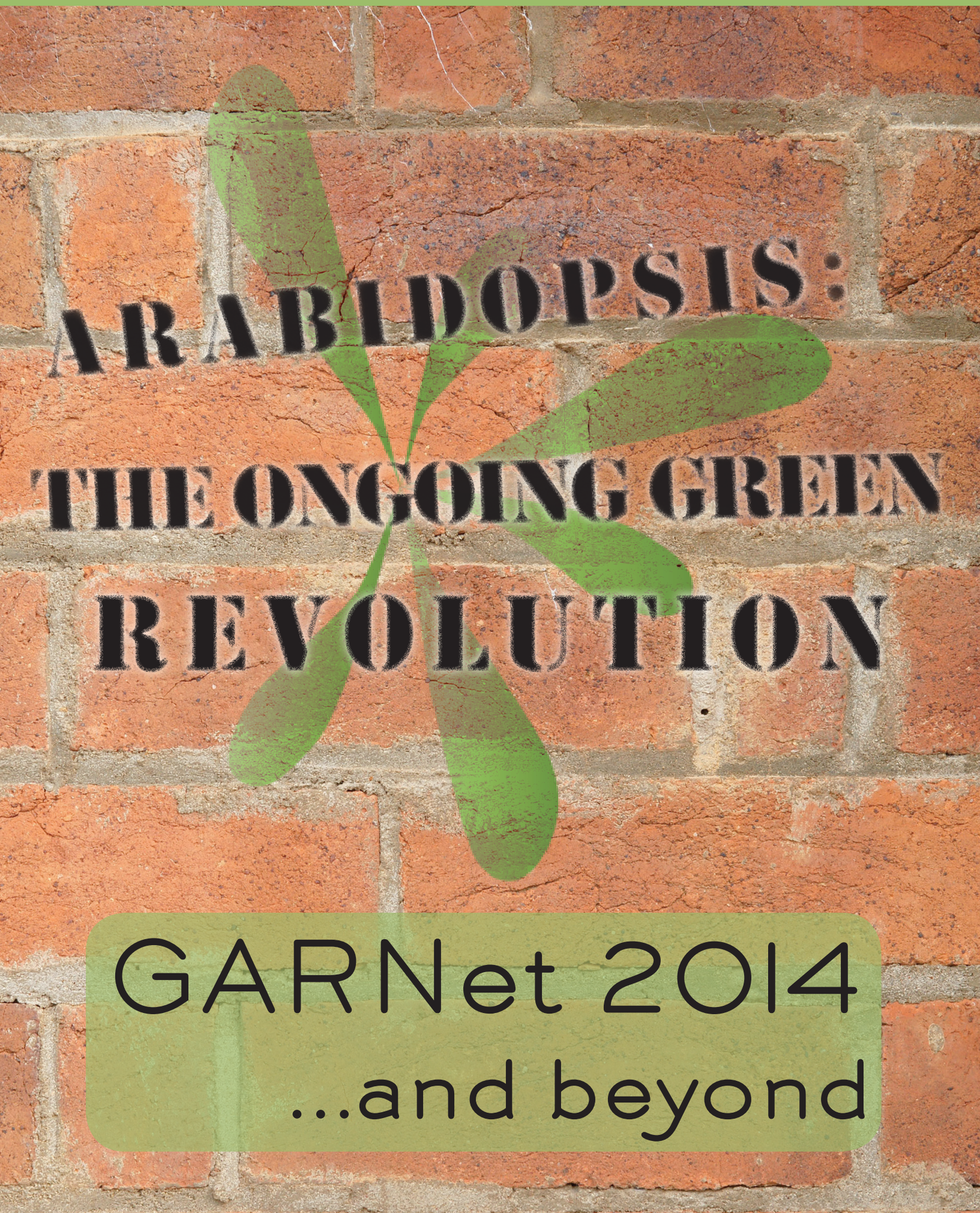
GARNish
December 2014 Edition 22



GARNet 2014
...and beyond

Welcome to the December 2014 Issue of GARNish

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As we approach Christmas and the New Year it's time to reflect on the year gone by – and what a busy year it has been!

Since the last issue of GARNish in June, the GARNet team has been keeping up to date with the latest plant science around the world by attending conferences in Dublin (FESPB-EPSO), Manchester (SEB), Portland, Oregon (ASPB) and Vancouver (ICAR). In fact, it was at ICAR 2014 that we heard Christine Queitsch, from the University of Washington, speak about PlantRegulome.org, a new online resource for plant scientists that provides open access to cis-regulatory element data for *Arabidopsis thaliana*. You can read more about this on pages 16–17.

We also hosted our own conference in September; GARNet 2014, *Arabidopsis: The Ongoing Green Revolution*. Attended by almost 100 plant scientists from across the country, this two-day conference was held at the University of Bristol (hence the Banksy-esque front cover!), with the poster session taking place in the brand new Life Sciences building. Officially opened by Sir David Attenborough a couple of weeks after our conference, this state-of-the-art facility will be a fantastic asset for research and teaching in Bristol. See pages 14–15 for more.

Then in November, GARNet was involved in organising a proteomics workshop led by Alex Jones at the University of Warwick. A few days later we were out and about again, this time visiting the University of Liverpool for our second Software Carpentry bootcamp of the year. Like the one we ran in April, this one was yet again over-subscribed, demonstrating the demand and need for basic training in computer programming among members of the plant science community. GARNet isn't planning to organise any more Software Carpentry bootcamps, but on page 12, we have put together our top tips to consider if you would like to arrange your own.

With BBSRC's renewed focus on plant science as part of its food security agenda, Arabidopsis researchers have been really successful in terms of funding applications this year. On pages 6–11 the PIs of some newly funded BBSRC grants tell us about their forthcoming projects, while as part of our feature on The Genome Analysis Centre on pages 20–23, Rob Davey explains the Collaboratively Open Plant 'Omics (COPO) project, which GARNet will be involved with. There's a Spotlight feature on the University of York, too (pages 24–30).

If you hadn't already heard our very own funding news, GARNet has also been awarded renewed funding for another five years, so we will be here supporting the UK plant science community until 2020! Our new PI is Jim Murray from Cardiff University, so GARNet will be based in Wales from 1st February 2015. See page 4 for more details.

Talking of BBSRC, Lisa visited the Great British Bioscience Festival in November (page 18); a celebration of 20 years of BBSRC-funded research and a great outreach opportunity for plant science.

Here's to the next five years of GARNet, and many more years to come of excellent UK plant research. Merry Christmas, Happy New Year, and best wishes to all for the rest of 2014 and beyond!

Twitter: Follow @GARNetweets and @weedinggems.

Also don't forget the **Weeding the Gems blog** at *http://blog.garnetcommunity.org.uk*. Please contact Charis at charis@garnetcommunity.org.uk if you would like to write a guest post!

Contents

Thanks to: Ruth Bastow, Mike Blatt, John Christie, Seth J Davis, Jonathan Jones, Gerhard Leubner, Hayley London, Christine Queitsch, Ari Sadanandom, Giovanni Sena, Gordon Simpson, Alessandra Sullivan, Mimi Tanimoto, Simon Turner and Alex Webb

The GARNet Committee

New GARNet Committee Members

GARNet's renewed funding for the next five years brings some changes to GARNet's organisational structure. First and foremost, we say 'goodbye and thank you' to Jim Beynon who is retiring from the University of Warwick and his position as GARNet PI. Going forwards, GARNet will be led by Jim Murray from Cardiff University, who has served as GARNet's Chair for the last three years.

Having been based at Warwick, GARNet's Communication & Liaison Officer Charis Cook will be moving to Cardiff to work with Jim M and continue in her role, but we say goodbye to Lisa Martin who has worked as the Research & Engagement Officer since July 2013.

There are changes to the GARNet committee too, with three members coming to the end of their three-year stints. Our thanks go to Malcolm Bennett (University of Nottingham), Heather Knight (Durham University), and Smita Kurup (Rothamsted Research) who have all been invaluable members of the team since 2012. In their places we welcome newly elected committee members Katherine Denby (University of Warwick), Ian Henderson (University of Cambridge) and Zoe Wilson (University of Nottingham), while existing committee member David Salt (University of Aberdeen) takes over from Jim Murray as Chair.

Jim Beynon posing with his very life-like Arabidopsis retirement cake! *Photo: Lisa Martin*

New GARNet publication: Data Mining with iPlant

GARNet has recently published a paper in the *Journal of Experimental Botany* that describes the successful 'Data Mining with iPlant' workshop we held at the University of Warwick last year. Written by Lisa, Charis and Ruth from the GARNet team, with help from Jason Williams and Naim Matasci from the iPlant Collaborative, a toll-free copy of this publication is available to download from the GARNet website at: *http://tinyurl.com/iplantpaper*.

We are planning new and exciting links with the iPlant Collaborative in the future, so watch this space!

Global Plant Council Update

Global Plant Council (GPC) Executive Director Ruth Bastow was busy over the summer promoting the GPC at conferences all over the world. In addition, the GPC Executive Committee met for their fifth Annual General Meeting in October. Hosted by the Society for Experimental Biology at Charles Darwin House in London, the AGM was attended by individuals representing 22 member organisations from five continents.

The first day of the AGM was dedicated to sharing news and updates on recent GPC activities including DivSeek (*http://www.divseek.org/*), the Digital Seed Bank, Biofortification and Stress Resilience. The second day focused on new initiatives including an online digital resource, the Plant Knowledge Hub, which aims to provide plant researchers across the globe with access to news, events, funding opportunities, educational and outreach resources, a directory of global research projects and other relevant information all in one place.

Attendees of the 2014 Global Plant Council AGM.
Back row L>R: Beat Boller, Antonio Costa de Oliveira, Ellen Bergfeld, Ariel Orellana, Crispin Taylor, Jim Beynon, Vicky Buchanan-Wollaston, Henry Nguyen, Rodomiro Ortiz, Zuhua He, Gustavo Habermann, Shahrokh Khanizadeh, Charis Cook, Nelson Saibo, Carl Douglas.
Front row L>R: Paul Hutchinson, Ruth Bastow, Russell Jones, Christine Foyer, Wilhelm Gruissem, Zhihong Xu, Karin Metzlaff, Mimi Tanimoto.

