost per sample
> 10x	16	£220
> 20x	8	£330
> 30x	6	£400
> 40x	4	£545
> 80x	2	£970
> 160x	1	£1,826

**These are exclusive of VAT, which would be charged if the work is undertaken on a contract rather than on a grant funded / research collaboration basis (see below).*

In addition to genome re-sequencing, for organisms such as *Arabidopsis thaliana* with a fully annotated reference genome, TGAC offers transcriptome analysis based on Illumina RNASeq or Roche 454 cDNA sequencing (RNASeq is typically based on a minimum of 25 million reads per sample with 50 base single or paired end reads). Further information about the services and analyses available can be obtained from TGAC project managers.

Working with TGAC

Researchers can interact with TGAC via two routes. BBSRC funded projects that involve collaboration with TGAC, for example in *de novo* sequencing or novel bioinformatic projects, require a completed Technical Assessment form (TAF) at the time of application (<http://www.tgac.ac.uk/projects/bbsrc-grant-submissions/>). The TAF will set out the aims of the NGS and bioinformatics work, plus include advice and input from TGAC staff on feasibility, experimental design, appropriate methodologies, and costs. A completed TAF will form part of the supporting information for the BBSRC grant application. Four weeks are

required for the consideration of an applicant's completed TAF by TGAC. BBSRC originally gave TGAC preferred supplier status for 'large-scale' NGS but guidelines have been relaxed, now accepting any UK academic partner and even overseas and commercial partners, but require applicants to justify their choice of service provider and collaborator with some proof of competence (BBSRC Research grants guidance notes 5.27).

It is also possible to gain access to TGAC facilities on a contract research basis via their subsidiary, Genome Enterprises Ltd (GEL). This avenue may serve much of the community's needs, given that much NGS of Arabidopsis will involve relatively routine procedures for sequencing, read-mapping, SNP detection, and SNP frequency calling. The specific requirements and costs of a project can be discussed with one of TGAC's Project Managers and a quotation will normally be received within 2-3 working days of an enquiry being received. Enquiries can be made by e-mail (enquiries@tgac.ac.uk), telephone (+44 1603 450861) or via the website (<http://www.tgac.ac.uk/contact-us/>). It is unclear that a TAF is required for BBSRC applicants who undertake contract research with GEL and the relatively low costs involved may be included as a directly incurred cost along with other contract services.

We understand that collaborative sequencing at TGAC can be funded by BBSRC at 80% fEC without incurring VAT, whereas sequencing at GEL can be funded at 100% fEC (Guidance note 2.59) but will attract VAT.

Sample submission and data delivery.

TGAC requires 1-5µg of genomic DNA or total RNA per sample for paired-end genomic sequencing or RNASeq on the Illumina platform and approximately 10-fold more for 454 transcriptome analysis. A document setting out recommended methods for sample preparation, quality-control, and shipment is available at: <http://www.genome-enterprise.com/content/files/services/TGAC+sample+guidelines.pdf> and an update was planned at the time of writing. For genomic DNA samples, nuclear DNA preparations are recommended to minimise organellar DNA contamination. Total genomic DNA samples are accepted but may require a greater depth of coverage and, in practice, it is possible to obtain 40x-fold coverage of the nuclear genome from

less than 3µg of total DNA isolated from flower buds. It may be possible in the near future to assess organellar genomic content during the QC stage to agree on an acceptable sequencing strategy.

TGAC will perform a quality control of all DNA/RNA samples upon arrival and will assess the suitability of such samples for library construction and subsequent sequencing. If the samples pass QC then they are deemed suitable for downstream work. If the library then fails TGAC will undertake one attempt to re-make the library at its own cost. Similarly if problems arise in sequencing libraries that have passed QC, TGAC will inform the client and re-sequence as soon as possible. Repeated failures will be discussed with the client.

Sequencing data is subject to quality control before being supplied via electronic download. As a general rule, 97% of data for samples of 100 million bases is delivered at Q20 or better (99% probability of correct base call) and these quality scores are substantiated in our subsequent analyses. This compares favourably with data from other commercial suppliers that have been used by colleagues in this Department (Dr. Steven Kelly, University of Oxford, pers. comm.). For RNASeq data, analysis is via a Bowtie – Tophat – Cufflinks pipeline (FPKM values, pairwise differential expression) and visualisation is in G-Browse, Ensembl or TGAC Browser). Bioinformatic tools, computing facilities, and services are also offered at various levels (<http://www.genome-enterprise.com/services/detail/url/bioinformatics>). For contract services, costs will be quoted for individual projects depending on the degree of TGAC involvement. In October 2012, a basic analysis involving read-mapping to reference genome, SNP detection, and SNP frequency calling was costed at approximately £900+VAT for up to 16 samples. More involved or novel bioinformatic projects can be entered into as collaborations with TGAC's bioinformaticians.


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Next Generation Sequencing

NGS Sequencing Services offered in the UK

Name	Services offered	Platform/Other comments
<i>University-based / publicly funded services</i>		
Biosciences, University of Exeter	<i>De novo</i> genome sequencing; Genome resequencing; RNA-Seq; Small RNA; ChIP-Seq; Meth-Seq; Bioinformatics analysis and support (by special arrangement)	HiSeq 2500
TGAC, The Genome Analysis Centre	Genome sequencing; RNA-Seq; Bioinformatics analysis	HiSEQ2000; Illumina GAIIX; Abi- SOLiD4; Roche 454 FLX Titanium
NBAF, Liverpool	Genome sequencing; <i>De novo</i> sequencing; RNA-Seq; ChIP-Seq; Epigenomics; Metagenomics	ABi-SOLiD5500xl; Roche 454 FLX; IonTorrent sequencer
School of Biological Sciences, University of Bristol	Genome sequencing; <i>De novo</i> sequencing; RNA-Seq; ChIP-Seq; MeDIP-Seq	Illumina GAIIX; IonPGM™ sequencer
<i>Commercial services</i>		
BGI	<i>De novo</i> genome sequencing; Genome resequencing; RNA-Seq; Small RNA; Metagenomics; Epigenomics; ChIP-Seq; Bioinformatics analysis and software.	Illumina HiSeq; AB SOLiD system; IonTorrent
GATC- Biotech, Germany	<i>De novo</i> genome sequencing; Genome resequencing; RNA-seq; Small RNA; ChIP-seq; Meth-seq; PacBio RS; metagenomics	PacBio RS; HiSeq 2000; Roche GS FLX+ System
LGC genomics	<i>De novo</i> genome sequencing; Genome resequencing; RNA-seq; Small RNA; ChIP-seq; Meth-seq; metagenomics	HiSeq 2000; Roche 454 FLX Titanium
Source BioSciences, Nottingham	Genome sequencing; RNA-Seq; ChIP-Seq; Bioinformatics solutions	Illumina GAIIX HiSeq 2000; Roche 454 FLX

Acknowledgements.

