GARNish
December 2015 Edition 24

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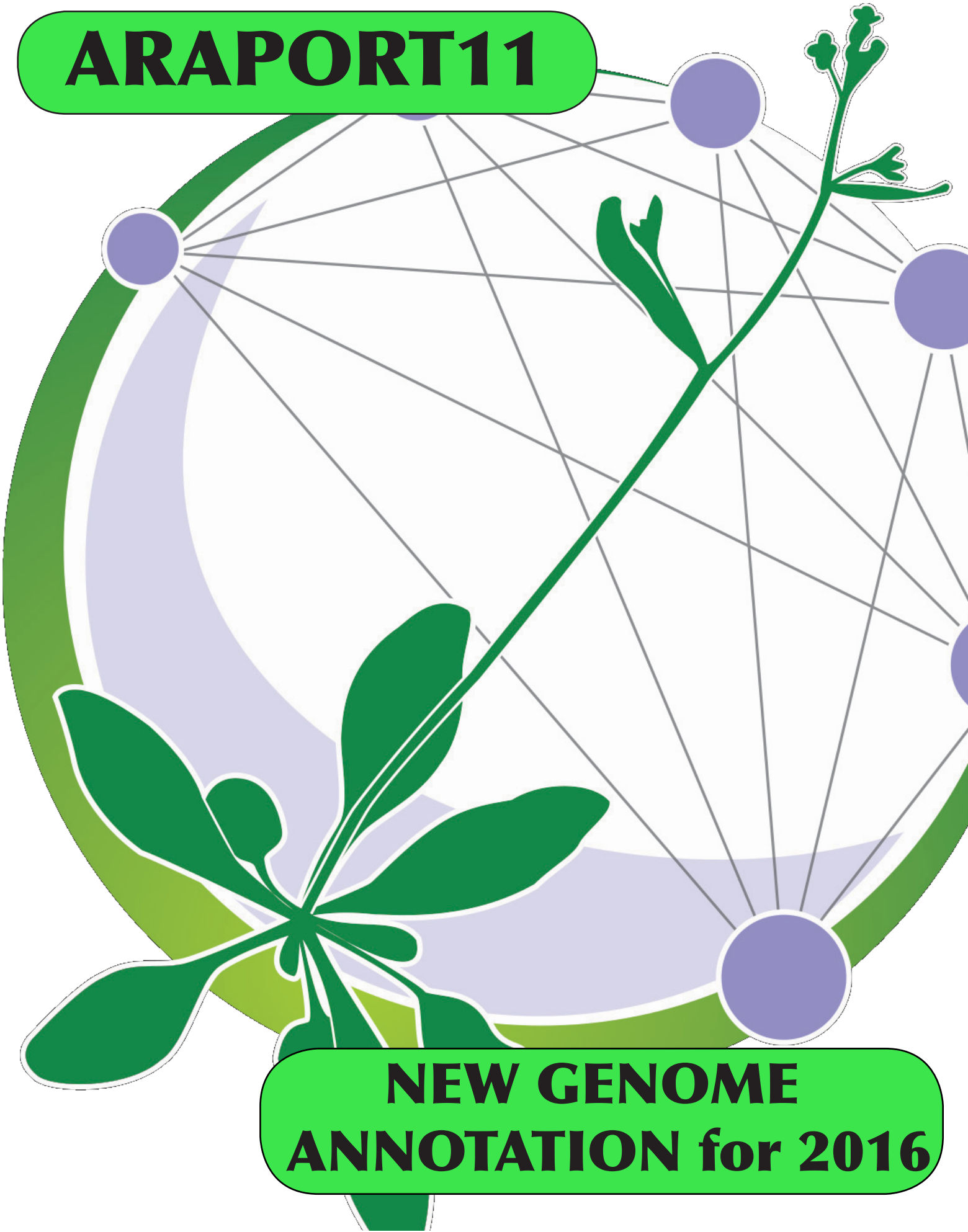


# NEW GENOME ANNOTATION for 2016

## Welcome to the December 2015 Issue of GARNish

### Geraint Parry, GARNet Coordinator

At the passing of each calendar year there is the obvious opportunity to look both back and forward. That is also the case at GARNet and we are excited to welcome a new cohort of academics to the Advisory committee. Christine Raines (University of Essex), Saskia Hogenhout (John Innes Centre) and Steven Spoel (University of Edinburgh) represent the present and future of UK plant science and will no doubt will bring great value to Committee decisions. On the flip-side we must bid fairwell to Anthony Hall, Cyril Zipfel and John Doonan whose excellent terms have ended. Anthony in particular has played a significant role in the grants with which GARNet have been involved over the past few years. He is a PI on the ongoing BBSRC iPlant grant (see page 6) and as the leader of the UoL GeneMill he is an integral member of the UK Plant Synthetic Biology community.

With reference to the recent GARNet election it was extremely gratifying to have over 170 UK plant science academics cast their votes. Thanks to all who contributed to the process.

With the UKPSF in a transition period (see page 4), we are fortunate that GARNet has a full-time coordinator to support UK plant science and it is worth reminding readers that we are not solely focused on Arabidopsis but that part of our mandate is to interact with researchers whose focus is on other plant species.

We are extremely excited about the program of meetings that GARNet is organising in 2016. In April we are hosting a workshop focussed on the strategies that plant scientists use to deal with the challenges of big data. The speakers at this meeting include Professor Nick Provart (BAR, Toronto), Professor Carole Goble CBE (Manchester) and Professor Geoffrey Boulton OBE (Edinburgh). More details can be found on page 5.

Later in the year Cardiff University is hosting our biennial GARNet meeting entitled '*GARNet2016: Innovation in the Plant Sciences*'. The keynote speakers include Ben Scheres (Wageningen), Niko Geldner (Lausanne), Cathie Martin (JIC) and Chris Town (Araport). All the details can be found at www.GARNet2016.weebly.com

In December GARNet will finish 2016 with a fantastic meeting held at Gonville and Caius College in Cambridge, organised by advisory board members David Salt and Ian Henderson. This workshop is entitled '*Natural genetic variation as a tool for gene discovery and crop improvement*' and the key-note speakers include Detlef Weigel (Tuebingen), Joy Bergelson (Chicago) and Magnus Nordborg (GMI, Vienna).

## Contents



Special thanks to: Katherine Denby, Lisa Martin, Joe McKenna, Richard Buggs, Andrew Thompson, Brian Forde, Agnes Chan, the new BBSRC grant holders and plant science researchers at QMUL, Cranfield and Oxford Brookes.



## The GARNet Committee

**David Salt**
University of Aberdeen
GARNet Chair Nov 2014–Dec 2016

**Jim Murray**
University of Cardiff
GARNet PI (from February 2015)

**Katherine Denby**
University of Warwick
Committee member Nov 2014–Dec 2017

**Antony Dodd**
University of Bristol
Committee member Jan 2013–Dec 2016

**John Doonan**
University of Aberystwyth
Committee member Jan 2012–Dec 2015

**Anthony Hall**
University of Liverpool
Committee member Jan 2012–Dec 2015

**Nicholas Harberd**
University of Oxford
Committee member Jan 2013–Dec 2016

**Ian Henderson**
University of Cambridge
Committee member Nov 2014–Dec 2017

**Sabina Leonelli**
University of Exeter
*Ex-officio* member

**Sean May**
Nottingham Arabidopsis Stock Centre
*Ex-officio* member

**Zoe Wilson**
University of Nottingham
Committee member Nov 2014–Dec 2017

**Cyril Zipfel**
The Sainsbury Laboratory, Norwich
Committee member Jan 2012–Dec 2015

**New Members starting their terms in Jan 2016:**

**Christine Raines:** University of Essex

**Saskia Hogenout:** John Innes Centre

**Stephen Spoel:** University of Edinburgh

Watch this space for updates as we further develop this meeting.

Even though we have a full 2016, we are already looking ahead to 2017 so if anyone has ideas about meetings or workshops with which GARNet might be involved then please get in contact.