The Global Plant Council has made vast progress in the past two years – and there is much more still to come! You can keep up to date with the GPC by joining the mailing list. Contact ruth@globalplantcouncil.org to sign up. The GPC blog is also a source of interesting plant science news and stories from around the world: *http://blog.globalplantcouncil.org*.

UK Plant Sciences Federation Update

Following the launch of the UKPSF report on the status of UK plant science in January, four working groups were established in the areas of Training and Skills, Funding, Translation, and Regulation, to develop mechanisms to implement the report's recommendations. Each group has developed a set of strategic plans for the UKPSF to work with the scientific community, policymakers, funders and educators.

A major plan to emerge – cutting across all of the priority areas identified in the report – is the development of a roadmap for UK plant science for the next 25 years.

The next annual UK PlantSci conference will take place at Harper Adams University on 14–15th April 2015. The meeting provides a unique forum for all those interested and working in the plant sciences to come together and share their knowledge and expertise. The programme includes the session topics: Plants and Agriculture; Trees, Forests and Environmental Change; Cells; Roots, Soil, Nutrients and Water; and Ecology, Environment and Biodiversity. There will be an early career session, and open floor and panel discussions. For more information visit the meeting website: *http://plantsci2015.org.uk/*.

Arabidopsis Information Portal

The Arabidopsis Information Portal (AIP, or 'araport') is now up and running at *http://www.araport.org*. An open resource for genome data, online tools, community news, jobs and more, you can find out more by visiting the website, or reading this paper in *Nucleic Acids Research*: *http://tinyurl.com/araport*.

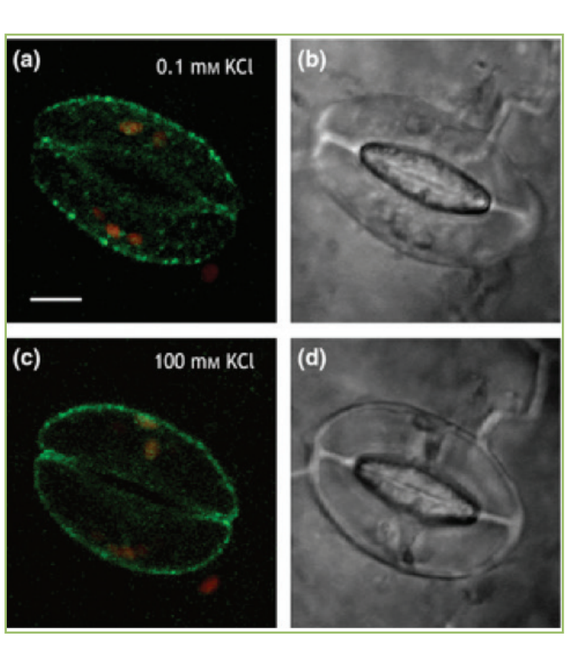
New Arabidopsis Grants

Arabidopsis researchers were very successful in the recent BBSRC responsive mode funding round. Here's a round-up of new grants awarded to members of our community. Congratulations!

Analysing GORK Clustering for Enhanced Stomatal Control

Mike Blatt, University of Glasgow

Mike Blatt has long researched the mechanisms of stomatal opening and closing. Stomatal transpiration is at the centre of a crisis in water availability and crop production that is expected to unfold over the next 20–30 years, so stomata present an important target for manipulating crop performance.



Mike Blatt: GORK-GFP fluorescence (a,c) and brightfield images (b,d) in a pair of guard cells in 0.1 mm KCl (a,b) and after transfer to 100 mm KCl (c,d). Scale bar: 5 µm. Images in (a) and (c) are overlaid, 3D projections of GORK-GFP(green) and chloroplast (red) fluorescence from z-stacks taken at intervals of 0.7 µm. *Reproduced from Eisenach et al. (2014), Plant J* ***78****, 203–14, with permission. © 2014 The Authors The Plant Journal © 2014 John Wiley & Sons Ltd.*

Stomatal movements are driven by solute transport, and consequent uptake/loss of water, across the guard cell membrane. Guard cells harbour ion channel proteins to facilitate cation flux for stomatal movement. Uniquely, the opening (or gating) of one class of plant ion channels is also sensitive to external K^+ concentration. These channels are found in guard cells of tobacco, Vicia and Arabidopsis; in the latter encoded solely by the GORK gene. Increasing K^+ outside moderates channel opening in parallel with the equilibrium voltage for K^+ and affects whole-cell conductance. These channels are the main pathway for K^+ efflux during stomatal closure, but their K^+-sensitivity constrains K^+ flux capacity, notably at higher external K^+. Quantitative systems modelling (see Wang, *et al*. 2014, *Plant Physiol* **164**, 1593–9) suggests that stomatal closure could be accelerated threefold with only a moderate increase in the flux capacity of these channels. Best estimates indicate that a threefold increase in the rates of stomatal closure could yield very substantial gains in water use efficiency by the plant (see Lawson & Blatt 2014, *Plant Physiol* **164**, 1556-1570).

Mike's lab previously uncovered evidence that the K^+-dependence of GORK gating is associated with its assembly in puncta (Eisenach *et al*. 2014, Plant J **78**, 203–14). These assemblies require the so-called 'voltage-sensor domains' (VSDs) of GORK, which are known to couple voltage to channel gating. It is likely that punta assembly is the mechanism behind the cooperative gating associated with external K^+. Over the next three years Mike will explore the mechanics of clustering of these channels. Clearly, these discoveries offer the means to explore a unique and fundamental property of this unusual class of K^+ channels in plants, and are likely also to pave the way to manipulating channel activity and, potentially, to enhancing water use efficiency of the plant.

A Complexity Science Approach to Plant Tissue Regeneration

Giovanni Sena and Henrik Jensen, Imperial College London

Tissue regeneration in multicellular organisms is a topic of great interest both in basic and applied

contexts. To shed new light on the mechanisms underlying tissue regeneration, this project intends to test experimentally a technical but intriguing hypothesis on the way cellular divisions are organised during regeneration.

The experimental case studied is that of Arabidopsis root tip regeneration following mechanical excision. Any significant improvement of our understanding on how roots can regenerate after a major injury opens the possibility of enhancing growth and resistance of plants of economic interest cultivated in challenging environmental conditions.

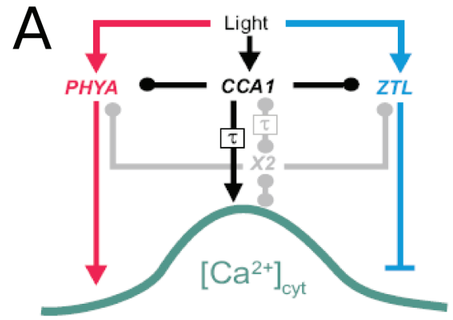
This project will study tissue regeneration from the novel point of view of complex systems, focusing on an original quantitative analysis of cell division dynamics. It will adopt a combination of high spatial and temporal resolution live imaging, statistical analysis of response distributions in temporal series of cell division events, and mathematical modelling of effective cell–cell interactions leading to intermittent activity.

The working hypothesis is that regeneration can be described as the emergent property of a complex dynamical system, and that the underlying statistics of cell division events carry crucial information on the fundamental mechanisms driving the process. In synthesis, the scientists will look for classic signs of scale-free behaviour in the temporal distribution of cell divisions during Arabidopsis root tip regeneration. A scale-free dynamic, one where no characteristic scale length or duration can be identified, is a classic hallmark of criticality observed, at least to some degree, in a variety of phenomena ranging from earthquake events to brain neuronal activity. The main question here addressed is whether this notion can be extended to complex phenomena in developmental biology.

A Linear Systems Toolkit for Biology

Alex Webb & Jorge Gonçalves, University of Cambridge, Seth J Davis, University of York

The collaborators have developed a tool set from Engineering to identify the causal connections in biological networks. They use linear time invariant (LTI) models to describe the dynamic relationships



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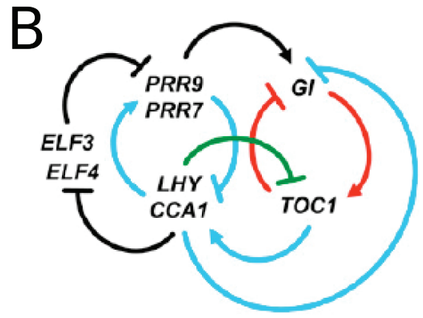

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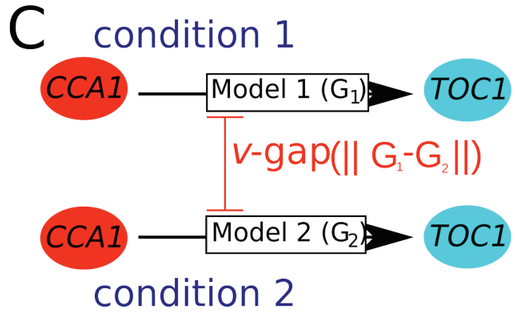


Alex Webb, Jorge Goncalves & Seth J Davis: Linear models can be used to describe biological systems where knowledge is sparse, such as the regulation of cytosolic free calcium by the circadian clock (A), and provide computationally light descriptions of the connections in complex networks, such as the circadian oscillator of Arabidopsis (B). We have adapted a new approach that computes the difference between the models obtained under different conditions, and we will use this Nu gap to identify causal changes in the circadian clock under different conditions (C).

in biological systems based on analysis of time series datasets. LTI models describe causal relationships in the network and have predictive power concerning the dynamical system. They have used LTI modelling to describe the circadian clock of Arabidopsis.