 Ian Moore thanks Chris Watkins (TGAC) and Mike Ball (BBSRC) for information and comments during the preparation of this article, and Dr. Steven Kelly (Department of Plant Sciences, University of Oxford) for sequence quality

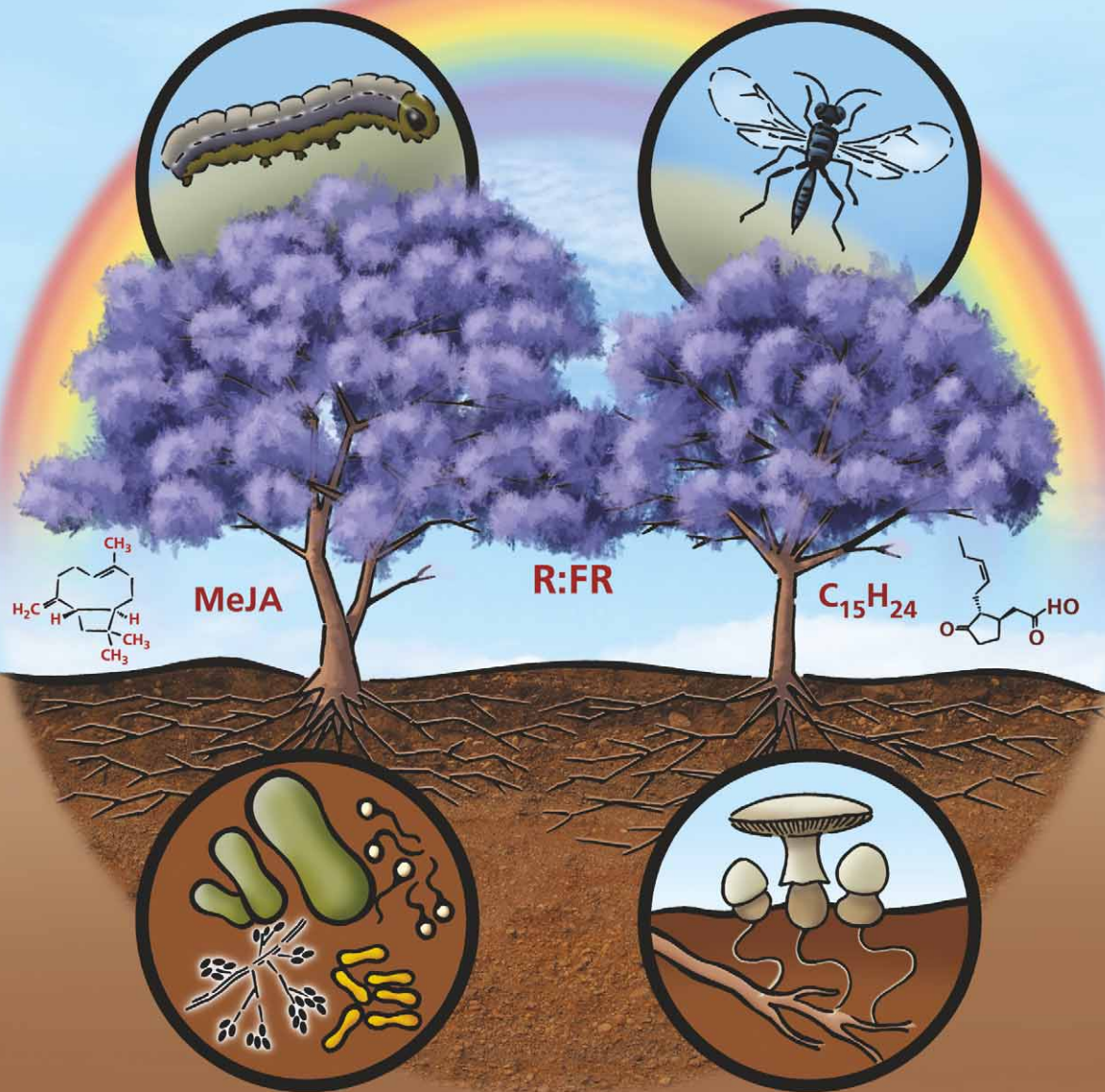
comparisons between service providers.

Thanks to Cyril Zipfel and Heather Knight for comments on the article.

32nd New Phytologist Symposium

Plant interactions with other organisms: Molecules, ecology and evolution

Universidad Católica, Puerto Madero Campus, Buenos Aires, Argentina
20–23 November 2013



Confirmed speakers

Marcelo Aizen Universidad Nacional del Comahue, Argentina
Amy Austin University of Buenos Aires and IFEVA, Argentina
Ian Baldwin Max Planck Institute for Chemical Ecology, Germany
Carlos Ballaré University of Buenos Aires and IFEVA, Argentina
Richard Bardgett University of Manchester, UK
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New
Phytologist

Teaching Tools in Plant Biology, to inspire the next generation

Mary Williams

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University faculty are squeezed between the need to teach and a system that evaluates them primarily by their research accomplishments. Years of preparation and training support their research endeavors, but there is little support for their role as teacher. A major objective of Teaching Tools in Plant Biology, a feature of the American Society of Plant Biologists' premier plant biology journal *The Plant Cell*, is to help instructors teach. The project was initiated by TPC Editor-in-Chief Cathie Martin of the John Innes Centre and is edited by Mary Williams, an experienced teacher of plant science, researcher, and winner of the 2011 ASPB Excellence in Education Award. Teaching Tools are designed to bridge the gap between textbooks and the research literature, by providing up-to-date, hyperlinked, online content, sometimes described as a "living textbook". Instructors and students can access materials electronically and use them as launch points for further study and inquiry. Importantly, Teaching Tools are revised and updated regularly by scientists so that instructors can be confident that they are presenting the most important, current information to their students.

Each Teaching Tool covers a key topic in plant biology through a review article written for undergraduates with links to primary literature and review articles, PowerPoint slides (examples can be seen in Figure 1) that provide both introductory and advanced material arranged into a coherent narrative, and a teaching guide that includes learning objectives and questions for discussion or assessment. The information in each Teaching Tool is drawn from the primary literature, and the content is peer reviewed. One of our users remarked, "It saves time I would've spent searching the literature," and another appreciates that these materials are "current, up-to-date, and all in one place."