Please enjoy this edition of GARNish that features an article from Araport about the new Arabidopsis Genome Annotation as well as information about new BBSRC grant funding, which includes a promising number of New Investigator Grants.

We also turn the Spotlight on the plant science departments at QMUL, Cranfield and the Bioimaging facility at Oxford Brookes.

Follow @GARNetweets on Twitter and Facebook. Please remember the '**Weeding the Gems' blog** at *http://blog.garnetcommunity.org.uk*. Please contact Geraint, geraint@garnetcommunity.org.uk if you would like to write a guest post.

## UK Plant Sciences Federation Update

Small but significant change has come to the UKPSF over the past couple of months. The full time UKPSF Executive Officer Mimi Tanimoto left her role to take up a post at Kew Gardens whilst at the same time the core funding supplied by the Gatsby Foundation and the Society for Experimental Biology (SEB) was coming to an end. The UKPSF has secured follow-on funding from the British Society of Plant Pathology, Biochemical Society and SEB but it is insufficient to maintain a full time position.
Moving forward the UKPSF will become a Special Interest Group of the Royal Society of Biology (RSB) and be adminstered as the *de facto* plant science arm of RSB. Unfortunately the lack of a full-time position will reduce the amount of time that RSB can devote to the UKPSF.
However in the recent (and perhaps final) UKPSF AGM, the RSB agreed to maintain the strong web presence that the UKPSF has developed (http://www.plantsci.org.uk/) and then focus on specific projects. In future this will depend upon gaining appropriate funding in addition to that already supplied by the member organisations.
In 2016 these will include:

**1.** Organisation of the UK Plant Science Conference; April 11-12th 2016 at the John Innes Centre

**2.** Imminent publication of reports prepared by the Working groups set up as a result of the 2014 'UK Plant Science: Current status and future challenges' report.

**3.** Support the development and publication of a Roadmap for the next 25 years of UK Plant Science. This is scheduled for publication in mid 2016.
The current UKPSF Executive board (http://www.rsb.org.uk/policy/groups-and-committees/ukpsf) will remain in place and they will liase with Alessandro Allegra, who is the member of RSB staff who will take on the role of 'UKPSF coordinator'. Elections to this Executive board will proceed as normal with three new members to be immediately elected.
The future of the AGM, where all member organisations could attend and learn about the activites of the UKPSF, is less certain but Mark Downs, Chief Executive of the RSB suggested that this type of meeting might occur on a six-monthly basis.
The lack of a full time officer will certainly impact the broader influence of the UKPSF but it remains to be seen how this new arrangement will develop. The RSB will certainly welcome any help maximise the effectivness of this new incarnation of the UKPSF.

## Global Plant Council Update

An update from the GPC Communications manager, Lisa Martin, who after spending a couple of years in a similar position at GARNet, *just can't stop contributing to GARNish!*

It's been a busy few months for the Global Plant Council (GPC) as we prepared ourselves not only for our Annual General Meeting, but also for our Symposium on Stress Resilience, held in collaboration with the Society for Experimental Biology (SEB). The meetings were held on either side of the International Plant Molecular Biology conference in the town of Foz do Iguaçu on the Brazilian side of the famous Iguassu Falls. You can read more about our Stress Resilience Symposium in the report on page 22.

At our AGM we reflected on the great work that the GPC has achieved over the last year. The GPC has played an important role in the development of DivSeek (www.divseek.org), a multi-stakeholder collaborative initiative that aims to 'unlock the potential of crop diversity stored in genebanks around the world'. The steering committee for this consortium-led project has now been established, and is formulating a workplan, so stay tuned for updates!

We have also been working with the American Society of Plant Biologists to develop 'Plantae', a digital platform that will be both an online resource hub for plant science, as well as a place where plant scientists can network, promote their research, discuss and interact. The website is currently in beta-testing mode with a full release due in 2016, but if you want to have a look around, you can sign up to be a beta-tester and give us your feedback at www.plantae.org.

At the AGM we also discussed our social media activities, which have dramatically increased awareness of the GPC around the world. Check out this blog post, written by one of our two New Media Fellows, Amelia Frizell-Armitage from the John Innes Centre, if you want some tips on how to use social media to promote yourself and your science, and to increase your following: http://blog.globalplantcouncil.org/future-directions/the-global-plant-council-guide-to-social-media/. Our other New Media Fellow, Sarah Jose from the University of Bristol, has set us up on Scoop. It (www.scoop.it/global-plant-council), and we also now have a Facebook page (www.facebook.com/GlobalPlantGPC) in addition to our English and Spanish-language Twitter accounts (@GlobalPlantGPC and @GPC_EnEspanol), so if you're not already following us or 'liking' us, please do!

Lastly, we thanked our outgoing Executive Board for all their hard work over the last three years, and we welcomed the newly elected one. Barry Pogson (Australian Society of Plant Scientists) will be our new Chair, Vice-Chair is Ariel Orellana (Chile's National Network of Plant Biologists), the Treasurer is Vicky Buchanan-Wollaston (SEB) and Carl Douglas (Canadian Society of Plant Biologists) and Yusuke Saijo (Japanese Society of Plant Physiologists) are Board Members.

With this new team in place, including our new President Professor Bill Davies from the University of Lancaster, whom we had welcomed earlier in the year, we look forward to lots more exciting activities in the coming year to help develop plant science for global challenges.

## GARNet/Egenis Workshop on 'Integrating Large Data into Plant Science: From Big Data to Discovery'

GARNet and the Exeter Centre for the Study of the Life Sciences (Egenis) are excited to announce this two-day workshop to be held in the picturesque Dartington Hall, Totnes, Devon on April 21st-22nd 2016. https://www.dartington.org/visit/stay/

The aims of this workshop are to:
1. Introduce examples of how researchers have re-used datasets in innovative ways.
2. Examine the infrastructure that exists to support the re-use of large datasets
3. Discuss the mechanisms by which the community deals with big data.

We have kind support from the ERC and the BBSRC so registration for this workshop will be free although sadly we can only select a limited number of delegates. If you are interested in attending please email the GARNet coordinator Geraint Parry (geraint@garnetcommunity.org.uk) with a short paragraph outlining why this workshop would be useful to you. The organising committee will then let you know by March 1st whether you have been successfully selected so that you can plan your trip to Devon.
More details can be found here: http://blog.garnetcommunity.org.uk/garnetegenis-meeting-big-data/

## iPlantUK: computational resources for large-scale data analysis

Katherine Denby, University of Warwick

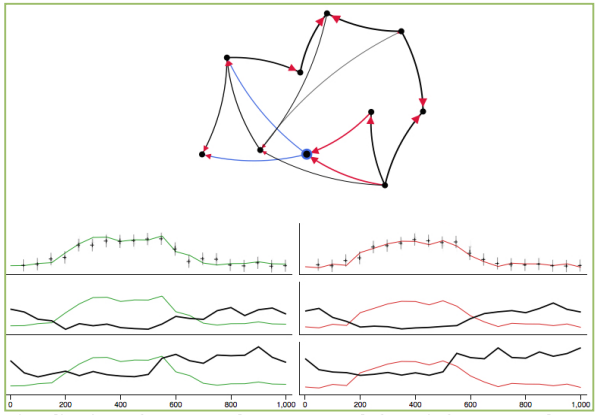
iPlantUK is a major BBSRC-funded collaboration between scientists at the University of Arizona, the Texas Advanced Computing Center, the University of Warwick, the University of Liverpool, the University of Nottingham, and The Genome Analysis Centre (TGAC) to set up a UK based node for The iPlant Collaborative. The iPlant Collaborative provides a high-performance computing environment and tools for scientists to share and analyse large-scale data effectively. Originally set up for plant scientists (hence the name), iPlant is now available for researchers studying all organisms other than humans. The iPlant platform allows research groups that lack either computational capacity or expertise to access extensive data storage, backup and compute power hosted in a number of globally accessible locations, and structured, integrated analysis applications and workflows. Researchers can work on large datasets using publicly available tools and pipelines in a single online location.

iPlantUK will establish a UK node of the iPlant Collaborative cyberinfrastructure to support the UK biological science community's data storage and analysis requirements. iPlant and iPlant UK are building a common international biological science platform that aims to prevent duplication of effort and funding by actively encouraging and supporting reuse of data, applications and resources.