The group plans to build on this advance by developing a new approach based on the Nu gap metric, which identifies the causal changes in a network in response to stimulation or perturbation. The Nu gap identifies those altered connections by measuring the degree of change in the LTI models that describe those connections. Identification of those network connections that have changed in response to treatment allows follow up studies to be focused exclusively on the affected nodes that represent primary candidate gene targets.

Preliminary studies demonstrate the utility of the approach. LTI modelling and Nu gap analyses of circadian transcriptomes of Arabidopsis have identified targets for metabolites in the circadian clock and the mathematical predictions have been confirmed through experimentation. LTI modelling with Nu gap analysis will be developed both theoretically and practically. Nu gap analysis will be applied to circadian datasets obtained both from model systems that are well understood, and from barley in which circadian networks are not fully understood. Using LTI modelling coupled with Nu gap analysis, transcriptional responses to pharmacological and genetic pertubations will be investigated. They will extend the utility of the LTI modelling with Nu gap analysis by incorporating non-transcriptional data. Theoretical developments will attempt to extend the power of Nu gap analysis to non-linear models. The goal is to bring LTI modelling and Nu gap analyses to the state where they can be widely implemented.

Diversifying Transcription Termination Function

Gordon Simpson, University of Dundee

We know a lot about how transcription initiates and how RNA polymerase II elongates across genes. However, the least understood aspect of the transcription cycle is how termination occurs. Surprisingly, the genetic analysis of Arabidopsis flowering time has been a fruitful source of novel insight into transcription termination: mutants from Maarten Koorneef's original and hugely influential screen for factors controlling flowering included *fy*, *fca* and *fpa*, all of which disrupt RNA 3′ end formation and termination.

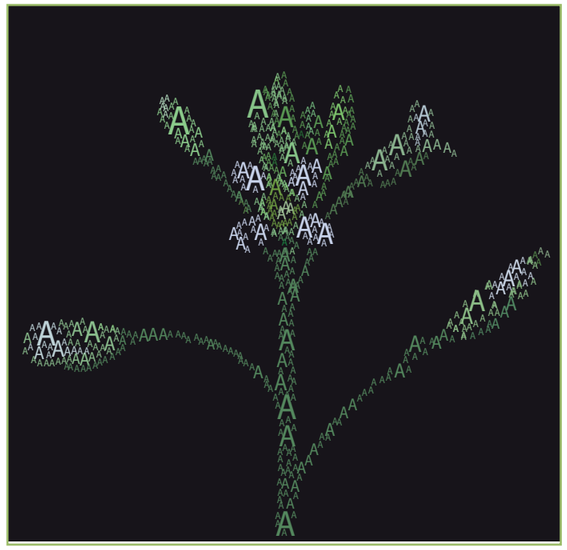
In order to understand how FPA controls gene-specific termination, the Simpson group developed a proteomics approach to identify proteins closely associated with FPA in living plant cells. One of the discoveries resulting from this approach was the realisation that paralogues of a highly conserved termination factor have evolved in flowering plants; it is speculated that these mediate gene-specific termination.

With the new funding from the BBSRC, Gordon and colleagues will combine their new proteomics procedure with ChIP-Seq and an integrated set of RNA-Seq approaches designed to reveal how the specialisation of the function of these factors comes about. In these ways, they should provide generally useful methodology for the design and analysis of related experiments and reveal the molecular basis by which termination can be a regulated process.

Gene-for-Gene Coevolution between Albugo candida and Arabidopsis: Mining Non-host Resistance Genes for White Rust Control in Brassicacae crops

Jonathan Jones, University of East Anglia

The obligate biotrophic parasite *Albugo candida* infects many distinct Brassicaceae. It causes white blister rust disease, resulting in significant losses of economically important oilseed and vegetable Brassica crops. *A. candida* consists of physiological races that each specialise on distinct hosts. The Jones group carried out genome sequencing of multiple *A. candida* races; comparison of these races revealed a mosaic-like genome structure. They also found that the strong immunosuppression ability of an adapted *A. candida* race enables colonisation of the host by a non-adapted race; this in turn could create novel races through sexual exchange and effector repertoire shuffling. Therefore, it is of great importance to identify and



Gordon Simpson is going to use proteomics to identify proteins closely associated with FPA.

clone broad-spectrum as well as race-specific resistance genes against this pathogen.

Some *A. candida* races can also infect various Arabidopsis accessions and this previously enabled the cloning of White Rust Resistance gene *WRR4* (encoding a TIR-NB-LRR R-protein) from Arabidopsis accession Col-0 (Borhan *et al*. 2008). A large number of Arabidopsis accessions were tested at adult leaf stage with Brassica-infecting *A. candida* races and found that all were resistant. Interestingly, this resistance is dependent on EDS1, suggesting that non-host resistance in Arabidopsis against Brassica-infecting *A. candida* race Ac2V is conferred by TIR-NB-LRR encoding *R* genes. To test the hypothesis that different Arabidopsis accessions might resist these races due to non-identical repertoires of *R* genes, the group screened "MAGIC" lines derived from 19 parents (Kover *et al*. 2009). They found 11 transgressive segregants that show different degrees of susceptibility to Ac2V. Two of these lines were fully susceptible to Ac2V, and enabled the group to carry out genetic studies to clone additional *WRR* genes.

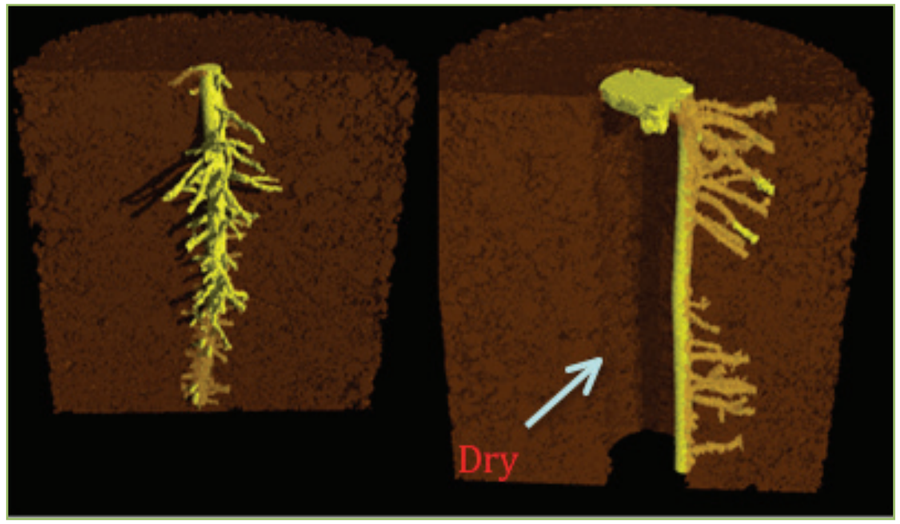
Furthermore, comparative and association genomics were carried out with the recently discovered novel class of CHxC (Kemen *et al*. 2011; reclassified as CX2CX5G and abbreviated to CCG) Albugo effector family and secreted proteins, and identified strong candidates for effectors recognised by the *WRR4*. This work then enabled the group to identify and characterize four CCG effectors from *A. candida* that are specifically recognised by *WRR4*.

With the new project, Jonathan and colleagues will mine Arabidopsis natural variation to expand *WRR* gene discovery against multiple races of *A. candida* through using novel approaches such as RenSeq (Jupe *et al*. 2013) and CrispR/Cas9/sgRNA system (Nekrasov *et al*. 2013). They will assemble multiple *WRR* genes with different combinations into a single T-DNA and transform into economically important crops such as *Brassica juncea*, *Brassica oleracea* and *Camelina sativa* for more durable resistance to multiple races of *A. candida*. Comparative and association genomics approaches were successful for the identification of effectors recognised by *WRR4*; they will use a similar approach to identify and characterise effectors recognised by the additional *WRR* genes. This work will be coupled with a newly developed PathSeq approach that enables CCG effectors to be specifically captured and sequenced from large numbers of *A. candida* field infections collected from multiple geographical regions. This, in turn, will allow prediction of the effectiveness of *WRR* genes against multiple *A. candida* races.

Hydropatterning: A Novel Mechanism Controlling Root Branching

Ari Sadanandom University of Durham &
Malcolm Bennett, University of Nottingham

Significant improvements in crop yields are urgently required to meet the food security needs of an increased world population by 2050. The degree of root branching determines the efficiency of water uptake and acquisition of nutrients in crops. Understanding the regulation of lateral root (LR) development is therefore of vital agronomic importance. The researchers on this grant have recently observed using a new form of X-ray imaging that root branching is profoundly influenced by the distribution of water in soil.



Ari Sadanandom and Malcolm Bennett: MicroCT images of maize reveals lateral root hydropatterning responses when roots are not in contact with water in soil.

Lateral roots form on the side of the main root in contact with water, but rarely on the dry side, using a mechanism termed 'hydropatterning'. LR hydropatterning occurs in both dicot and monocot species and therefore appears to be a highly conserved adaptive root trait.

Mutant studies in Arabidopsis revealed that LR hydropatterning is dependent on posttranslational modifications (PTMs) on the auxin response (transcription) factor ARF7. This proposal investigates whether LR hydropatterning is dependent on ARF7 (and its target genes) being differentially regulated on wet and dry root sides through PTMs and whether this is a highly conserved mechanism in land plants. This multidisciplinary project aims to exploit these new insights and uncover the mechanistic basis of LR hydropatterning.