Teaching Tools can support a wide variety of teaching styles. For example, the lecture notes or slides can be used by students as supplement-

tal reading to augment their textbooks, or the instructor can incorporate selected slides into a formal lecture. Alternatively, the materials can be used as resources and offer the foundation for in-depth classroom discussions of primary literature. Each topic is conveyed in two sets of slides; a full set of about 100 slides, and an abridged set of 24 slides that highlight the major topic themes and are intended for use in introductory courses.

Ultimately, Teaching Tools in Plant Biology will cover all the major topics in plant biology at a level suitable for advanced undergraduates. A set of ten lectures that covers each of the major plant hormones was completed in 2011, and these lectures have been updated since their initial publication to incorporate the most recent breakthroughs. For example, putative receptors for salicylate and strigolactone hormones were identified after the corresponding Tools were first published, but this new information was included when the Tools were revised. Several lectures on the theme of biotic interactions of plants (including microsymbionts, arthropods, and pathogens) have been published, and more, are coming soon. Lectures on the theme of plant physiology will be published during 2013 and will include Teaching Tools on water uptake and movement, mineral assimilation, photosynthesis, and so forth.

An important objective of biology education is to teach students the processes of scientific data gathering and interpretation. Biology is an empirical science, in which knowledge and understanding come from experiments and models are continually refined and modified to incorporate new data. Students need to learn how to design and analyze experiments and interpret this information. To support this objective, Teaching Tools in Plant Biology slides include summary models as well as explanations of key experiments, and figures from research papers and descriptions of classic and groundbreaking experiments. Each Tool points out unanswered questions and areas of current and future research, to help students recognize the importance of the future contributions that they might make. Another user remarked, "Students really appreciate and like the way the information has been presented."

Periodically we publish Tools on topics of broad societal interest, such as human nutrition, medic-

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Inspiring the Next Generation

inal plants, and biofuels. Whether they become researchers or not, the students we are educating now are going to be faced with social and environmental challenges that demand a solid understanding of the roles of plants in ecosystems and human endeavors. Teaching Tools in Plant Biology highlights the applications of plant science to improving agriculture, the environment and human health, with the objective of enlightening and inspiring students.

Teaching Tools in Plant Biology is available by institutional or personal subscription to The Plant Cell and to ASPB members; a pay-per-view option has just been added. Access to the first six Teaching Tools, including the highly accessed "Why Study Plants?" is unrestricted. Have a look and tell us what you think, and please inform your students and colleagues about this innovative educational resource.

Placing plant science in contemporary context

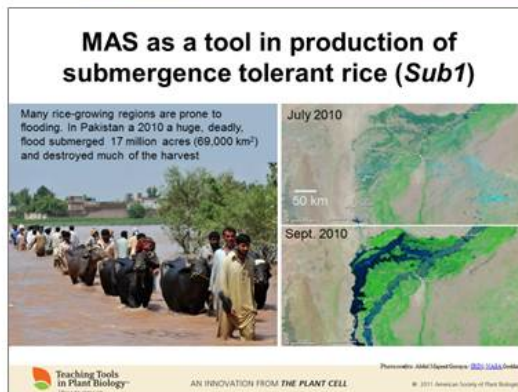
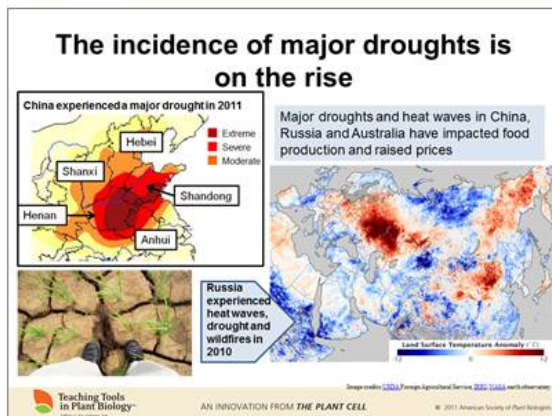
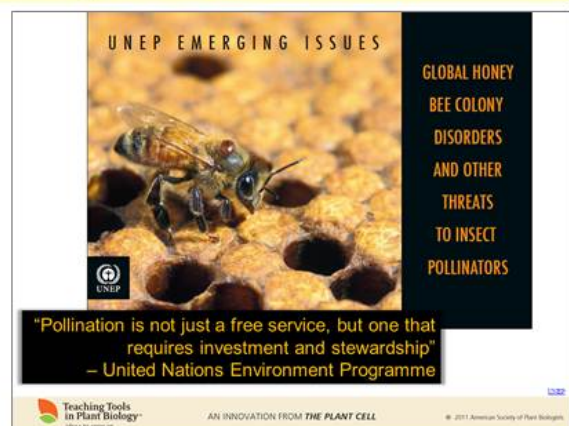
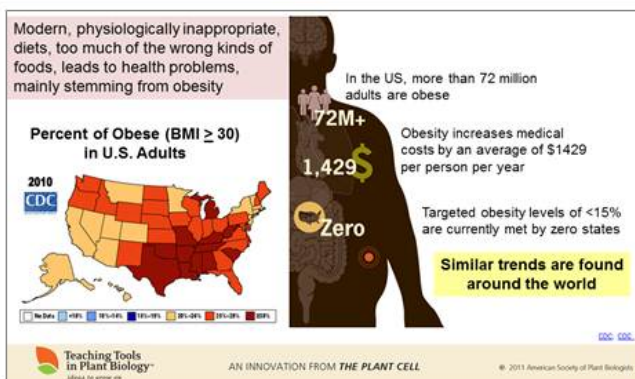


Figure 1: Teaching Tools slides are designed to convey information visually, as illustrated by this set that highlights societal and environmental issues being addressed by plant scientists.

1001 *Arabidopsis thaliana* genomes and GWAS

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To understand the causal relationship between genomic variation and phenotypic variation, genome-wide association studies (GWA) have become the general approach.¹ These analyses have become routine in *A.thaliana*, and the number of published GWA studies is still increasing dramatically. Although most analyses to date have been conducted with a relatively small sample size, the recent release of dense (250k) SNP data for over 1,300 accessions² will enable much larger studies. In addition, online tools that enable GWA analyses on the fly have been developed (see Fig.1), which will further facilitate the use of GWA. Recently, over one hundred *Arabidopsis* genomes collected from around the world have been released.⁴⁻⁶ Their analysis reveals several differences within the *thaliana* lineage, including millions of single nucleotide polymorphism (SNPs), structural variants (SVs), and copy-number variants (CNVs). These data already enable evolutionary and functional studies but do not completely match the data used in GWA. Efforts are presently under way to completely sequence more than 1,000 accessions,⁷ and this raises a question: to what extent will these additional sequences add to our understanding of the genotype-phenotype map in *A.thaliana*?