### iPlant Collaborative UK

iPlantUK will host computational tools developed in BBSRC-funded projects, enabling them to be globally and easily accessible. Currently iPlantUK is establishing workflows for analysis of next generation sequencing data and adapting suites of tools for transcriptome analysis/network modelling, and image-based phenotyping. For all tools, clear user documentation will be provided. The computational hardware infrastructure for iPlantUK will be set up at The Genome Analysis Centre (TGAC) in Norwich. TGAC provides the National Capability for computational infrastructure in the UK, and as such is perfectly situated to provide technical foundations and bioinformatics expertise for the iPlantUK node. The TGAC team, led by Dr Robert Davey, is deploying, configuring and maintaining the complex iPlant virtualised computing environment in order to run the UK node, facilitate federation with the iPlant node in the US, as well as optimising next-generation sequencing analysis tools developed at TGAC for the platform.

The Liverpool team, led by Anthony Hall, is building software workflows for genome analysis in polyploids. These will enable researchers to use up-to-date wheat genome information or custom polyploidy genomes and carry out SNP scoring, analysis of homologous gene expression and mapping-by-sequencing. This team is also evaluating multiple mapping-by-sequencing algorithms to establish optimal pipelines for Arabidopsis, barley and custom diploid organisms. For Arabidopsis researchers, iPlantUK will provide detailed SNP information and a workflow for design of CRISPR/Cas9 constructs for knocking out target genes. These tools will be complemented by workflows for RNAseq analysis and *de novo* genome assembly. Some of these workflows have already been built and are available on iPlant (for example, Tuxedo suite PE up to 4 conditions); these will be hosted on iPlantUK when the UK node is deployed and user documentation provided.




**Visualisation of gene regulatory network from inference tool. Both photos on this page from iPlantUk.**

The Warwick programmers, led by David Wild, are integrating a number of systems biology tools developed in the PRESTA (http://warwick.ac.uk/presta) project into the iPlant environment. These include a set of tools for determining differential gene expression in time series transcriptome data, along with network inference and modeling algorithms. Tools for analysing co-expression across multiple time series, promoter conservation and sequence motifs, as well as genome-wide chromatin footprinting data will also be incorporated. Output from each tool will be formatted to allow easy integration of different tools and common workflows will be set up to guide users.

Image analysis is the focus of Tony Pridmore's team at Nottingham. His team is working to incorporate several image-based phenotyping applications into iPlantUK, all of which are based on the Root System Markup Language (RSML) developed by the Centre for Plant Integrative Biology (https://www.cpib.ac.uk/) and colleagues. This tool set includes software for phenotyping root system architectures from both 2D and 3D images and a viewer for visualising and extracting features of interest from RSML files. The availability of these RSML tools on iPlant UK will encourage further sharing and interoperability between phenotyping tools within the community.

Initial information on the iPlantUK project and team is available on our website – http://iplantuk.org. Look out for further information and announcements of tool releases as the project progresses. We will also be talking about iPlantUK at the Plant and Animal Genome conference in January 2016 at the iPlant workshop (https://pag.confex.com/pag/xxiv/webprogram/Session3121.html) and at the GARNet meeting in September 2016 (www.GARNet2016.weebly.com).

BBSRC bioscience for the future

## New Arabidopsis Grants

Arabidopsis researchers continue to be very successful in BBSRC responsive mode funding rounds. Here's a round-up of grants awarded to members of our community in the BBSRC Responsive Mode 2014 Round 3 and 2015 Round 1. Congratulations to the PIs and the researchers in post working on these exciting projects!

### Does the N-end rule pathway of targeted proteolysis control the plant immune system?

Mike Holdsworth

University of Nottingham

The capacity of plants to survive adverse conditions and reach reproductive maturity critically depends on their ability to continuously adapt to changes in the environment, particularly in response to pathogens. Many studies have identified the control of protein stability as a major regulator of plant responses during invasion and propagation of pathogens, showing that modulation of the stability of key regulatory proteins is required for adaptation to pathogenic infections.

The N-end rule pathway of targeted proteolysis is a ubiquitin proteasome system mechanism that controls protein degradation dependent on the N-degron, a specific motif mainly determined by an N-terminal (Nt-) destabilizing amino acid residue, targeting the proteins for degradation. This pathway has been extensively studied in animal and yeast systems, where it was shown to have an important role in developmental processes, including apoptosis. Recently in our group the first plant physiological substrates of the N-end rule pathway were identified as the GroupVII ERF transcription factors, which were shown to be the major regulators of plant oxygen and nitric oxide (NO) sensing, through the Cysteine-Arginine branch of the pathway (Cys-Arg/N-end rule pathway).

Our recent unpublished experiments show that the N-end rule pathway is involved in the regulation of the plant immune response, revealing the importance of an as yet undiscovered substrate(s) with Nt-Glutamine (Q), a separate branch of the pathway that utilises the enzyme Glutamine Amidohydrolase (NtQ-amidase; NTAQ). This is the first time that a function for this branch of the pathway has been discovered in plants.

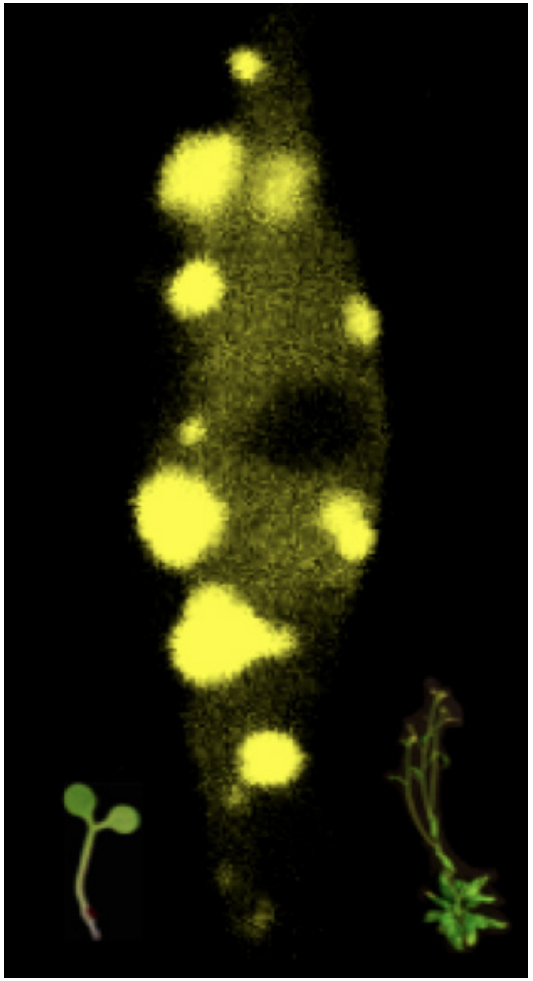
In this project we will investigate the hypothesis that the N-end rule pathway mediates previously undiscovered key aspects of plant responses to pathogens by controlling the stability of specific substrate proteins with an N-terminal glutamine.