Photoreceptor Engineering to Modulate Plant Growth

John Christie, University of Glasgow

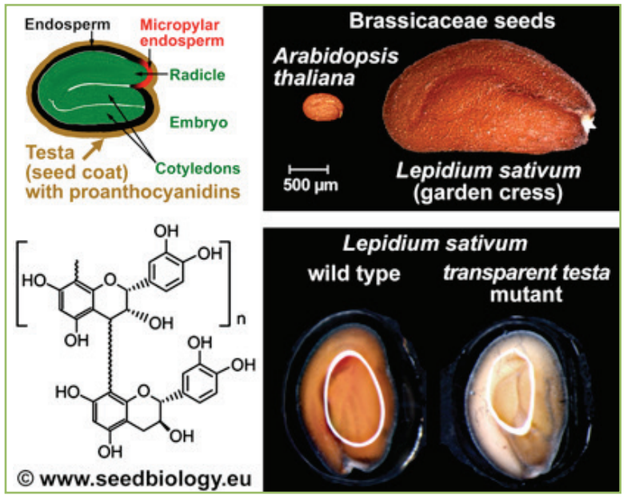
Light is critical for coordinating plant growth and development. Blue light (320–500 nm) in particular acts to regulate a wide range of responses that serve to promote growth. These processes include chloroplast relocation movements, leaf positioning and expansion, stomatal opening and phototropism, all of which influence a plant's photosynthetic competence by improving efficiency of light capture, reducing photodamage, and regulating gas exchange between leaves and the atmosphere. Collectively, these responses elicit dramatic effects on plant growth and are controlled by phototropin blue-light receptors. As a result, manipulation of phototropin receptor activity offers additional opportunities to increase photosynthetic performance and promote growth under specific light conditions. A major outcome of this work will be to establish a structural and functional blueprint for constructing engineered photoreceptors directed at optimising photosynthetic productivity under specific light conditions. This proposal therefore offers an additional approach to coordinate stepwise enhancements in photosynthetic performance with an aim to increasing yield that should ultimately offer new strategies to grow crops more efficiently.

Proanthocyanidins in Cereals and Brassicacae: A Cross-Species Approach on their Roles for Seed-Coat Biophysical Properties, Dormancy and Germination

Andrew Phillips, Rothamsted Research & Gerhard Leubner, Royal Holloway University of London

Led by Gerhard Leubner, this project will look at the roles of condensed tannins, or proanthocyandins (PAs), in the seed coat of many plant species, taking a cross-species approach with Brassicaceae seeds and cereal grains to elucidate their possible roles in determining the biophysical properties of the seed coat. This includes its mechanical strength/resistance and permeability to oxygen or plant hormones. These are proposed to be key properties underlying coat-imposed dormancy as well as germination speed, uniformity and seed vigour.

The project benefits from published genetic and biochemical knowledge acquired from *Arabidopsis thaliana* transparent testa mutants, but the Royal Holloway (RHUL) experiments are aimed at moving beyond Arabidopsis to the Brassicaceae as a large and economically important angiosperm family. The use of the larger seeds of *Lepidium sativum* (garden cress) will allow Tina Steinbrecher, the biomaterial engineer of the team at RHUL, to conduct quantitative biophysical analyses. A transparent testa cress mutant and PA-deficient wheat grains as well as PA-related transgenic lines of cress and wheat are key for these experiments. Andy Phillips and Alison Huttly from Rothamsted are interested in the relationship between PAs in wheat grain and pre-harvest sprouting. The team aims to integrate the molecular biomaterial science results from the cross-species approach to understand the roles of PAs in seed coats.



Andy Phillips and Gerhard Leubner are collaborating to investigate the roles of proanthocyanidins in seed coats.

Unravelling the Organisation, Composition and Dynamics of the Plant Cellulose Synthase Complex

Simon Turner, University of Manchester

The crystalline structure of plant cellulose microfibrils have useful structural properties, but is also very hard to break down and use for biofuel or other industrial applications. CESA proteins are the catalytic components of the cellulose synthase complex (CSC). Modifying cellulose synthesis to improve its properties for industrial use is precluded by poor knowledge of the composition and organisation of the CSC. This project aims to exploit recent breakthroughs and apply novel methods for looking at protein–protein interactions.

Protein cross-linking has been widely applied in the mammalian field, but it has not been used extensively in plants. The Qi and Kitagiri (*Plant J.* **57**, 932–44) study on the composition of rare membrane proteins complexes has arguably not had the coverage it deserves. A similar approach can be used to address problems such as the organisation of the plant cellulose synthase complex. This group has developed methods allowing the purification of CESA proteins even in the presence of strong detergents, so as to overcome problems associated with purification of the CSC and can be coupled with chemical crosslinking to identify interacting proteins. Furthermore analysis of the CESA proteins suggests many cysteines are not essential and can be removed. Consequently, they will also take a targeted cross-linking approach based upon removing non-essential cysteines from CESA proteins that will simplify both interpretation of the crosslinking data and help identify specific sites at which the proteins interact. In a complementary approach they will also use proximity-dependent biotin identification. By combining these approaches and looking at both primary and secondary cell wall cellulose biosynthesis the group aims to understand how different CESA proteins are organised to make up the rosette, what constituents of a core complex are required to make cellulose, and identify components that are involved in trafficking and/or localisation of the CSC.

Running a Software Carpentry Workshop

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We've organised two Software Carpentry bootcamps for plant scientists this year, one in April at the University of Warwick, and one in November co-organised with the Centre for Genomic Research at the University of Liverpool. Both events were extremely popular, with a long waiting list for each!

GARNet isn't planning to organise another Software Carpentry bootcamp for the foreseeable future, but the good news is, it's really easy to organise your own bootcamp. Here are our top tips for running your own workshop.

1. Budget and plan
Software Carpentry events are not free. When we organised the Warwick Bootcamp, Software Carpentry was subsidised by the Mozilla Foundation, but since the recent move to its own Software Carpentry Foundation, events now command a fee (TBC) – it's still a non-profit organisation though.

Software Carpentry trainers are volunteers but you will need to be able to reimburse their travel, food and accommodation expenses. They can come from anywhere in the world, so budget for transatlantic flights! Other costs you will need to think about include venue hire, and travel, food and accommodation for the workshop participants.

2. Contact Software Carpentry
If you're in the UK, Aleksandra Pawlik from the Software Sustainability Institute (SSI) is your point of contact for organising Software Carpentry events: email admin-uk@software-carpentry.org. Aleksandra and her colleagues will discuss ideas for your bootcamp with you over Skype and/or email. Software Carpentry requires core topics to be covered, but the programme can be tailored to the needs of your attendees.

Decide on a date. When this has been identified, Software Carpentry will put out a call for volunteer trainers from their global network.

3. Arrange logistics
While Software Carpentry will take care of the programme and the trainers, you'll need to organise logistics at your venue. Make sure your venue has good WiFi (and don't forget to arrange guest access), a few wired internet access points just in case, enough plug sockets for attendees to plug their laptops in, a projector and screen, and somewhere to have tea/coffee/lunch close by.

If you want your delegates to benefit from networking as well as training, try to make a block booking at a hotel and definitely arrange dinner on the first night of the bootcamp.

4. Publicise and take registration
For our first event, we advertised via our mailing lists and accepted trainees on a first-come first-served basis. It worked fine that time, but be aware Software Carpentry is growing in popularity and you will likely be over-subscribed, so be clear on your criteria for accepting people. For our second event, we took applications and selected trainees who fit our scope. Both models worked.

4. Find helpers
Software Carpentry recommends having one helper for every six attendees or so - these should be people who are comfortable with coding so they can help attendees with questions or problems. There is no discipline-specific content in a Software Carpentry bootcamp, so your helpers don't have to be plant scientists!

For more tips, read our blog at: http://tinyurl.com/software-carpentry-blog.

GARNet 2014 - Arabidopsis: The Ongoing Green Revolution

Lisa Martin
GARNet
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GARNet hosted a UK Arabidopsis research conference at the University of Bristol in September. GARNet 2014, entitled *Arabidopsis: The Ongoing Green Revolution,* was attended by almost 100 plant scientists from all over the country for two days of excellent plant research presentations, panel discussions and networking opportunities.

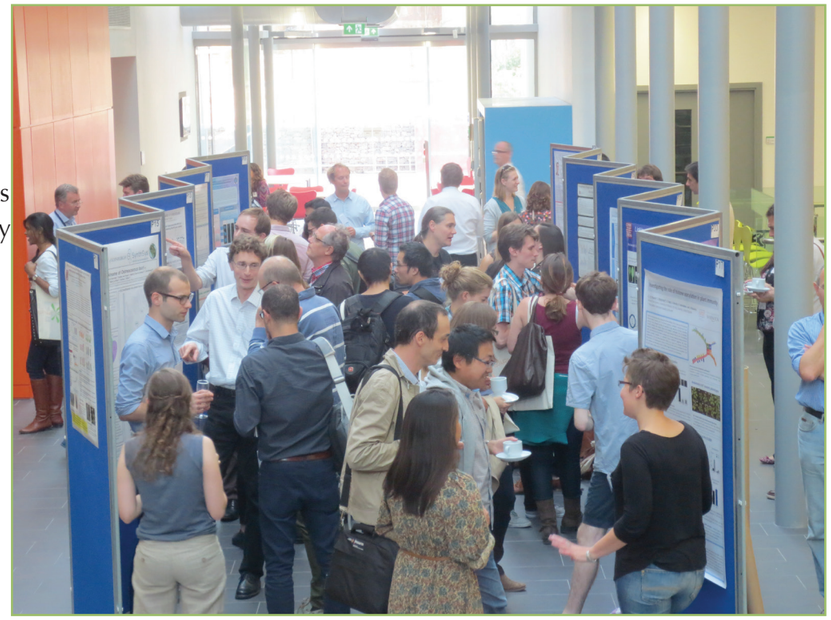
There were five themed sessions during the conference, beginning with Physiology & Productivity on the morning of the 9th September. Alistair Hetherington from the host university gave the opening plenary lecture, speaking about his work on the response of stomata to environmental signals, followed by a presentation on plasticity in roots by Miriam Gifford from the University of Warwick. Steve Penfield from Exeter also spoke about his work on understanding how plants respond to environmental temperature at key life history effects. The session talks were concluded by the first of our student/early career researcher prize-winners, Beatriz Lagunas from the University of Warwick. Beatriz works with Miriam Gifford and provided further insights on the genetics control of root archictecture.