The answer has two parts: one regards the use of this data for GWA; and the other concerns the general picture of the *A.thaliana* genome.

Starting with the latter, it is noteworthy that even though we are speaking of full genome sequences, the current data are in fact far from complete genome sequences. We are able to call SNPs (and to a lesser degree SVs) with relatively low error rates in the unique part of the genome, but we have only a basic idea about the remaining parts of the genome. We have very little idea of the amount of large structural variants, although some examples have already been seen. Experiments using Flow Cytometry suggest a nearly

10% difference in genome size between different *A.thaliana* accessions,⁸ the source of this variation being far from clear. It is clear, however, that massive genomic differences, including chromosomal fusions and large translocations, exist between *A.lyrata* and *A.thaliana*; these two species diverged only about 10 million years ago.⁹ The Brassica genomes may be more flexible than a naïve glimpse at their DNA sequence would imply. The above argues that even though the *A.thaliana* genome might be one of the best understood genomes at the moment, there is still much that we do not understand. The hope is that once a thousand or more genomes of the same species are available, we can really start tackling these questions.

In regard to first point association mapping, it is important to be aware that it is unlikely for the actual causal variant(s) - for any given phenotype - to be present in the 250k data (they only represent ~ 2-4 % of the SNPs that are still segregating). Although these data may show significant associations in the GWA analysis, linkage disequilibrium (LD) with causative variants will often be the driving force behind these associations. That is, although the resolution in GWA is better than in classical QTL studies (using recombinant inbred lines from single crosses), it is still coarser than single-base-pair resolution. Having full sequence data – and therefore potentially the causative polymorphism (meaning both SNPs as well as SVs, which are as likely to cause phenotypic differences) in the dataset – should help in theory. But there are still many reasons (e.g. epistasis and allelic heterogeneity) why a non-causative marker may still be a better descriptor of the phenotype, than the causative one.¹⁰ In these cases, use of more sophisticated models might be necessary. In this respect, extensions to classical GWA models, analyzing multiple phenotypes or loci together, have been proposed.^{11,12} The combination of both, higher marker density and specific GWA models, should increase the power of the analysis. To add an extra layer of complication, it is increasingly clear that additional data, such as expression and methylation data, influence the relationship between genotype and phenotype. Efforts are underway to produce these data as well.¹³

The vision is that all of these data and tools will

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1001 Genomes Resource

be combined with the amazing phenotypic resources in *A.thaliana*, and hosted in one common location, thus becoming an unparalleled resource for the entire Arabidopsis community.

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The screenshot displays the GWAPP web application interface. At the top, there is a navigation menu with links for HOME, ACCESSIONS, UPLOAD PHENOTYPES, ANALYSIS, and HELP. Below the menu, a 'Welcome to GWAPP' section provides a dataset key and a 'Quick Start' section. The main content area is divided into seven steps, each with a thumbnail image showing the corresponding web interface:

- Step 1 - Upload Phenotypes:** Shows the 'Upload phenotypes form' interface.
- Step 2 - Verify Phenotypes:** Shows the 'Phenotypes' table and 'Statistics' section.
- Step 3 - Create Dataset (Optional):** Shows the 'Filler Box' and 'Geographic Distribution' map.
- Step 4 - Apply Transformations (Optional):** Shows 'Current phenotype distribution' and 'Transformed phenotype distribution' histograms.
- Step 5 - Run GWAS:** Shows the 'GWAS methods' and 'Leading Indicator' section.
- Step 6 - View Results:** Shows the 'Search genes' and 'SNP info' section.
- Step 7 - Run Step-Wise GWAS (Optional):** Shows the 'Selected SNP' and 'Run step-wise GWAS' section.

Fig1: Screenshot of GWAPP. A tool, to perform GWA analysis on the fly. The tool is hosted at <http://gwas.gmi.oeaw.ac.at>.

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Spotlight on the University of Bath

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 Bath and the University of Bristol.

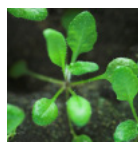
Spotlight on the University of Bath



The plant research groups at the University of Bath include a wide diversity of researchers involved in many aspects of plant biology. Research themes encompass reproduction, evolution and conservation of plants, tropical plant biotechnology and pathology, plant-microbe interactions, defence and hormone signalling, and algae as an alternative fuel. More detail of each PI's research can be found below, or by visiting www.plantresearch-bath.org/.

The plant group is housed within the Biology and Biochemistry department, which has recently been ranked second in the country by The Sunday Times University guide, reflecting the high satisfaction of our students and the quality of both staff and outgoing students. The diversity of research groups within the department allows valuable collaborations with bioinformaticians, biochemists, protein structure specialists, etc.

We have a large number of plant growing facilities, including a dedicated GM house, glass-houses, walk-in chambers, and growth cabinets, and we offer undergraduate, masters and PhD courses for students interested in pursuing plant sciences (www.bath.ac.uk/bio-sci/admissions/). The group is keen to support prospective independent research fellows and informal enquiries are very welcome.



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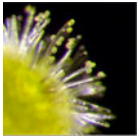
http://www.bath.ac.uk/bio-sci/contacts/academics/richard_cooper/

Plant-pathogen interactions

Innate Immunity: how plants recognize pathogens. Microbial pathogens release conserved molecules which elicit host defences. These MAMPs (Microbial Associated Molecular Patterns) include chitin from fungi, flagellin and lipopolysaccharide (LPS) from bacteria. MAMPs are recognized by PRR receptors, trigger calcium ion influx, signalling pathways and subsequently myriad defences. The Cooper lab was the first to show: bacterial peptidoglycan (PGN) is recognized by plant cells; Arabidopsis cells recognize simultaneously multiple MAMPs to avoid pathogen camouflage; Large MAMPs (PGN, LPS) need first to be degraded to pass through the plant cell wall matrix.

Microbial Pathogenicity: suppression of host innate immunity. Pathogens have evolved arsenals of suppressive molecules in order to counteract MAMP-induced defences. Bacterial extracellular polysaccharides (EPS) are required for full virulence, and provide protection from desiccation and antimicrobials. It was revealed that chelation of calcium ions by polyanionic EPS of diverse pathogens, prevents calcium influx in plants to the cytosol from the apoplast. Defence signalling is suppressed in this way.

Plant defences and sustainable control of tropical diseases: The Cooper lab also undertakes applied research on diseases of some major tropical crops including cassava, cacao and oil palm. Methods of screening disease resistant lines to the major pathogens of oil palm, *Fusarium oxysporum* and *Ganoderma*, have been improved or developed. The lab's method of eradicating *Fusarium* from oil palm seed is in commercial use. DNA probes for rapid and specific detection of *Fusarium* for seed quarantine are being developed. *Ganoderma* infection and epidemiology is ongoing; genetic studies show the importance of basidiospores in its spread.