### Transcriptional regulation of plant growth in nuclear micro domains.

Eirini Kaiserli

University of Glasgow
New Investigator Grant

The focus of this project is to investigate the role of novel regulators of plant growth and development in response to environmental stimuli. We will use genetics, next generation sequencing and super-resolution microscopy to elucidate the mechanism of action of TZP (TANDEM ZINC FINGER PLUS3), a novel transcriptional regulator that integrates light, hormone and clock networks to control major plant developmental transitions (Loudet *et al.*, 2008 PNAS, Kaiserli *et al.*, 2015 Dev Cell). In particular, the existence of "transcription factories" and the translocation of active gene regions towards areas enriched in transcription factors, chromatin remodeling enzymes, photoreceptors and components will be investigated using the model plant species, *Arabidopsis thaliana*. TZP is the only protein in Arabidopsis containing both Zinc Finger (ZF) and PLUS3 domains. Studies in yeast and human proteins have revealed that PLUS3 domains function in chromatin re-organisation by mediating the recruitment of gene regulatory proteins and RNA-processing factors to chromatin during transcription (de Wier *et al.*, 2013 PNAS ). The role and molecular function of PLUS3 domains in plant proteins remains elusive. We will investigate the transcriptional activity of TZP PLUS3 *in vivo* and *in vitro* and employ a whole-genome approach to identify *in planta* RNA and DNA targets for TZP. To obtain information on the 3D structure, content, environment and complexity of nuclear photobodies we propose to use super-resolution microscopy as well as DNA and RNA Fluorescence In Situ Hybridisation (FISH) on transgenic Arabidopsis lines expressing fluorescently tagged TZP and TZP-interacting proteins.



**Eirini Kaiserli:** Nuclear architecture reflects key transition points during a plant's life-cycle. Confocal image analysis of TZP tagged with a fluorescent marker shows dynamic nuclear localisation in response to light. TZP sub-nuclear compartmentalisation correlates with changes in gene expression required for regulating plant growth and development (adapted from Kaiserli *et al.*, 2015 Dev Cell).

### N-terminal acetylation as a signal for protein degradation controlling plant development and stress responses:

Daniel Gibbs

University of Birmingham
New Investigator Grant

Targeted protein degradation (proteolysis) via the ubiquitin proteasome system (UPS) is an essential cellular process of physiological importance, and in plants plays a key role in almost all aspects of development and stress response. Increasing our understanding of the signals and components controlling protein stability via this system therefore has the potential to identify new targets for crop improvement.

The N-end rule pathway, a highly conserved division of the UPS that destroys proteins based on the nature of their N-terminus (Nt), has emerged as a critical regulator of development and environmental signal-sensing in plants (Gibbs *et*

**Dan Gibbs: Rosette phenotype of wild type (left) and Ac/N-recgonin loss-of-function mutant (right) plants**

*al.* 2014 Trends Cell Biol). Recent studies in yeast and mammals have now identified a novel branch of the pathway that specifically degrades proteins that have been Nt-acetylated (called the 'Ac/N-end rule pathway'). Despite the fact that more than 70% of proteins undergo Nt-acetylation in plants, the functional relevance of this modification has remained elusive (Gibbs 2015 Trends Plant Sci). Therefore, we hypothesised that one function for this protein modification might be in the control of protein half-life via the previously undiscovered plant Ac/N-end rule pathway.

We identified putative homologues of yeast Ac/N-end rule-associated enzymes in Arabidopsis and crop plant genomes. These include Nt-acetyltransferases (NATs), which co-translationally add acetyl moieties to the exposed alpha-amino group of Nt-residues, and specific E3 ligases (called Ac/N-recognins) that bind to and ubiquitinate Nt-acetylated target proteins. Remarkably, a vast majority of these proteins have not been studied previously. We found that loss-of-function mutations in the genes encoding these components have several shared growth and stress-related phenotypes in Arabidopsis - including altered germination, ABA and drought responses, as well as growth and chlorophyll defects. Furthermore, artificial 'reporter proteins' were found to accumulate to higher levels in Ac/N-end rule mutants than in wild type plants. These preliminary studies indicate that the Ac/N-end rule is present in plants and that it regulates a range of important processes.

In this BBSRC-funded project we will functionally characterise the structural and enzymatic components of this novel proteolytic pathway in Arabidopsis to demonstrate that Nt-acetylation acts as a context-specific degradation signal in plants. We will link the activity of this pathway to diverse growth, development and stress responses, and use targeted and screening approaches to identify physiological substrates. Collectively these studies will open up a new area of research into plant proteolysis and signal transduction, and provide new insight into the functional relevance of this major but enigmatic protein modification.



## Photoreceptor Optimisation of Plant Water Use.

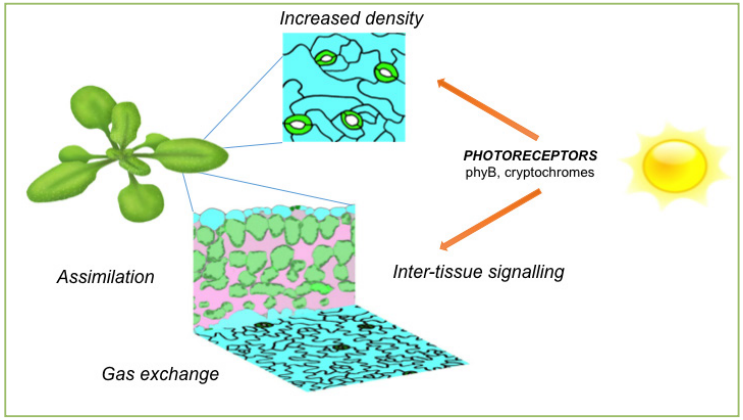
Stuart Casson

University of Sheffield

New Investigator Grant.

The research in my lab is focused on how plants respond to environmental conditions and in particular, the impact this has on plant development and performance. Much of our research utilises stomatal development as a model to study plant-environment interactions. It has long been known that light signals modulate stomatal development, with leaves that develop under higher irradiances having significantly increased stomatal densities. We, along with other groups, were able to demonstrate that this response is regulated by photoreceptor signalling, with the red/far-red light receptor phytochrome B (phyB) having a dominant role (Casson et al., 2009, Current Biology, Kang et al., 2009, Plant Cell). Whilst stomata are limited to the epidermis of the leaf, we demonstrated that phyB can act in a tissue specific manner, outside of the epidermis, to regulate light mediated stomatal development (Casson and Hetherington, 2014, Current Biology). This work raised questions about how signals from different tissues are integrated and in particular, the role of tissue-specific and inter-tissue photoreceptor signalling in mediating changes in stomatal development.

These factors form the basis for the research to be undertaken in this project which aims to investigate how photoreceptor signalling balances plant water use and productivity through changes in stomatal development (Figure 1). The research will focus on dissecting the inter-tissue mechanisms regulating stomatal development in response to light and investigate the regulatory network downstream of the photoreceptors in different tissues. By manipulating components of these networks the final aim is to determine whether it is possible to uncouple the trade-off between water use efficiency (WUE) and carbon assimilation in phyB leaves.




**Stuart Casson: Stomatal development on the leaf surface is positively regulated by light and growth at higher irradiances leads to increases in stomatal density. These developmental changes are phyB and cryptochrome dependent. However, these changes in epidermal development are not specific to signalling within the epidermis and involve inter-tissue signalling between the inner tissue of the leaf and epidermis.**

Crop yield is highly water dependent and globally, approximately 80% of all freshwater that is abstracted is used for agriculture. Increases in global population, industrial demand and changing global climate are predicted to increase competition for fresh water resources, severely impacting on food and water security. A major outcome of this proposal will be to establish the role of photoreceptor signalling networks in regulating this process through both tissue specific and inter-tissue signalling. Modulating these signalling networks presents a means of manipulating the trade-off between water use and photosynthesis to generate plants with improved performance.

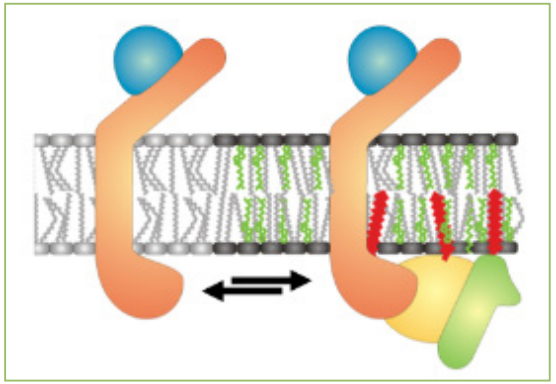
## Receptor-like kinase palmitoylation: resolving a crucial feature of plant cell signalling.