After lunch, networking and a chance to peruse our exhibitors' stands, the afternoon session on Genome Biology kicked off with Siobhan Brady – all the way from the University of California Davis – who gave an enigmatic presentation on spatiotemporal gene regulatory networks in plant roots. Siobhan was followed by new GARNet committee recruit Ian Henderson from the University of Cambridge and current committee member Antony Dodd from Bristol. Finally, we heard from the second prize-winner of the day, Emily Hawkes from the John Innes Centre, who gave a fascinating overview of her PhD project looking at the evolutionary conservation of antisense transcripts known as *COOLAIR* and their regulatory role in Arabidopsis.

Andrew Millar (University of Edinburgh) takes the mike during the Synthetic & Systems Biology discussion with fellow panellists Mathew Hindle, Leah Band, Siobhan Braybrook and session Chair Claire Grierson. *Photo: Charis Cook*

After the day's scientific sessions, delegates moved from the Chemistry department lecture theatre to the University of Bristol's brand new Life Sciences building – not even officially opened yet! Gary Foster gave group tours of this fantastic new asset for science teaching and research, while the rest of us browsed the posters, chatted with the poster presenters, had a glass of bubbly and feasted on GARNet-branded cupcakes!

Following an excellent conference dinner at the Bristol Marriott hotel on the Tuesday night, Day Two had three scientific sessions. In Natural Variation we heard from Maarten Kournneef from the Max Planck Institute for Plant Breeding Research in Germany as the plenary speaker, Adrian Brennan from Durham, and Javier Agusti from Oxford. Monika Mierzwinska was our poster prize-winning speaker here, giving an excellent talk on 'natural variation in endodermal development and plant mineral nutrient homeostasis'. Former GARNet PI Andrew Millar (Edinburgh) opened the Systems & Synthetic Biology session, followed by Siobhan #2, Siobhan Braybrook from the Sainsbury Laboratory in Cambridge, mathematician Leah Band from Nottingham, and prize-winner Matthew Hindle from Edinburgh.



The GARNet 2014 poster session was held in the University of Bristol's brand-new Life Sciences building. *Photo: Charis Cook*

Finally, in Plant Interactions with their Environment, where the plenary speaker was another guest from the Max Planck Institute, Paul Schultze-Lefert, we also heard from GARNet committee member Cyril Zipfel, Bristol University's Kerry Franklin, and Nottingham PhD student Sophie Berkhan.

A highlight of the conference was the panel discussions at the end of each session. Here, the speakers – including the poster prize-winners – took questions from the floor and discussed key issues emerging from the talks. It was great to see many students and early career researchers getting involved in the conversations.

You can download selected presentations from GARNet 2014 by visiting our blog at: *http://blog.garnetcommunity.org.uk/garnet-2014-presentations/*.

Plantregulome.org: an atlas of Arabidopsis thaliana cis-regulatory elements

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If you have ever wondered about the promoter accessibility of your favorite *Arabidopsis thaliana* gene, its nearby regulatory elements and motifs, or its involvement in transcription factor networks, then plantregulome.org is for you.

Cis-regulatory elements can be delineated by their chromatin accessibility (1) using DNase I-seq (2). Using this technique, Sullivan and co-authors generated nucleotide-resolution maps of regulatory DNA and derived transcription factor (TF) networks for *A. thaliana* seedlings before and after exposure to light and heat (3). These data sets, along with unpublished data sets, including *A. thaliana* root cell types, hormone treatments, seed coat epidermis, and diverse *A. thaliana* accessions, are easily viewed and downloaded at plantregulome.org (Figure 1).

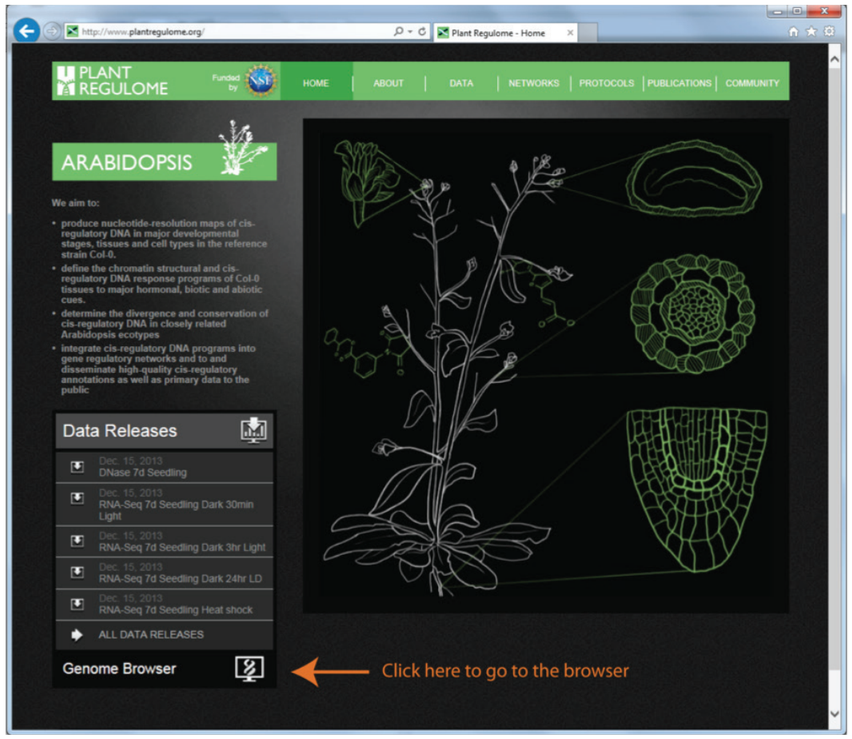

Figure 1: PlantRegulome.org

The Plant Regulome browser is run by a modified version of the UCSC Genome Browser system (Figure 2). The browser can be reached from links at the bottom of the homepage (Figure 1) and data page. Once in the browser, tracks can be selected by clicking track links (e.g. "Light/Dark DNase (24mil)") and selecting track options. Gene names (e.g. AT1G01010) or genome coordinates can be used to navigate the genome. Read-depth normalised data from Sullivan *et al*. 2014 have their own tabs. Tracks with motif instances for hundreds of *A. thaliana* TFs (3-8) can be added by clicking the "FIMO scans" tab.

TF networks from Sullivan *et al*. 2014 (3) can be viewed by navigating to the networks page. Select TFs from the "genes" menu, and conditions from the "sample types" menu. Additional regulatory interactions can be added using the options at the top left of the page. The "regulatory profile" of individual nodes can be viewed by clicking the node of interest. Note: the networks tool can be choosy about web browsers; Firefox works well.

Last but not least, plantregulome.org provides access to raw and post-processed data, including alignments and DHSs (data page), and a full DNase I-seq protocol (protocols page).

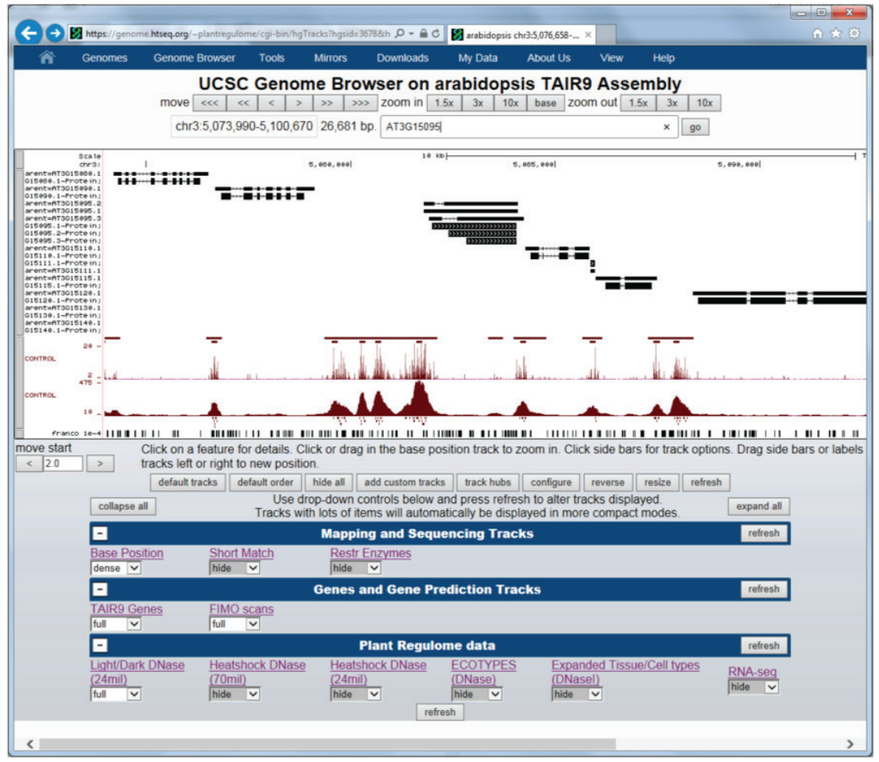

Figure 2. Plant Regulome browser. From top to bottom the following tracks are shown in this browser image: genes (black), hotspots (large burgundy bars), DNase I hypersensitive sites (also called DHSs or peaks; small burgundy bars), per-base cleavage (fine-scale histogram), DNase I cleavage density (also called signal; smoothed histogram), footprints (burgundy ticks), and motifs (black bars).