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Cell-cell communication during plant reproduction; reproductive development

Research in the Doughty group is centred on aspects of plant reproductive biology, with a particular focus on understanding how cells communicate with one another at various stages of this exquisitely regulated process. In recent years much progress has been made in elucidating the molecular basis for recognition events that lead to the rejection of 'self' or closely related pollen by classic self-incompatibility (SI) systems, however, comparatively little is known about the regulators of compatible interactions.

Work in the lab is addressing this gap in our knowledge by examining the role of pollen-borne proteins that are involved in the earliest steps of the pollen-stigma interaction. Compatible interactions must activate processes that initially permit effective hydration of pollen and this is likely to be established by protein interactions at highly focussed regions of the stigmatic plasma membrane. Small cysteine-rich proteins (CRPs) are of particular interest as not only are they important components of the pollen coat but they are firmly established as important regulators of various steps in the reproductive process. A range of molecular genetic approaches are being utilised to gain a full understanding of the role of pollen CRPs in early pollination events and to identify their stigmatic targets.

In collaboration with the Scott Lab at Bath, the group aims at understanding how seed size is regulated in *Arabidopsis*. Early stages of seed development involve endosperm proliferation without the formation of cell walls, followed by cellularisation of the endosperm later in development. It is now clear that the timing of this cellularisation event is a crucial determinant of seed size and work is focusing on factors that potentially interrupt cell-cell signalling which bring about this important developmental process. The group are also investigating the regulation and mechanism of tetrad dissolution during pollen development. This step, which separates the developing microspores of the tetrad, involves that action of a

suite of β 1,3 and β 1,4 glucanase enzymes. A combination of molecular genetic and proteomic approaches are being deployed to dissect this crucial phase of reproductive development.



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Evolutionary genetics, complex trait evolution, ecological adaptation

The Kover lab is interested in the genetic basis and evolution of complex traits such as flowering time, seed size, germination rate, and response to drought and temperature, etc. The aim of this research is to understand how genetics interacts with an organism's ecology to determine the evolution of traits under natural selection. To reach this goal the lab has developed a number of resources that allows improved mapping of quantitative traits in *A.thaliana*, which includes the densely genotyped set of MAGIC lines (Multiparent Advanced Genetic InterCross); and resequencing the 19 parental accessions that were used to produce the MAGIC lines. The group continues to develop more resources for these lines to improve mapping efficiency and accuracy. They also use a direct approach to determine the adaptive value of candidate genes, using experimental evolution. This approach allows the lab to investigate what genes underlie response to selection, and what are the pleiotropic consequences of genetic changes. Finally, the Kover group is also interested in investigating gene by environment interactions, as well the genetic basis of plasticity, under both field and laboratory settings.



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Seed development, plant reproduction, and algae biotechnology

Seeds are the most important agricultural prod-

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Spotlight on the University of Bath

uct, accounting for at least 70% of the world's food supply. With rising population and diminishing availability of agricultural land, it is increasingly urgent to improve crop yields; increasing seed size is one route to this goal. A major interest in the lab is the mechanism of seed growth regulation. The Scott group is investigating this from several angles by looking at the effect of crossing *A.thaliana* plants of different ploidies on alterations to the cell cycle in endosperm, alteration of gene expression, and changes in pattern of imprinting.

The lab also collaborates with Drs James Dougherty and Susan Crennell (University of Bath) to solve a long-standing issue in plant reproductive biology – the identity and regulation of the glucanases responsible for releasing microspores from the post-meiotic male tetrad. The callosic 'barrier' around the tetrad separates the walls of adjacent microspores, allowing them to develop individually. In order for pollen development to proceed, the tetrad walls must be dissolved to release the microspores. The immediate aim of this project is to identify the genes encoding the enzymes responsible for degrading the tetrad walls.

The lab is also interested in several aspects of algal biotechnology including: isolating thermotolerant species from the hot waters of the Roman Baths; reducing product recovery costs by weakening the algal cell wall via mutagenesis and selection; combining wastewater cleaning and algae biomass production to reduce input costs. These projects are in collaboration with Dr Chris Chuck (Chem. Eng) and Dr Chris Bannister (Mech. Eng), both of the University of Bath.



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www.evolutionarygenetics.org

Genetic architecture, quantitative genetics, evolutionary theory

The Wolf lab focuses on the genetic architecture of complex traits. The research emphasis is mainly on components of genetic variation that tend to be ignored or under-appreciated in analyses of genetic architecture. These include

maternal effects, epigenetic effects, indirect genetic effects, and gene interactions. The lab integrates theoretical, computation, and empirical approaches to understand how these sources of variation structure the genotype-phenotype and influence evolutionary dynamics. They use several different model organisms to achieve their goals, including plant, animal, and microbial models. Plant based research has mainly focused on the genetic basis of interactions (e.g., competition) between plants, using primarily QTL mapping and candidate gene approaches in *Arabidopsis thaliana*.



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The molecular basis of signal transduction in plants

S-acylation of eukaryotic proteins is the reversible attachment of palmitic or stearic acid to cysteine residues, catalysed by protein S-acyl transferases (PATs) that share an Asp-His-His-Cys (DHHC) motif. Previous evidence suggests that in *Arabidopsis* S-acylation is involved in the control of cell size, polarity and the growth of pollen tubes and root hairs. Using a combination of yeast genetics, biochemistry, cell biology and loss of function genetics, the roles of a member of the PAT family, AtPAT10, have been explored. In keeping with its role as a PAT, AtPAT10 auto-S-acylates, partially complements the yeast *akr1* PAT mutant, and this requires Cys192 of the DHHC motif. In *Arabidopsis* AtPAT10 is localised in Golgi and tonoplast. Loss-of-function mutants have a pleiotropic phenotype involving cell expansion and division, vascular patterning, and fertility that is rescued by wild-type AtPAT10 but not by catalytically inactive AtPAT10C192A. This supports the hypothesis that AtPAT10 is functionally independent of the other *Arabidopsis* PATs. Our findings demonstrate a growing importance of protein S-acylation in plants, and reveal a Golgi and tonoplast located S-acylation mechanism that affects a range of events during growth and development in *Arabidopsis*.

Mathematics in the Plant Sciences Study Group VI

25-28 March 2013
Nottingham



If you are a plant or crop scientist who would like a willing team of mathematicians to work on your research problem at this meeting, please contact Susie Lydon (susannah.lydon@nottingham.ac.uk).