Piers Hemsley
University of Dundee and James Hutton Institute
New Investigator Grant

Cellular membranes divide eukaryotic cells into many diverse functional compartments and separate the inside of the cell from the outside world. Each of these membranes has a distinct population of proteins associated with it, performing a wide range of tasks such as transmitting signals from one side of the membrane to the other or regulating the flux of metabolites between compartments. To coordinate these processes a high degree of regulation is required at the level of protein function.

One post-translational modifications (PTMs) regulating protein function is the fatty acid based S-acylation or palmitoylation. This modification is the only known reversible lipid modification of proteins and, based on our own and others data, is thought to affect up to a third of all membrane proteins (~10-15% of the total proteome). By comparison, the better known but non-reversible, lipid based modifications N-myristoylation, farnesylation, geranylgeranylation and GPI-anchors are only thought to account for 2.5% of the total proteome. S-acylation has been implicated in a wide variety of processes including trafficking proteins to specific membrane compartment, regulating protein-protein interactions, protein microdomain partitioning, directly regulating protein activity and regulating protein stability or turnover.

The reversibility of S-acylation allows it to act in an analogous manner to phosphorylation whereby proteins can undergo rounds of S-acylation and de-S-acylation in response to stimuli. Our lab is particularly focussed on understanding how these cycles are regulated and what are the functional outcomes of S-acylation and de-S-acylation. We published the first snapshot of the Arabidopsis S-acyl proteome, identifying nearly 600 proteins as being S-acylated, and have since expanded this data further. Many of the proteins identified belong to the Receptor-like kinase (RLK) superfamily.



**Piers Helmsley: Palmitoylation (red) is able to change the signalling responses at the plasma membrane.**



RLKs are one of the most important families of receptors in plants, being responsible for perceiving the majority of extracellular stimuli such as pathogens, cell wall stress or hormones.

Understanding how RLKs are regulated is therefore of paramount importance for a wide range of research fields and applications. We have since established that the signalling outputs of many RLKs are regulated by changes in S-acylation state in response to ligand binding. RLKs with altered S-acylation states show altered signalling outputs indicating that S-acylation is required to modulate correct responses.

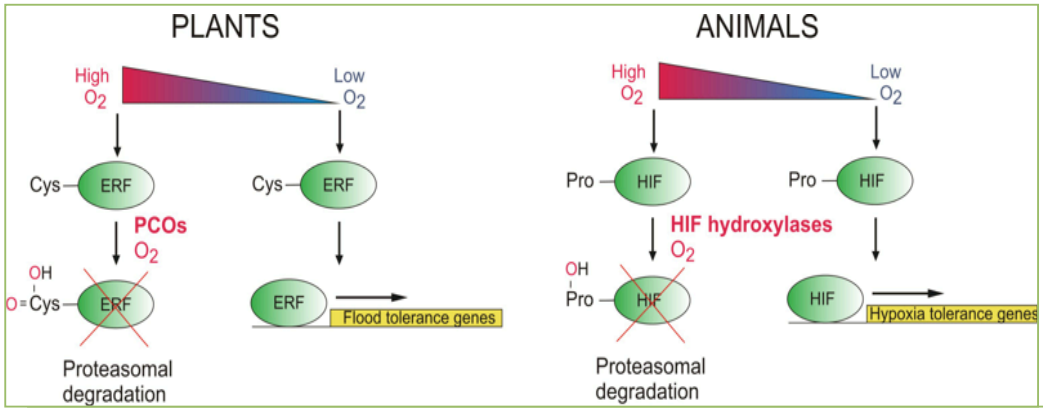
In this project we aim to use model RLKs to place S-acylation state changes into the known regulatory framework of RLK signalling and identify the enzymes required for regulating S-acylation state changes.

## Hypoxia Sensing in Plants: Role of the Plant Cysteine Oxidases.

Emily Flashman
University of Oxford
New Investigator Grant

All aerobic organisms must have regulatory systems in order to respond to low oxygen (hypoxia), either by metabolic reconfiguration or by physical changes to increase oxygen delivery. In animals, this hypoxic response is mediated by the Hypoxia-Inducible transcription Factor, HIF. HIF levels are regulated by acutely oxygen-sensitive enzymes, the HIF hydroxylases; hydroxylation targets HIF for proteasomal degradation but HIF hydroxylase activity reduces in hypoxia, elevating HIF levels and inducing the hypoxic response. The hypoxic response in plants is mediated by Group VII ethylene response factors (ERF-VIIs). Similar to HIF, levels of the ERF-VIIs are regulated in an oxygen-dependent fashion: oxidation of their N-terminal cysteine residues renders them targets for the N-end rule pathway (NERP) and proteasomal degradation (a process which also requires NO in planta). In hypoxia, this N-terminal cysteine oxidation is reduced and ERF-VII levels are stabilised to elicit the hypoxic response (Gibbs *et al*, 2011, Nature. Licausi *et al*,

**Emily Flashman: Hypoxic response mechanisms in plants and animals. Understanding the role of the PCOs will allow targeted manipulation and upregulation of ERF-VIIs to enhance flood tolerance**



2011, Nature) ERF-VIIs in rice and Arabidopsis are known to regulate responses to flooding, a major cause of hypoxia in plants.

The mechanism of N-terminal cysteine oxidation was elucidated in 2014, when teams led by Francesco Licausi and Joost van Dongen identified a set of enzymes in Arabidopsis which catalyse oxidation of the ERF-VII N-terminal cysteine residues in an oxygen-dependent manner (Weits *et al* 2014 Nature Comm). These enzymes, termed the Plant Cysteine Oxidases (PCOs), were found to regulate ERF-VII levels and consequently gene expression, influencing submergence tolerance. The identification of oxygen-dependent enzymes as regulators of the ERF-VIIs and thus the hypoxic response in plants raises the possibility that the PCOs may act as plant oxygen sensors, similar to the HIF hydroxylases in animals (see figure). It also raises the exciting possibility that manipulating the activity of these enzymes could artificially upregulate ERF-VII levels and improve flood tolerance.

Elevated ERF-VIIs are already known to confer submergence tolerance when artificially stabilised in Arabidopsis and barley, and also in rice varieties containing the gene encoding the ERF-VII SUB1A which, unusually, is not degraded via the NERP. The advantage of manipulating ERF-VII levels at the point of PCO activity is that it allows the possibilities of 'fine-tuning' the hypoxic response and of temporal control.

The aim of our BBSRC-funded project is therefore to characterise the role of the PCOs in plant oxygen-sensing and identify ways to modify their activity. We will conduct biochemical, biophysical, structural and kinetic investigations of the PCOs, and thus identify how they interact with both the ERF-VIIs and oxygen. This will include characterising their capacity to act as oxygen sensors, i.e. how their activity correlates with oxygen concentrations.

Most excitingly, this detailed molecular understanding will enable us to rationally design mechanisms to either chemically inhibit or genetically fine-tune PCO activity, particularly with respect to oxygen, and thus artificially elevate ERF-VII levels. Our initial focus will be on the Arabidopsis PCOs but we will also look at whether PCOs from other species, particularly crops, could also perform oxygen-sensing roles. Mechanisms we identify to modulate PCO activity in Arabidopsis could then be translated into nutritionally or commercially relevant plants.