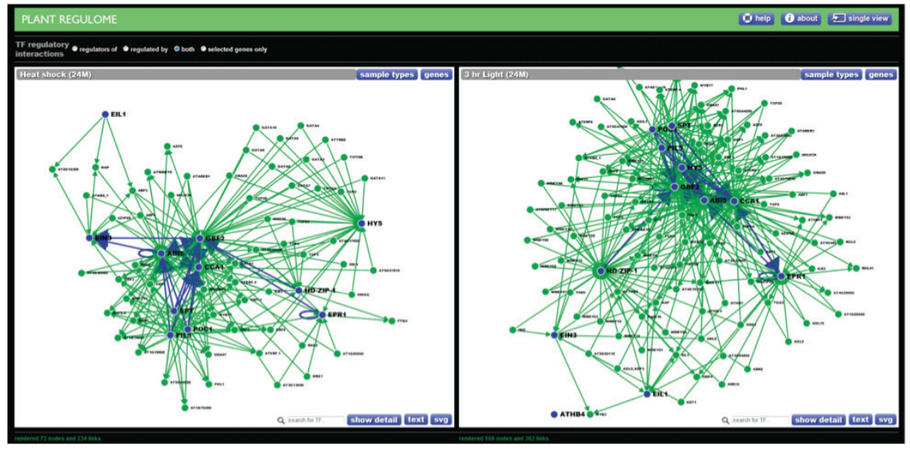

Figure 3. Networks display. Side-by-side networks from heat and light treatments. Selected genes are in blue. Regulatory interactions involving selected genes are in green.

Acknowledgments

Plantregulome.org was created by Richard Sandstrom, Michael Buckley, and Audra Johnson; artwork by Rae Senarighi.

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The BBSRC Great British Bioscience Festival

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The Great British Bioscience Festival was held in a marquee in Museum Gardens, Bethnal Green, London, on the 14th and 15th of November. Celebrating 20 years of BBSRC and showcasing the best of British biotechnology and biological sciences research, this free public event attracted over 6,500 visitors over two days. I went along to see to see the exhibits, and also to help out on the Society of Biology stand!

The diversity of exhibits at the Festival was staggering, fascinating, and covered all kinds of topics in the life sciences. You could walk through a giant, inflatable model of the gut, learn about bioluminescence to make your own glow-sticks, discover the amazing relationship between bees, flowers and static electricity, and explore the microscopic world of cells and organelles via 3D-printed models.

The BBSRC Great British Bioscience Festival attracted over 6,500 people over two days. *Photo: Lisa Martin.*

The atmosphere at the Festival was brilliant, and it was great to see so many children and adults engaging with real scientists and getting enthused about biology. On Friday afternoon, I spent two hours on the Society of Biology stand helping small children to make paper 'fortune tellers', which we then used to teach them a little bit about biologists who have changed the world with their amazing discoveries. This very simple activity was well received - especially the competition to win a cuddly virus or skin cell!

It was really great to see plant science so well represented, too!

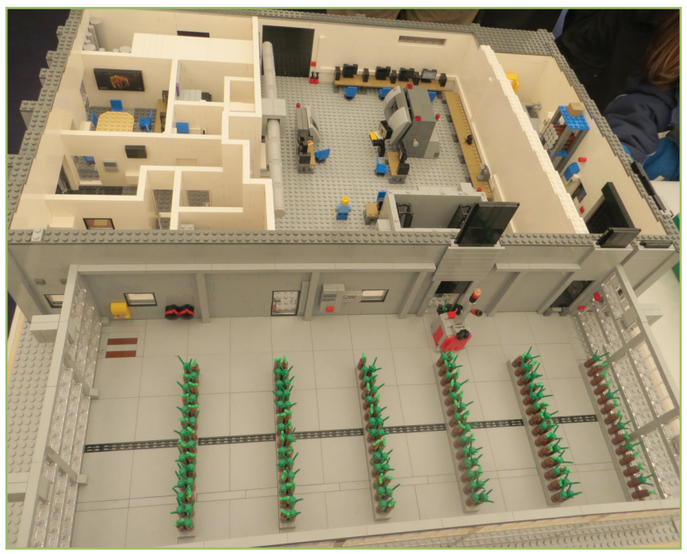
A team from IBERS at Aberystwyth University had a giant plant pot at the centre of their exhibit on grasses. The 'super plant' in the pot was a model representing oats, ryegrass and Miscanthus and was used to demonstrate how studying plants can help scientists solve problems such as how to make better biofuels, or how to breed crops that are resilient to climate change. Children loved looking down the microscope at different plant cells both here, and on the exhibit about 'the complex life of sugars'.

Aberystwyth University's giant plant pot contained a 'super plant' made up of ryegrass, oats and Miscanthus. *Photo: Lisa Martin.*

Genetic modification of plants was the subject of the exhibit from Rothamsted Research and the University of Stirling, which explained research to create *Camelina sativa* plants capable of producing omega-3 fish oils. This exhibit generated lots of interesting discussion on the ethics and benefits of GM technology.

Purple tomatoes were just one aspect of the John Innes Centre's exhibit, which looked at how plants can be used as factories to 'grow' useful natural products. *Photo: Lisa Martin.*

GM technology was also one of the topics up for discussion on the John Innes Centre's 'Nature's Factories' stand. This showcased a range of projects from Norwich, including the development of purple tomatoes that have been genetically engineered to produce the cancer-fighting pigment anthocyanin, and the use of traditional crop breeding methods to develop Beneforté 'super-broccoli', which has high levels of glucoraphanin to keep the heart healthy. Visitors to the exhibit could also try their hand at making some body scrubs and lotions using natural scents from plants such as mint and lavender.



The brilliant Lego model of the plant phentyping facility at the University of Nottingham's Sutton Bonington campus.
Photo: Lisa Martin

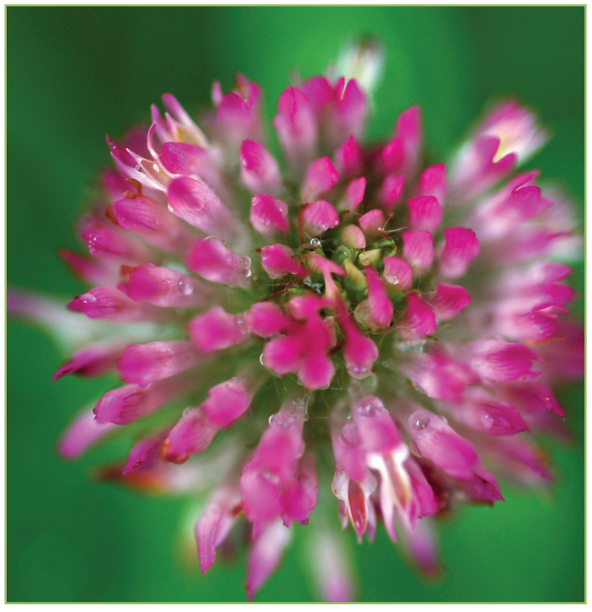
The University of Nottingham clearly had a lot of fun preparing their exhibition for the Festival, which featured a Lego model of the new Hounsfield plant phenotyping facility at CPIB. The helpers on the stand explained how scientists are using X-ray computed tomography to study the shape and growth of roots, 'the hidden half of plants'. There's a brilliant YouTube video showing a stop-motion animation of the Lego model in action! *http://youtu.be/X9mfQnfZ0Zg*.

Spotlight on The Genome Analysis Centre

TGAC
The Genome Analysis Centre™

Researchers at The Genome Analysis Centre (TGAC) work on the development and application of advanced genomics and computational tools to address key scientific questions in plants, animals and microbes and their interactions with the environment. Plant research programmes are focused on the characterisation and understanding of genetic diversity and its relation to relevant traits.

TGAC is a world-class leader in the generation of genomics and bioinformatics resources for plant sciences, and in the creation of software platforms to make them accessible to the wider scientific community. TGAC works closely with partners at Norwich Research Park, and with national and international collaborators, to advance bioscience to promote a sustainable bioeconomy.



Sarah Ayling's group seeks to understand complex plant genomes, such as that of red clover, *Trifolium pratense*. *Photo: Malgorzata Kaczor.*

Thanks to Hayley London, TGAC Marketing and Communications Officer, for coordinating this article.

Sarah Ayling
http://www.tgac.ac.uk/bioinformatics/computational-genomics/sarah-ayling/

Computational Biology

Sarah's group is interested in the development of assembly approaches for complex plant genomes, and works with a variety of species with large, repetitive and/or polyploid genomes, such as barley, red clover, lolium, ash tree, and hexaploid bread wheat.

As part of the EU TransPLANT project, the group is establishing an online resource to provide guidance to researchers embarking upon plant genome sequencing projects. The Assembly Knowledge Base (*http://assemblykb.tgac.ac.uk/*) provides sample datasets from species with different genomic characteristics and quality control metrics for input datasets and the resulting assemblies; a range of assemblies are provided, generated using different combinations of sequencing technologies and assembly pipelines. Through comparison with a user's own project requirements, the Knowledge Base aims to provide decision support when planning a genome assembly project.

Sarah's group is also interested in the identification and characterisation of genetic diversity and its effects for traits of agronomic interest. They are working on a number of projects to re-sequence individuals from mutant populations, diversity panels and genebanks in order to identify genetic variants that can be linked to traits of interest. They work with several crop species, including wheat, barley, rice and pea, and use a range of sequencing techniques from reduced-representation approaches such as RAD-seq and target-enrichment, to whole genome resequencing as appropriate. We have also recently established a collaboration with the John Innes Centre to develop approaches to analyse high throughput field-phenotyping data for crops.

Matt Clark
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Plant and Microbial Genomics

Matt's group aims to apply the latests sequencing and informatics approaches to better understand the genetics arms race between plants and their microbial pathogens. Plant pathogens significantly affect crop yields and are one of the largest selection pressures driving plant evolution; conversely plant defences select for pathogens able to modulate or evade host responses. By studying fundamental biological processes, the group ensures their findings have potential impact outside of academia, e.g. in food security. By working with collaborators the group can improve crop breeding strategies, and can further leverage genomics expertise for tangible benefits such as identifying novel antibiotics from Streptomyces bacteria.

Late blight on the underside of a potato leaf. Matt Clark's group studies the relationships between plants and pathogens. *Photo: Howard F. Schwartz, Colorado State University.*

As a partner in the International Wheat Genome Sequencing Consortium to sequence the genome of hexaploid bread wheat, the Clark group is helping to accelerate progress in global food security by providing valuable databases and interface formats for wheat breeders and scientists worldwide.