For more information about how study groups work and previous successful problems, visit www.cpiib.ac.uk/events/mpssg/

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Spotlight on the University of Bristol

Spotlight on the University of Bristol



Plant Science research and teaching in Bristol are on a rapid upward trajectory. Two out of five new academic appointments are plant scientists (Heather Whitney and Antony Dodd). In addition, Bristol has a fundamental role in the BBSRC wheat genome project, driven by Keith Edwards and Gary Barker. The University is committed to the future of plant science, becoming the first UK University in nearly 50 years to create a new botanic garden. The University incorporates Fenswood Farm, which houses additional plant growth facilities and field trial facilities. Plant sciences in Bristol interconnects with the Food Security and Land Research Alliance (Bristol, Exeter, Rothamsted <http://www.fslra.ac.uk/>), including access to North Wyke experimental farm platform in Devon. Doctoral Training in the School includes World Class Bioscience and Food Security PhD studentships within the BBSRC-funded South West Doctoral Training Partnership (<http://www.bris.ac.uk/swdtp/>). Overall, plant science in Bristol is on the up – literally too – we move in 2013 to the top floor of the new Life Sciences building!

The strength of Bristol's research and teaching lies in its breadth. The unifying theme is our desire to understand biological complexity at all scales - from molecules to ecosystems. Research at Bristol is in four interwoven themes: 1) Evolution, 2) Animal Behaviour and Sensory Biology, 3) Plant and Agricultural Sciences, 4) Ecology and Environmental Change. "Animal Behaviour and Sensory Biology" is the 'brand' that Bristol is best known for, described as 'world leading' at the last RAE, with two members of the University Centre for Behavioural Biology, Alasdair Houston and John MacNamara, recently elected FRS.

The new grouping "Plant and Agricultural Sciences" reflects growing strengths and the global need for research in Food Security (a BBSRC strategic theme). Plant scientists at Bristol perform a wide range of research from model organism molecular, cell and systems biology (Antony Dodd, Kerry Franklin, Claire Grierson, Alistair Hetherington) to biotechnology, pathology (Andy

Bailey, Gary Foster), ecology (Jane Memmott, Heather Whitney, Marion Yallop), and evolution (Simon Hiscock and Jon Bridle), all within a lively and highly collegiate environment.

The theme of Evolution is at the heart of the mission for the new Life Sciences building, and will incorporate expertise from Chemistry (Steve Mann, investigating proto-life), Earth Sciences (palaeobiology, Mike Benton, Phil Donoghue, Emily Rayfield), Computer Science (protein structure databases, Julian Gough) and Social Medicine (human genome analysis, Ian Day), plus three new appointments in phylogenomics (Davide Pisani, Seirian Sumner, Jakob Vinther). Bristol aspires to be a world centre for evolutionary biology and Omics technologies will be at the heart of this.

The final theme "Ecology and Environmental Change" focusses on climate and environmental change (NERC strategic theme) and links strongly with the newly formed University of Bristol Cabot Institute (<http://www.bristol.ac.uk/cabot/>), a hub of interdisciplinary research activity to address how humanity might live sustainably in the face of environmental uncertainty.



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<http://www.bris.ac.uk/biology/research/plant/pathology/>

Fungal plant pathology and fungal biotechnology

Andy's research interests are based around the biology of fungi. Several different areas are researched including; the biology of plant pathogenic fungi, fungal viruses, transformation and manipulation of basidiomycetes and fungal biotechnology including natural product production by fungi. These areas often overlap, for instance in the case where a secondary metabolite is also used as a virulence factor for establishing disease.

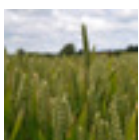
Andy also has interests in genome analysis and has been involved in the generation and analysis of genome data for species such as *Mycosphaerella graminicola*, responsible for *Seporia tritici* leaf blotch on wheat and *Agaricus*

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bisporus, the common cultivated button mushroom.

Much of the research has its basis in the establishment of effective genetic transformation systems for the fungus, to allow investigations into gene function and providing a means to manipulate gene content or gene expression and these tools and techniques have been developed for a large number of different ascomycete and basidiomycete species.



Gary Barker

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Bioinformatics for wheat genetics.

Gary Barker is a bioinformatician, with a primary interest in the development and application of wheat genetic markers.

Wheat is one of the world's, and certainly the UK's, most important crops. We need to be able to grow more wheat on less land with lower inputs to meet population growth predictions, and this comes at a time when many fear that yields are plateauing. The UK wheat pre-breeding program funded by BBSRC aims to introduce novel genetic diversity into modern UK wheat germplasm by generating novel synthetic wheat varieties and by bringing in novel alleles from non-cultivated wheat and wild relatives. At Bristol we are using state-of-the-art sequencing, bioinformatics and genotyping to generate dense genetic maps for wheat. Marker-assisted selection is then used to speed up the lengthy process of generating stable, commercially viable new varieties with novel useful phenotypes. See www.cerealsdb.uk.net for more information.



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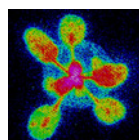
Ecological and population genetics

Jon's research group collaborates closely with

Jane Memmott's, and uses field experiments and molecular and quantitative genetics to explore how species' interactions evolve in response to climate change, and the effects of local adaptation and genetic diversity on the success of plant translocations.

The evolution of pollination networks in response to climate change may be critical for population persistence, as well as in stabilising networks affected by species loss. At the same time, variation in species' responses may create mismatches between the timing of flowering and insect emergence. In collaboration with the Avon Wildlife Trust, the group are testing the role of local adaptation in shaping biotic interactions in the cowslip *Primula veris*, a plant of UK conservation interest, as well as the potential for its interactions with its pollinators to evolve in the future.

Plant translocation and reintroduction may be crucial for ecosystem health and species conservation with rapid climate change. Should seed be sourced from nearby sites to preserve local adaptation, or combined across several populations to maximise genetic diversity, providing the local environment with the widest range of plant characteristics to favour following translocation? Policy on reintroductions often specifies that material used should be from local sites, but this may be counter-productive. The group are collaborating with the Somerset Wildlife Trust, and are using molecular genetic techniques to test whether introducing appropriately adapted populations improves the success of reintroductions of a UK BAP species, *Sium latifolium* (Greater Water Parsnip).



Antony Dodd

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Circadian biology

Antony Dodd investigates how the circadian clock controls cell physiology and signal transduction, in order to understand how circadian regulation optimizes plant performance. The circadian clock produces a biological estimate of the time of day. Circadian regulation is crucial because circadian

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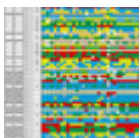
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timekeeping increases photosynthesis, productivity and seed production, and regulates plant water use, so contributes to crop yield and ecosystem productivity. The Dodd lab investigates the following questions:

1. How does the circadian clock control photosynthesis? There are circadian rhythms of photosynthesis, but it is not known how the circadian clock regulates the photosynthetic apparatus within chloroplasts. The group are investigating the nature of the signalling pathways that couple the circadian clock with the photosynthetic apparatus.