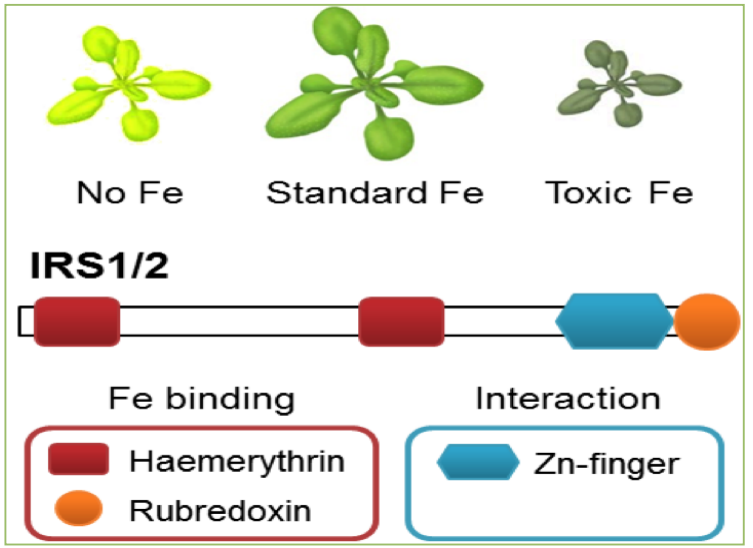
## Functional characterization of Iron Regulator Sensor (IRS) proteins in plants:

Janneke Balk, Jorge Rodríguez-Celma, Nick Le Brun

John Innes Centre and University of East Anglia

Iron (Fe) is an important micronutrient both for plants and animals. Iron deficiency anaemia is a widespread disease in humans and Fe is a limiting factor for crop growth in many arable soils. However, deficiency is not the only problem: in excess, Fe can cause serious oxidative damage and induce cell death. Therefore, its uptake and accumulation needs to be tightly regulated and Fe levels inside cells must be sensed. The Fe sensing mechanism is well known for bacteria, yeast and mammals: Fe is sensed via regulatory proteins that sense the level of Fe either as a free ion or as biologically active cofactors (Fe-S or heme) and regulate the expression of Fe homeostasis genes.

Recently a new Fe sensing protein, FBXL5, has been discovered in mammals and acts in protein turnover. Depending on the Fe levels in the cell, FBXL5 promotes the degradation of an Fe regulatory protein, which in turn controls the gene expression of Fe homeostasis genes, giving a fast response to local Fe levels. However, no Fe sensing mechanism is known for plants. The previously identified transcription factors are not known to bind Fe, and no relation between Fe-S biosynthesis and Fe homeostasis has been yet discovered.




**Janneke Balk: Fe deficiency and toxicity symptoms (top) and the domain structure of the IRS proteins (below)**

The Balk group has been studying the Fe-S assembly pathways in plants for many years, and the Le Brun group has been working in the field of iron metabolism for >20 years. Dr. Rodriguez-Celma recently joined the Balk group to enhance his plant physiology skills with biochemical techniques. During a postdoc position in Taiwan, he studied the transcriptomics responses to Fe deficiency in Arabidopsis and discovered two new candidate genes that may be involved in signalling the Fe status of the plant cell. The genes are provisionally named *IRS1* and *IRS2*, for Iron-Regulated Sensor, and they have partial homology to *FBXL5*. The proteins have several putative Fe binding domains, known as haemerythrin and rubredoxin domains, and a RING Zn-finger domain that is likely to mediate protein-protein interactions. The proteins are also predicted to have ubiquitin ligase activity, so a mechanism analogous to the FBXL5 complex in mammals would be plausible.

This project aims to characterize the metal binding properties of the IRS proteins and how Fe binding affects folding and protein interactions. In order to function as sensors our candidates will need to bind Fe and interact with other proteins controlling Fe homeostasis, targeting them for degradation depending on the intracellular Fe levels. We will test the Fe binding properties and thermodynamics by recombinant protein expression and advanced spectroscopic and analytical techniques. We will try and identify their interacting partners *in vitro* using yeast-two hybrid analysis and co-immunoprecipitation. To test how they function *in vivo* we will also characterize *irs* mutant lines in Arabidopsis for iron homeostasis phenotypes. The longer term aim is to unravel the entire Fe signalling cascade, which can then be manipulated to biofortify crops with iron. This will help to combat Fe deficiency in humans, especially if lower meat consumption becomes more important in order to address climate change.

## Reframing the GM Debate

Geraint Parry,
GARNet Coordinator

On a daily basis most plant scientists might not be too concerned by the politics surrounding the use of genetic modification or advanced genetic technologies. However these are areas of policy that might greatly impact future research, funding and employment opportunities. Currently, even with the moratorium on use of GM plants across the European Union (EU), UK funding levels have broadly been maintained. However if this policy persists it might negatively impact available future funding. Conversely if there is a change in public and political opinion toward these genetic technologies then that might open new avenues of research and sources of funding.

In February 2015 the cross-party Science and Technology Committee provided a report to the UK government entitled 'Advanced genetic techniques for crop improvement: regulation, risk and precaution'. This 102-page document, for which GARNet provided written evidence, contained 44 conclusions and recommendations for the incoming government to consider. The entire document can be found here: http://www.publications.parliament.uk/pa/cm201415/cmselect/cmsctech/328/32802.htm

In mid October, the new Conservative government supplied a response to this report that includes answers to a number of the original recommendations. This 13-page response can be found in full here: http://www.publications.parliament.uk/pa/cm201516/cmselect/cmsctech/519/51902.htm

Below are highlighted some of the recommendations and the government responses that might be of interest to GARNish readers:

***Recommendation:*** The Government (GOV) should initiate a reframing of the public debate in this area by moving away from the simple notion of 'GM' in its future policy communications. These communications should be presented in a way to encourage constructive public debate about the science-based evidence supporting the safety of GM crops.
***Response:*** GOV agrees that this reframing is needed but notes that some stakeholders would view a removal of the term 'GM' with some suspicion. Therefore GOV will continue to use 'GM' when appropriate. GOV also takes note of the debate surrounding the term 'new breeding technologies (NBT)', whose status in EU legislation needs to be clarified. GOV takes the position that necessary regulation of these techniques should be pragmatic and proportionate to the overall objective. However when addressing a lay audience, GOV will attempt to make it plain to that audience exactly what they are discussing. GOV maintains its manifesto promise to make science-based decisions on GM and their public communications will highlight agricultural innovations, including use of GM crops. GOV does not think that there is a requirement to consider the assessment of non-safety factors in the decision making process surrounding whether to engage with the growing of GM crops.

***Recommendation:*** GOV should undertake a review of the intellectual property landscape particularly in reference to agricultural technologies and the impact it might have on commercialisation of all types of new crops.
***Response:*** GOV will wait until the EU publish a report on a similar topic and then decide whether to undertake a national review.

***Recommendation:*** GOV should publicly acknowledge that GM crops pose no greater inherent risk than conventionally bred crops. Relevant areas of GOV.UK should be updated to reflect this position.
***Response:*** GOV accepts this point and, where appropriate, already reflects it in its communications.

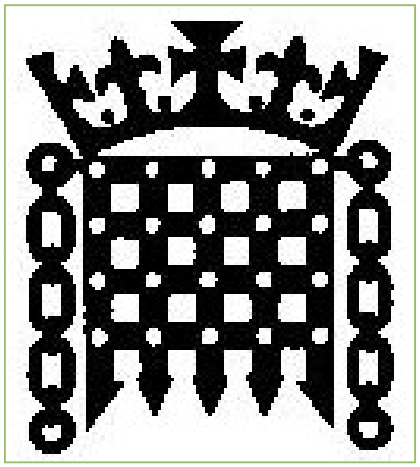
***Recommendation:*** GOV should formally adopt a move to regulate novel plants in a trait-based manner and develop this framework so that it will inform EU future discussions. GOV should publicly state its commitment to major EU reform of the legislative framework for GM organisms and GM crops. The role of the Advisory Committee of Releases to the Environment (ACRE) should be expanded to consider all novel crops, not just GM varieties.
***Response:*** GOV is currently focused on encouraging the EU to operate GM authorisation in a timely manner but feels that in the short term, it is improbable to reform policy toward the use of 'trait-based assessment'. GOV feels that this might have a negative impact given the increased number of assessments that would have to be conducted. The current GM cultivation Directive is making process, albeit at a slow rate. This type of analysis would be required for every novel crop so GOV feels it is in its best interest to attempt to influence the EU only on this current legislation. GOV feels that an expansion of ACRE remit would be linked to the move to a trait-based assessment. GOV concedes that this type of system might be more logical but it is not appropriate to pursue this course domestically in the absence of any real prospect of a corresponding change in the EU regime. The recommended changes to the remit of ACRE would likely require additional primary legislation to be adopted, which would be time-consuming and costly. GOV feels this would currently represent unnecessary expenditure.