Matt's group also works with the potato, which has no existing populations of mutant genotypes that may impact directly (e.g. tuber traits) or indirectly on crop yield and quality. To assist this process, the group is sequencing a high quality draft genome of self-compatible diploid *Scleroderma verrucosum*, which has a very high level of late blight resistance. This provides a state-of-the-art technological platform for identifying functional resistance genes from any plant species, which offers a more rapid alternative to traditional approaches. Working with collaborators, they aim to realise the full potential of the potato and tomato genomes to enable more rapid cloning of functional resistance genes, by exploiting existing populations segregating for virus (PVY), potato cyst nematode (*Globodera pallida*) and late blight resistances, allowing them to combine searches for resistances effective against three of the most economically important potato diseases.

Robert Davey
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Sequencing Informatics

New experimental technologies have opened the way to new, data-generative approaches to plant research, particularly within the genomics field but also high-throughput transcriptomics, proteomics and metabolomics. Furthermore,

GARNish

Spotlight on The Genome Analysis Centre

Rob Davey and his group will be working closely with GARNet on the Collaboratively Open Plant 'Omics project.

publication models are moving away from the traditional "data late" approach, and are shifting to "data early", with particular pressure being made by funding agencies to see data publicised quickly. Alongside the wealth of these large plant science datasets held in public and private laboratories around the globe, there are many tools to help researchers disseminate, analyse and publish those datasets. However, the disparate nature of the tools, data formats and scientific problems in light of this expansive experimental development has resulted in a lack of interoperable, production-quality software available for data analysis and dissemination.

A newly funded BBSRC project, Collaboratively Open Plant Omics (COPO), will address this disparity. The community demands a framework for the description, deposition and publication of datasets, but also that enables the identification and citation of datasets, increasing transparency and reproducibility. By developing high quality, stable interfaces to and with existing virtualised resources the Davey group will tie together services to: (i) develop and use community-accepted standards for data representation, (ii) facilitate data submission to persistent archival resources, (iii) enable seamless transition from data to analysis platforms, and (iv) track metadata for linked publication and data citation.

David Swarbreck

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Genome Analysis

The Genome Analysis group uses computational approaches and next-generation sequencing to improve genome annotation and understand the complexity of eukaryotic transcriptomes and gene regulation. Precise patterns of spatial and temporal gene expression are crucial for growth and development of multicellular eukaryotes and their response to the environment. Protein synthesis therefore requires tight regulation with multiple layers of regulation including transcription initiation, post transcriptional modification, mRNA degradation and translation. The group apply RNA sequencing coupled with complementary data (Chip-Seq, BS-seq, ribosomal profiling, HiC etc) to explore the complexity of eukaryotic transcriptional landscapes.

The production of a high-quality reference genome annotation for a species is of critical importance for any downstream analyses such as conservation, variation, and assessing functionality of a sequence. Due to large genome sizes, high repeat content, heterozygosity and polyploidy, plant genomes present significant challenges for genome assembly. As such most of the 50+ sequenced plant genomes are of a draft standard and highly fragmented. This research involves the development of sequencing, assembly, and annotation strategies to characterise transcriptome complexity including coding and non-coding transcripts, alternative splice variants and small peptides. The group works mainly on higher eukaryotes such as plants (Ash, Rubber, Willow, Barley, and Wheat) but also on smaller eukaryotic genomes.

Whole genome duplication has occurred extensively in plants with many important crop species displaying hallmarks of autopolyploidy or allopolyploidy. Polyploidy is recognised as a major evolutionary force shaping the evolution of plants, increasing biodiversity and providing new material for evolution. This group is interested in understanding evolution of expression, alternative splicing, and function of genes duplicated by polyploidy events and characterising the changes in gene expression and regulation in polyploid species and interspecies hybrids.

Follow TGAC on Twitter: @GenomeAnalysis
www.tgac.ac.uk

Spotlight on the University of York

THE UNIVERSITY of York

We've featured the University of York in GARNish before, but that was in 2005 and a lot has changed since then! Many thanks to Seth Davis for coordinating this article.

Researchers at York address fundamental problems from across plant biology including physiological adaptation, plant nutrition, primary and secondary metabolism and intracellular and intercellular signalling. These scientists use diverse approaches spanning classical molecular genetics and biochemistry through post-genomic and advanced imaging technologies.

Impact is gained from these studies within three research centres working within the university structure. These are the Centre for Novel Agricultural Products (CNAP), the York Environmental Sustainability Institute (YESI) and the Biorenewables Development Centre (BDC).

Together, a unified force works to create basic and translational findings that address:
i) health and disease,
ii) sustainable production of foods and fuels
iii) ameliorating the effects on environmental change.
These are the three global challenges that the Department of Biology at York has prioritised and provides examples of how plant biology research benefits society.

Ian Bancroft

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CNAP Chair of Plant Genomics

Ian's research focuses on the relationships between genome evolution and the control of characteristics of plants that are of relevance to food security, health or sustainability. His group uses *Brassica napus* (a species that includes oilseed rape and several other crop types) as a model for polyploid genomes and has developed computational approaches for the deployment of "second generation" sequencing technologies to analyse molecular variation.

Exploiting comparative genomics and the transcriptome as a means of analysing both gene sequence variation and gene expression variation, either directly or via a network of collaborations, the Bancroft group is uncovering the genetic bases of a range of traits (including seed oil composition, seed co-products and the suitability of straw as feedstock for bio-alcohol production) in a range of species (including *B. napus* and *Triticum aestivum*.

Neil Bruce

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CNAP Chair in Biotechnology

The major research themes of the Bruce laboratory are microbial metabolism, biocatalysis and environmental biotechnology. A primary goal is to understand how microorganisms have adapted to utilise xenobiotic compounds as carbon and nitrogen sources for growth. The enzymes mediating these pathways often have potential commercial applications as recognition components in biosensors, as biocatalysts for synthetic chemistry, for the production of biofuels and for the bioremediation of soil and ground water.

The Bruce lab is now engaged in extensive structural analysis of a number of these enzymes using X-ray crystallography and is also focusing on generating carefully designed mutant forms of a number of these enzymes to understand their catalytic mechanisms. A principal theme of our research is the biodegradation, biotransformation and phytoremediation of explosives.

Seth J Davis

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http://www.york.ac.uk/biology/research/plant-biology/seth-davis/

Chair of Plant Biology

Plants experience daily and seasonal changes in light and temperature. Processing these signals is key for fitness. To anticipate rhythmic changes, plants have evolved a timing mechanism termed the circadian clock.

The Davis working group is engaged with defining the framework of the core-clock mechanism, initiating a mechanistic understanding of light and temperature inputs to this oscillator and characterising various outputs from this timer under simulated and natural field conditions.

Julia Ferrari

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Lecturer in Herbivore–Natural Enemy Interactions

Julia's research focuses on ecological and evolutionary aspects of plant–herbivore–natural enemy interactions. She is particularly interested in the evolution of specialisation and ecological speciation in these systems. Many insects are infected with bacterial symbionts that can have strong ecological effects on their hosts. They can, for example, increase the resistance of insects to natural enemies such as pathogenic fungi. Julia's group investigates how the symbionts affect their hosts' ecology. The group is particularly interested in how multiple partners in these systems interact and co-evolve. Most of her current work uses the pea aphid, *Acyrthosiphon pisum*, as a model system. Her group found that the pea aphid is a complex of host-adapted populations that show a gradient of differentiation between populations, both in their host use and genetically. These host specialists also differ in which bacterial symbionts they carry, suggesting that the bacteria help the aphid to feed on certain plants.

Ian A Graham

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Head of Department and Weston Chair of Biochemical Genetics

Plants make an amazing array of chemical structures – Ian's team is interested in working out how they do this, plus how they can be developed to make useful molecules.

He has two main areas of interest: one focused on understanding the regulation of processes associated with seed germination, and the other focused on discovering and improving the production of high value chemicals in plants. Current projects range from lipid signals and transcription factors that control seed dormancy and germination to the development of novel oilcrops such as *Jatropha curcas* and medicinal crops such as *Artemisia annua* and *Papaver somniferum* (opium poppy).

Sue Hartley

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Director, York Environmental Sustainability Institute

Plants are at the centre of a complex web of interactions with other organisms which seek to exploit them. Sue's research focuses on the chemical basis of the interactions between plants

and these other organisms.Her particular interest is grasses (both native species and crops), and their silicon-based defences against herbivores.

Grasses take up silicon in unusually high amounts and deposit it in their leaves in the form of hard granules (phytoliths), or as spines on the surface. These make leaves more abrasive, so herbivores avoid feeding on plants containing high levels of silicon. The abrasiveness of these structures has profound impacts on the performance of agricultural pests and other herbivores, reducing their growth and feeding efficiency irreversibly.

Sue has pioneered new X-ray based methods of silicon analysis in plants (Reidinger et al. 2012) and demonstrated that silicon is an inducible defence: silicon levels increase when plants are attacked and they increase the number and size of silicon-containing spines in response to herbivory.

Half of our most important food crops are silicon accumulators and Sue has shown that crops can use silicon-rich spines as a defence. There is increasing interest in harnessing silicon to make agriculture more sustainable and less reliant on chemical inputs: as well as providing resistance to pests, silicon protects crops from pathogens and alleviates abiotic stresses, such as drought. A better understanding of the biochemical and genetic mechanisms underpinning silicon accumulation in plants will not only provide insights into an important area of plant biology, but will also enable the development of strategies for improving the resilience of crops to environmental change and the pests and diseases which threaten our food supply.

Mike Haydon
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Lecturer in Sugar Signalling

Plants must sense and adapt to environmental changes to grow efficiently and respond to stress. These adaptations can occur over timescales ranging from minutes to generations. Research in the Haydon lab aims to understand the cellular and molecular bases for how plants sense environmental signals to adapt their physiology and development.