2. Circadian organization of the proteome, phosphoproteome and membrane transport. Little is known of how the circadian clock organizes the proteome in terms of protein abundance and post-translational modification. The Dodd lab are using proteomics strategies to investigate this question with a particular focus on membrane systems, which are a crucial focus in plants for abiotic stress responses, photosynthesis, water fluxes and signal transduction. They are also investigating the role of specific protein kinases in circadian oscillator function and the coupling of the circadian clock with circadian-regulated cell physiology.

3. How is the circadian clock tailored to physiologically-relevant cell types? A small number of cell types in plants have a disproportionately large impact on water use and stress tolerance. This includes the stomatal guard cell and root endodermis. The Dodd group are investigating how circadian regulation in these cell types optimizes plant performance because the environment is characterized by 24 h cycles of water availability.



Keith Edwards

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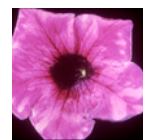
<http://www.cerealsdb.uk.net/>

Wheat genomics and pre-breeding

Keith's research covers the board areas of wheat genetic and genomics; he was the PI on the BBSRC funded project to generate, in collaboration with Liverpool and the John Innes Centre, a 5 fold sequence coverage of the Chinese Spring

wheat genome, data that was placed in the public domain in August 2010. Following on from the sequencing success, Keith, via the BBSRC funded wheat improvement strategic program, has focused his efforts on converting the information to SNP-based markers for use by wheat breeding companies, work that has resulted in the release of over 100,000 wheat SNPs to the wheat community. Keith was awarded the 2011 Royal Agricultural Society of England's research medal for his contribution to UK agriculture.

Recently Keith has expanded his research program to include a study of homoeologous and homologous recombination, to achieve this he is currently developing a number of deletion and transgenic lines for genes known to be involved in recombination. It is because of the problems in growing and crossing wheat within the university system that Keith is now a big fan of the wheat variety "Apogee". Apogee is a rapid cycling wheat (9-10 weeks) making it ideal for undergraduate studies. Keith received his first transgenic Apogee wheat from Rothamsted in September and he is looking forward to letting his level III practical project students loose on the material over the coming academic year.



Gary D. Foster

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Molecular plant pathology and biotechnology

Gary's research is focused on investigating a range of interconnecting themes that include plant virology, plant pathology, plant molecular biology, molecular mycology and biotechnology. The interdisciplinary approach to this research is one of the strong selling points, along with a vibrant lab community and the strong supervisory team, which has been supported by a range of funding sources continuously since 1992. This has included funding from the BBSRC, DEFRA, LESARS, Royal Society, the Wellcome Trust, DfID/ODA, Rothamsted International, and collaborative funding with agricultural industries and institutes, such as CSL-York, HRI-Wellesbourne, RHS-Wisley, PBI-Unilever. Funding has also come from international partnerships and collab-

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orations that have created research links/interchanges and visitors to the research group. The molecular mycology and biotechnology areas have also covered projects on drug discovery and manipulation including a major collaboration with GSK on antibiotic discovery and development. This work continues through a large team exploring the potential of basidiomycetes to produce compounds of interest to industry and medicine.

Current research themes within the lab cover a range of topics in plant pathology, including plant pathogen-stomatal interactions, changes in leaf surface upon pathogen attack which is also linked to how insect vectors perceive plants. This in addition to more direct and molecular studies on specific viruses which at present include the serious diseases of Pepino mosaic virus which is causing significant losses in tomato, as well as Cassava brown streak virus, a cassava virus that is affecting large parts of East Africa and threatening a staple food crop for much of the region and which is now reached epidemic proportions. Work also continues on a range of fungal pathogens, including basidiomycete pathogens such as those in *Armillaria*, which links nicely with the drug discovery team within the group.



Kerry Franklin

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Light and temperature-regulation of plant development

Light and temperature are two of the most important environmental stimuli regulating plant development. Plants perceive light using specialised information transducing photoreceptors which include the red and far-red light-absorbing phytochrome family. The Franklin lab focuses on investigating the interactions between light and temperature signalling in *Arabidopsis*. A primary research interest of the group is the interaction between light quality and temperature signalling pathways in the regulation of plant architecture. We have shown that some shade avoidance responses of the model species, *Arabidopsis thaliana*, are modulated by ambient growth tem-

perature and have identified a number of genes which are regulated by phytochrome in a temperature-dependent manner. These include the CBF regulon of genes involved in cold acclimation and freezing tolerance. The group have also established that the phytochrome-interacting factor PIF4 functions as a key regulator of plant architectural responses to elevated temperature, thereby operating as a central hub of light and temperature signal integration. They are currently investigating the parallels between shade avoidance and high temperature signalling and the fitness costs/benefits of such plasticity.

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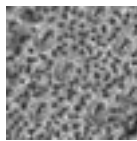
Claire Grierson
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Root development

Claire Grierson's research has three linked strands: Root hair development, Theoretical approaches to biology; and Interactions between roots and soils. By dissecting root hair growth in *Arabidopsis*, Grierson, her team, and international collaborators identified numerous genes with important roles, showed how auxin flows sustain root hair growth, and revealed how dynamic interactions between molecules could establish polar growth in root hair cells. Fundamental theoretical collaborations include characterising the surprisingly wide range of behaviours of even very simple biochemical circuits, and tackling how network structure might contribute to function. Grierson is developing new research to discover what plants contribute to root-soil cohesion, addressing questions such as "why are plants so hard to uproot?", "how can roots help to prevent soil erosion?", and "how might roots be affected by climate change?". She continues to use *Arabidopsis* for most of her experiments because of its unsurpassed power for empirical plant genetic research, but has ongoing research with Keith Edwards and others on root hair development in cereals.