***Recommendation:*** GOV should produce a short document that details its understanding of the precautionary principle and how it will use this principle as a guide to policy making.
***Response:*** In 2000 the EU commission set out their approach to the precautionary principle, which included the recommendation that use of the principle should be: 'based on the fullest possible scientific evaluation (including determining the degree of scientific uncertainty at each stage); be preceded by a risk evaluation and an evaluation of the potential consequences of inaction; involve the greatest possible transparency; and take into account principles of risk management'. GOV is happy with this current explanation and does not think it needs further clarification.

***Recommendation:*** GOV should work with the National Academies to provide a new online 'hub' of information about emerging topics in science

and technology, including issues surrounding climate change and the use of advanced genetic technologies. In addition GOV should initiate a more substantive dialogue on the future of the UK food system.

***Response:*** GOV already works closely with relevant organisations and does not believe there would be any added value in a new 'hub', especially considering the additional resources that this would require at a time when expenditure is under tight control. Additionally, in light of the recent science budget review, GOV cannot guarantee continued funding for the ScienceWise program. With regard the future of the UK food system, GOV highlights a number of initiatives that already address the issues of 'Food and Farming Strategy', 'Global Food Security' and 'Food Standards'. They feel that these are currently sufficient to inform the public dialogue on this topic.



It is gratifying that the UK government agrees that it should promote science-based decision-making on issues surrounding GM crops and that they agree to promote the evidence that states these crops pose no more safety risk compared to comparable non-GM crops. However GOV will not move to describe the adoption of novel crops as being generated through 'novel breeding techniques' as they feel removing the term 'GM' might arise suspicion.

With regard most other aspects of their response, GOV is reluctant to commit further funding toward the public understanding of these technologies and this likely reflects an uncertain funding environment. In the case of future regulations, GOV will follow the lead of the EU since it feels that the latter is making some progress in allowing the cultivation of GM crops in a member-state specific manner. It will take a wait-and-see approach as to how the applications for the eight-types of GM crop that are currently awaiting EU approval are judged.

In the short term it appears that GM-policy will have an 'as-you-were' feel to it but given the positive movement of the EU (from the scientists point of view) in this area this is perhaps not a bad thing. The major issue remains separating the public perception of this technology from that surrounding their safety concerns and the influence of big businesses. Hopefully as individual scientists we can all do our part to inform the public so as to spread a positive message about the future use of this technology.

GARNish
Araport: The Arabidopsis Information Resource
21

# Araport: A platform for data sharing, discovery and integration in the 21st century developed for (and by) the community.

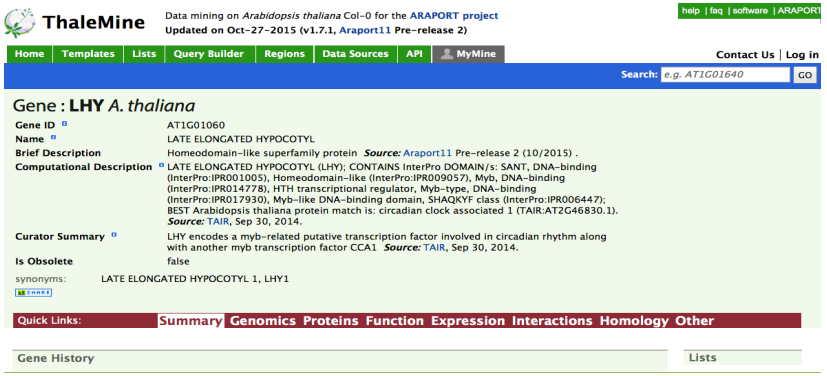
Agnes Chan and Chris Town,

Araport, JCVI.

Araport is an initiative funded by the National Science Foundation and the Biotechnology and Biological Sciences Research Council. It was established after a series of community workshops to give Arabidopsis and other plant scientists direct access to a new generation web-based data platform. Users can browse and analyse a wide array of data already available through Araport, and publish their own data modules for community sharing and building analysis workflows. The Araport data platform consists of three major components: ThaleMine, JBrowse, and Science Apps [1]. In addition, Araport has also taken over the responsibility for updating and revising genome annotation and the reference genome sequence. A series of tutorials is available to help users analyse and access Araport data.

**Araport11.** In our first set of updates, comprehensive updates to both structural and functional annotation of the *Col-0* Arabidopsis ecotype have recently been completed and submitted to NCBI for final review. An official release is expected in early 2016. Araport11 contains updates to gene structures and isoforms derived from over 100 publicly available RNA-seq datasets along with annotation contributions from NCBI, UniProt, and individual research groups. The latest Araport11 data release is available through several Araport components: ThaleMine, JBrowse, Science Apps, and FTP download. The reference genome sequence will be revised in 2016 using a combination of existing long and short read data generated from the PacBio and Illumina platforms. Araport11 represents a significant improvement on the previous TAIR10 annotation and an important new resource for all Arabidopsis researchers. Details of Araport11 annotation effort can be found at https://www.araport.org/data/araport11.

**ThaleMine** is based on the popular model organism data warehouse InterMine [2]. It currently houses a wide array of Arabidopsis genomic information including coexpression, orthologs, interactions, pathways, publications, alleles, germplasm and phenotypes. The data are collected from major data sources such as NCBI, UniProt, BAR, Phytozome, BioGrid, IntAct, KEGG, and many others. Users can browse Gene Reports, run Gene List enrichment analysis, run predefined data queries (Templates), export data tables, and save/share gene lists and data queries. In addition, on-the-fly programmatic access is available through built-in ThaleMine web services. Tissue-based gene expression derived from public RNA-seq datasets will be integrated into ThaleMine in the near future. See details of ThaleMine at https://apps.araport.org/thalemine/begin.do.

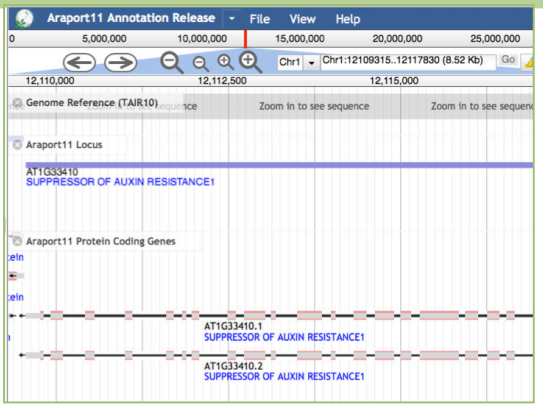



**The ThaleMine Interface when searched with the LHY gene**

**JBrowse** is a next generation fast response genome browser [3]. It currently hosts a collection of over 100 data tracks that includes a number of data sources accessed in real time. This both fulfils our commitment to a data federation model and also ensures data currency. Examples of data tracks include the latest Araport11 gene structure updates and over 100 RNA-seq datasets used in the Araport genome reannotation effort, TDNA-seq (Ecker lab), 1001 genomes variants (1001 Genomes Project), epigenetic marks (EPIC-CoGe), chromatin states [4] and whole-genome alignments (Phytozome). In addition to the large collection of data tracks from which to choose, users can also upload and view their own sequence alignments (e.g. BAM files) or genomic features (e.g. GFF files) for side-by-side comparisons. In the near future, users will also be able to directly publish their own data tracks for sharing with the community, or reuse the Araport JBrowse tracks in other JBrowse instances. See details of Araport JBrowse at https://apps.araport.org/jbrowse/?data=arabidopsis.

**Science Apps.** A growing collection of modules (providing data or analysis capabilities) will serve as building blocks for creating discovery workflows. The modules will be built and shared by the research community for interoperability and reuse. Users can review the currently available set of Science Apps, and provide comments and feedback on what modules they would like to see or contribute. A Developers' Workshop is planned for Spring 2016 for users interested in Science Apps development. See details of Araport Science Apps at https://www.araport.org/apps/catalog.