For example, Mike's recent research revealed a role for light-dependent production of sugars (i.e photosynthesis) in adapting internal molecular rhythms in Arabidopsis to daily changes in environment. Ongoing research in the lab is investigating how plants sense changes in internal sugar levels and how this information is integrated into classical modes of light sensing through photoreceptors.

A second aspect of research in the Haydon lab aims to understand the role of the plant cell wall in sensing and responding to environmental signals. The plant cell wall is a complex and dynamic structure, which forms a barrier between the cellular and external environment. It provides strength to otherwise formless plant cells, but must be highly plastic to allow physiological and developmental adaptations.

We aim to identify cell wall components that sense the external environment and elucidate the cellular pathways that drive dynamic modifications of plant cell walls.

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Lecturer in Arbuscular Mycorrhizal Fungi Symbiosis

Microbes, (bacteria, archaea, fungi) are key functional groups in ecosystems, acting as a drivers of major transitions in nutrient cycles.

The Helgason research team focuses on variation in biodiversity, distribution and function of key microbial groups in field-based systems. Recent advances in next-generation sequencing technologies allow the microbiome of field systems to be studied in detail, and current research projects use these technologies to understand nutrient cycling in agriculture and epidemiology in honeybees.

A major research area in the group is the Arbuscular Mycorrhizal Fungi (AMF). These symbionts are key conduits of mineral nutrients between plants and soils, and variation in AMF communities has the potential to affect large scale ecosystem function.

Research by the group includes determining what controls AMF biodiversity, including host plant effects, water and oxygen availability, and soil environment, and how these factors affect fungal fitness and evolution. This is studied using manipulative field experiments, molecular and bioinformatic approaches.

Jane K Hill
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Habitat Degradation and Climate Change on Biodiversity

Jane's research focus is on the effects of habitat degradation and climate change on biodiversity (with particular emphasis on temperate and tropical insects). Her team is studying climate-driven range shifts of species at their leading-edge and trailing-edge range boundaries, and the factors affecting species' ability to respond to climate and habitat changes.

The group is doing this via the analysis of historical records, collecting new field data, and the development of theoretical models. They are exploring potential methods for promoting adaptation of biodiversity to climate warming, for example by examining whether improving habitat connectivity will aid species' range shifts, and the role of Protected Areas.

Jane is also investigating methods for conserving biodiversity in tropical habitats, including logged forests and oil palm plantations.

Angela Hodge
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Reader in Plant–Soil–Microbe Interactions

Angela's research centres on plant–soil–microbe interactions, particularly those involving mycorrhizal fungi and nutrient cycling in soil systems. She is particularly interested in how roots proliferate in, and capture nutrients from, complex organic patches in soils and the subsequent environmental controls upon this nutrient capture response.

Another key mechanism by which plants can enhance resource capture is through the formation of symbiotic associations with mycorrhizal fungi. The group investigates how the fungus alters the ability of the root to respond to nutrient patches and the response of the fungus directly in nutrient-rich patches using both mechanistic and ecological approaches.

Phil Ineson
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Global Change and Ecology

Phil's group has particular interests in the role of soils in global change, and in the application of stable isotope approaches to ecological research.

Research is varied in scale, ranging from assessments of the carbon fluxes and inventories of terrestrial ecosystems, through to extracting

nucleotide sequences from functional groups of soil bacteria. The research has pioneered techniques in the field tracing and measurement of carbon fluxes, and utilises state-of-the-art equipment, both in the laboratory and the field, in order to identify and quantify major sources and sinks for the major 'greenhouse' gases.

Phil has pioneered stable isotope approaches to following the pathways and fate of carbon through plant–soil systems, identifying how these will change as the atmospheric CO_2 concentration rise, and also characterising the organisms involved in processing the carbon in the soil.

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Lecturer in Post-Transcriptional Control of Gene Expression

Louise has a long-standing interest in RNA biology and the post-transcriptional control of gene expression. A particular focus is RNA silencing, which is a conserved mechanism of gene regulation in eukaryotes and is involved in controlling endogenous gene expression and defence against invasive nucleic acids such as viruses.

Interestingly, RNA silencing can promote epigenetic changes such as DNA methylation and histone modification, and one idea is that these pathways contribute to phenotypic plasticity in response to environmental change.

Currently the Jones lab is using a combination of molecular and genetic approaches to investigating the connection between RNA silencing and DNA methylation and its wider significance.

Frans Maathuis
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Reader in Plant Nutrition

Plant nutrients and toxic minerals are typically present in ionic form – Frans' group studies the molecular mechanisms of ion uptake and translocation. Studies are conducted to elucidate how K^+ is taken up and distributed throughout plants, through identification and characterisation of K+ membrane transporters. Plant stress research focuses on detrimental effects of the global and increasing problem of salinity, and in particular on molecular pathways for Na^+ uptake and how these are regulated by cyclic nucleotide signalling.

More recently, investigations have started to identify and characterise membrane transporters involved in the uptake and distribution of arsenic in Arabidopsis and rice. Techniques to study these subjects include: electrophysiology, transcriptomics and (phospho)proteomics. The Maathuis team has discovered types of non-selective ion channels in Arabidopsis roots that are regulated by cyclic nucleotides and that these second messengers play important roles in plant salt tolerance and potassium nutrition. We were the first to report on the function of NIP aquaporins in plant arsenic uptake.

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CNAP Director and Chair in Materials Biology

Simon's research encompasses various aspects of plant cell wall biology. The cell wall plays a key role in the control of plant growth and morphogenesis by regulating the rates of cell expansion through changes in extensibility. Plant cell wall extensibility is under dynamic control and the molecular mechanisms underlying extension are a major research interest. Expansins are key proteins that regulate cell wall extensibility and we study these proteins at the level of biochemistry and molecular genetics. The cell wall is a complex fibre composite material composed of a range of different polysaccharides. The McQueen-Mason team studies the contribution of different matrix polysaccharides to cell wall extensibility and elasticity, as well as the genes and enzymes involved in their biosynthesis.

Plant biomass is one of the greatest reserves of fixed carbon on the planet, is viewed as a potential replacement for fossil fuels, and is largely composed of cell walls. The group uses our knowledge of cell walls to advance the development of second generation liquid biofuels from plant biomass in three distinct areas. Firstly, Simon is coordinating a large international project, which aims to optimise plant cell walls for biofuel applications by making them more readily converted into fermentable sugars for alcohol production. Secondly, the team has initiated a major programme for the discovery of novel enzymes for converting plant biomass into fermentable sugars. Finally, they are investigating the production of liquid biofuels from plant biomass from municipal waste.

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Lecturer in the Soil–Plant–Atmosphere System

Kelly examines multiple aspects of the soil–plant–atmosphere system for exchange of nitrogen, sulphur, chlorine, bromine and iodine. The volatile forms of these gases are involved in all of the most important climate change issues, from global warming to global cooling to ozone formation and loss.

The lab is focused on examining the atmospheric and environmental impacts of changing the way we manage land (e.g. the impact of increased demand for biofuels). The Redeker team uses growth chamber and greenhouse-grown plants to identify the parameters most important in controlling the emissions of these important trace gases. An understanding of the enzymatic and genetic drivers that produce the emissions of interest is also required.

Recent efforts include the developed methodology to pursue an intensive study of microbial diversity within forested soils and how changes in this community affects fluxes of trace gases to the atmosphere. Kelly has identified differences in thermal adaptation between Arabidopsis ecotypes in the secondary metabolism process that generates methyl halides.

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Lecturer in Mycorrhiza Formation

Michael's lab is taking a molecular genetic and functional genomics approaches to identify and characterise genes involved in the development and functioning of arbuscular mycorrhizas. Mycorrhizas ("fungal roots") are based on the symbiosis between plants and soil-borne fungi. They help the plant to acquire mineral nutrients and improve stress tolerance. Forward genetic screens in the model legume *Medicago truncatula* are used to identify new mutants affected in mycorrhiza formation.

A number of mutants have been isolated so far. Molecular cloning of the affected genes in some of these mutants is under way. Identification and

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characterisation of these genes will elucidate the mechanisms underlying the molecular communication between plant and fungus. Novel mutants affected at an early stage in mycorrhizal symbiosis have been identified in *M. truncatula*. These are currently being characterised, and molecular cloning of the affected genes is under way.

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Reader of Teaching and Scholarship in Leaf Shape

Richard's main research aim is to investigate how, and why, plants make leaves of different shapes.

He has used genetics to identify genes with roles in leaf development, and designed computer software to measure leaf shape and size variation. The team is now focusing on the genetic factors affecting shape variation and aims to understand how this is regulated at the genetic level. They have assessed leaf shape variation in plants from, for example, different genetic backgrounds grown in different conditions.

The group is also interested in how variation in leaf shape evolved, and a further aim is to uncover how the functional significance of leaf shape variation has changed over time. It was discovered that computational methods can be used to rapidly assess variation of leaf shape and size.

Using these methods Richard aims to determine the significance of leaf shape variation in Arabidopsis and a wide variety of other model plant species.

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Comparative Genomics of Rhizobia and Other Microbes

Microbes are everywhere and their activities are vital for all "macrobes" like us. Microbes are hard to see, and hard to tell apart, but advances in our ability to study DNA have led to rapid and accelerating progress in our knowledge of microbes in the environment, including those that interact with plants, animals and fungi.

In the Young group, they study the population genetics, molecular phylogeny and comparative genomics of rhizobia and other bacteria. They also use molecular approaches to study the ecology and diversity of mycorrhizal fungi.

Bioinformatics plays an important role in teasing new understanding from the masses of data. One recent discovery is that, whereas bacterial taxonomy reflects the core genome, ecological adaptation is conferred by an accessory genome that is partially independent of this. Bacteria do not have "second chromosomes", but may have chromids that are derived from plasmids.

Another finding is that the main symbionts of Mimosa species are betaproteobacteria in the genus Burkholderia. Finally, the group discovered that the nuclear genomes of arbuscular mycorrhizal fungi can have multiple coexisting gene versions, but the mitochondria do not.