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Alistair Hetherington

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Signal transduction pathways controlling stomatal function and development

The research in Alistair Hetherington's group centres on understanding, at the cellular level, how plants respond to a changing environment. Hetherington is interested in identifying the components present in the intracellular signalling pathways responsible for coupling extracellular stimuli to their characteristic responses. To investigate this, his group focus on stomata, the pores found on the surfaces of leaves. Environmental signals regulate both stomatal development and the aperture of the stomatal pore and current interests lie in the regulation of stomatal aperture and development by carbon dioxide, ABA and changes in atmospheric relative humidity. At the cellular level the group maintain a strong interest in calcium-based intracellular signalling with ongoing research into long chain phosphorylated sphingoid base signalling and the mechanisms responsible for encoding information in, and decoding information from, stimulus-induced calcium elevations (calcium signatures). More recently, through work on stomatal evolution, there is an increasing interest in the evolution of signalling pathways. Although most of the work is in *Arabidopsis*, recently research has involved the model lower plant *Selaginella* and the cereals barley and wheat. The cereal work, which is carried out with colleagues at Bristol and elsewhere, is in the context of Food Security and is focussed on investigating the potential of modifying stomatal behaviour and development with the aim of improving water use efficiency. This later area relates to Living With Environment Change research and in this context Alistair Hetherington's group are also interested, together with other colleagues in Geography at Bristol, in using crop albedo as a possible bio-geoengineering strategy to combat global warming.



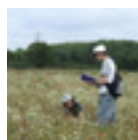
Simon Hiscock

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Plant ecological and evolutionary genetics

Research in Simon's lab seeks to understand fundamental processes in plant evolution, such as adaptation and speciation, using genetics and genomics to study the interacting forces of mating system, interspecific hybridization, and polyploidy. Much of this work has focused on three taxonomically 'difficult' groups: *Senecio* (*Asteraceae*), *Sorbus* (*Rosaceae*), and *Orobanche* (*Orobanchaceae*). Current research projects include: (i) the genomic basis of adaptation and speciation in the genus *Senecio* (*Asteraceae*), (ii) the molecular genetic basis of pollen-stigma recognition and self-incompatibility in *Senecio*, (iii) the genetic basis of mating system (self-incompatibility) variation and evolution in *Senecio*, (iv) genetic divergence, mating systems, and ongoing evolution in the genus *Sorbus* (*Rosaceae*), (v) local adaptation and genetic divergence in holoparasitic broomrapes (*Orobanche*). Funding for this work has come from NERC, BBSRC, The Leverhulme Trust, Royal Society, The Linnean Society (COSyst), and BSBI. Collaborators include: Richard Abbott (University of St Andrews), Dmitry Filatov and Stephen Harris (University of Oxford), Mark Carine (NHM), Tim Rich (National Museum of Wales).



Professor Jane Memmott

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Community ecology

Jane's research interests in ecology include pollination ecology, invasion ecology, agro-ecology, biological control, urban ecology and restoration ecology. A theme that runs through many of her projects is the use of ecological networks (food webs or pollination networks) as a tool to answer a variety of environmental questions. For example does restoration ecology restore ecological function, are ecosystem services affected by farming approach and how do aliens integrate

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into ecological networks?

Jane works as both a pure and an applied ecologist and is particularly keen on working at the interface between the two disciplines. A wide variety of techniques are used by her research group, from field observation to field experiment, from theory to molecular approaches. Plants form the bottom layer of all her food webs and one of the areas her group is particularly interested in is whether positive and negative effects can cascade upwards from these plants, rippling through the associated ecological network. For example, work recently published in *Science*, demonstrated that some farmland plant species were disproportionately well-linked to many other species and these were the ones to target when conserving biodiversity in agroecosystems.



Patricia Sanchez-Baracaldo

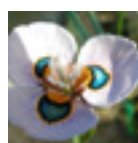
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<http://www.bristol.ac.uk/biology/people/patricia-sanchez-baracaldo.html>

The evolution of cyanobacteria and biogeochemical cycles

Cyanobacteria have played a fundamental role in the Earth's history, enabling the rise of atmospheric oxygen. Patricia's work on the evolution of cyanobacteria uses phylogenomics, molecular clock analyses and ancestral character state reconstruction. Her research has revealed that cyanobacteria first evolved in freshwater environments (2.7 Ga = billion years ago) and later they started colonising marine environments at around the Great Oxygenation Event (2.3 Ga). The origination and diversification of cyanobacteria had a profound impact on global biogeochemical cycling and the climate of the early Earth. Her current research focuses on understanding how the colonisation of marine environments by different groups of cyanobacteria has had an impact on biogeochemical cycles such as nitrogen, oxygen and carbon. Patricia's interdisciplinary approach combines evolutionary biology and an Earth system modelling. Other areas of research in her lab include: 1) the evolution of nitrogen fixation, 2) the generation of new genomic data to study the evolution of glacial cyanobacteria by

assessing how many times they have adapted to extreme cold habitats during the Earth's history, and 3) the use of molecular phylogenetics to understand the evolutionary processes that some plants groups have used (e.g. new morphological traits) to adapt and colonise extreme high elevation ecosystems in Andean mountains.



Heather Whitney

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Interactions at the plant surface

Heather's research focuses on how the structure of the plant surface can influence both biotic and abiotic interactions. At the moment this includes a range of projects from how the plant surface interacts with water and temperature to how bees grip onto the petal surface. One major project is an investigation how the plant surface interacts with light, in particular, how structural colour and iridescence is produced by the plant surface and how this be of benefit to the plant either through the light transmitted (for photosynthesis), or through the light reflected (photoprotection, temperature control or, in flowers, attraction of pollinators). This is an interdisciplinary project looking at every aspect of iridescence from its structure, development and occurrence to the impact it has on plant growth and interactions with other organisms such as insects. Heather therefore uses a range of techniques to investigate these interactions including plant molecular biology, optical analysis, biomimetics and animal behavioural assays.



Marian Yallop

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Ecosystem change

Marian's work focuses on various aspects of the structure and function of freshwater ecosystems in changing environments. One research area uses benthic diatoms as indicators of ecological

status in both rivers and lakes. The Yallop group work on a number of aspects of lake functioning with a key interest in lake state switching, growth of periphyton, phytoplankton and submerged macrophytes. In compliance with recent legislation (Water Framework Directive) they have been involved in the development of predictive tools, using benthic diatoms, to assess the ecological status of rivers and lakes in the UK. These tools primarily detect eutrophication but ongoing work examines the impact from other agrochemical pressures. In addition to work in temperate environments the group is involved in an interdisciplinary collaboration to investigate how algal communities in extreme conditions, such as those growing within glaciers, may function and evolve in response to climate change. Critically, these algae may produce screening pigments to protect them from UV or high irradiance, and these pigments in turn may potentially reduce albedo of snow and ice and actually promote surface melt, thereby promoting their growth in addition to melting the ice sheet.



UK PlantSci 2013

University of Dundee

16th - 17th April

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David Baulcombe (University of Cambridge)

Paul Birch (University of Dundee)

Rob Edwards (Fera)

Beverley Glover (University of Cambridge)

Charles Godfray (University of Oxford)

Sarah Gurr (University of Oxford)

Mike Holdsworth (University of Nottingham)

George Lomonosoff (John Innes Centre)

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