**Tutorials.** A series of Araport tutorials is available to help users access and analyse data in ThaleMine and JBrowse. For example, there are ThaleMine tutorials for running gene list enrichment analysis (e.g. GO enrichments), and comparing two gene lists (e.g. intersection). There are also JBrowse tutorials for uploading data files located on a user's own computer or remote locations (e.g. URLs shared by collaborators) for side-by-side track viewing, and for finding Arabidopsis mutant germplasms through T-DNA and TDNA-seq tracks. The tutorials can be found at: https://www.araport.org/tutorials.




**The JBrowse Interface when searched with the SAR1 gene**

Araport is a multi-institutional initiative started in 2013. Participating institutes include J. Craig Venter Institute (PIs: Chris Town [lead], Jason Miller, Agnes Chan), Texas Advanced Computing Center (PI: Matt Vaughn), and the University of Cambridge (PI: Gos Micklem). For questions and comments, please contact the Araport team at araport@jcvi.org.

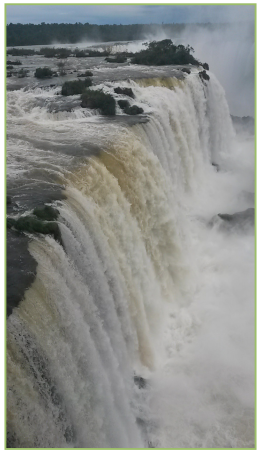
1. Krishnakumar, V., et al., Araport: the Arabidopsis information portal. Nucleic Acids Res, 2015. 43(Database issue): p. D1003-9.
2. Kalderimis, A., et al., InterMine: extensive web services for modern biology. Nucleic Acids Res, 2014. 42(Web Server issue): p. W468-72.
3. Skinner, M.E., et al., JBrowse: a next-generation genome browser. Genome Res, 2009. 19(9): p. 1630-8.
4. Sequeira-Mendes, J., et al., The Functional Topography of the Arabidopsis Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States. Plant Cell, 2014. 26(6): p. 2351-2366.

## Report from GPC/SEB Stress Resilience Symposium and Discussion Forum

Lisa Martin
GPC Outreach Manager
lisa@globalplantcouncil.org

It's a strange thing to be packing for 38ºC weather while the temperature at home in England steadily plummets towards 0ºC. Nevertheless, leaving a cold and rainy London behind, Team GPC took to the skies on 21st October and touched down in tropical Foz do Iguaçu, a resort town on the Brazil/Argentina/Paraguay border.

Iguaçu is best known for its spectacular UNESCO World Heritage waterfalls, but we – that is myself, Executive Director Ruth Bastow, and our two New Media Fellows Amelia Frizell-Armitage and Sarah Jose – were in town for three different reasons. As well as attending the International Plant Molecular Biology conference, followed by the GPC's Annual General Meeting, we were also running a Stress Resilience Symposium in collaboration with the Society for Experimental Biology (SEB) on 23rd and 24th October.



**It's a tough conference location for Team GPC! *Photo: Lisa Martin***

We've all heard the stats before: by the year 2050, the world's population is predicted to reach more than 9 billion. To be able to feed all these extra people, we need to increase crop production by around 60%, all the while our existing crops and cropping systems are threatened by climate change and dwindling natural resources. Urgent action must be taken to achieve global food security and to provide the world's hungry and malnourished with enough – and sufficiently – nutritious food to eat.

Recognising that plant scientists have an enormous role to play in helping to meet this challenge, the intention of the GPC/SEB Stress Resilience Symposium was to bring together experts from around the world to discuss current research efforts in developing stress resilience, showcase new approaches and technologies and build new networks and collaborations to help contribute to global efforts to develop crops and cropping systems that are better able to deal with fluctuating and stressful environmental conditions

**Day 1 – the Symposium**
The first day of the Stress Resilience meeting was given to knowledge exchange.

*Food Security Challenges*
After a welcome from the new GPC President Professor Bill Davies (Lancaster University, UK), the first session of the day focused on how scientists are helping to overcome existing and emerging barriers to food security. Matthew Reynolds gave an overview of the crops and climate change research at CIMMYT in Mexico, and was followed by CGIAR's Jean-Marcel Ribault, who described the collaborative approach to developing food crops, with stress resilience in mind, being taken by partners involved in the Generation Challenge Program (GCP, not to be confused with GPC!). The aim of this programme, he said, is to improve the germplasm in farmers' fields, focusing on six staple crops, the integration of data management, and building capacity for the future.
We also heard from Lancaster's Martin Parry, who described his group's work to translate findings in Arabidopsis to capture more carbon and improve water and nutrient use efficiency of crops; Bob Sharp from the University of Missouri (USA) spoke about trying to understand root responses to drought; Matthew Gilliham from the University of Adelaide (Australia) focused on improving crops' salinity tolerance; and finally Warwick's Sarah Harvey, who studies the effects of oomycete pathogens on plants, changed tack by exploring how the biotic stress posed by pathogens might change as the climate changes.



*Improving stress tolerance in variable environments*
Chaired by Vicky Buchanan-Wollaston, who is both the SEB Plant Section Chair and now the newly elected GPC Treasurer, the session after lunch took a closer look at some specific stress-related challenges. Drought tolerance was a popular topic, with Andrew Borrell of the University of Queensland (Australia) speaking about his work to elucidate the molecular and physiological basis for the Stay Green trait, which gives greater sorghum yields under drought conditions; Vincent Vadez from ICRISAT describing how investigating the way in which plants use water under drought-free conditions can help understand their responses under drought stress; and INRA's François Tardieu discussing the high variability in "drought tolerant" alleles, and the differing effects those alleles can elicit in different plants under different environmental conditions.
Scott Chapman also provided some insights into the modelling work going on at Australia's CSIRO, which is helping crop breeders to decide which traits to focus on to adapt to different sources of stress, and Lyza Maron from Cornell University (USA) spoke about her work to understand aluminium toxicity and tolerance in rice.

*Innovating for Stress Resilience*
In the next session, we heard about some exciting projects being carried out across the globe that are advancing our understanding of stress resilience in plants. Chile's Ariel Orellana gave a fascinating talk, illustrated with some beautiful photographs, of how mining the genome of a desert flower could provide valuable insights into stress tolerance. *Cystanthe longiscapa* lives in the barren, extremely dry Atacama desert – its seeds can lie dormant for many years, yet germinate rapidly and explode into a short-lived riot of deep pink flowers on the very rare occasion that rain should fall.

*Cystanthe longiscapa* bursting into flower *Photo: Juan Benavente Baghetti Flickr*

Speaking about the part her lab played in the PRESTA project, Warwick's (and GARNet's!) Katherine Denby showed us some of the complex, intricate transcriptional network models used to predict, test and reveal interactions between genes involved in Arabidopsis' defence against *Botrytis cinerea*, while China's Xinguang Zhu explained that when it comes to photosynthesis, it's not all about the leaf. His research has shown that simply increasing the photosynthetic rate of the leaf can in fact have negative consequences for canopy photosynthesis – his 3D internal leaf models simulating cell structures, water and metabolite movement were quite stunning.
Finally in this session, Elizabete Carmo Silva from Lancaster University talked about high-throughput phenotyping in the field, and potato root architecture was the theme of the presentation made by Awais Khan from the International Potato Center in Peru.

*Last but not least…*
At the end of a fascinating day of great science, we heard some short talks from up and coming

researchers whose posters had been selected for an oral presentation: make sure to look up the awesome work of rising stars Elizabeth Neilson from the University of Copenhagen, Nicolas Franck from Universidad de Chile, Cristina Barrero-Sicilia from Rothamsted, and Amelia Frizell-Armitage from the John Innes Centre!

**Day 2 – the discussion forum**

But the Stress Resilience Symposium didn't end there… The next day a smaller group of invited experts returned to the meeting venue for some in depth discussion and debate. The aim of the day was to prepare the ground for a forthcoming GPC report, which will highlight the specific challenges facing plant science in terms of developing stress resilient crops and cropping systems, and outline some potential solutions that the plant science community – and those beyond it – can initiate to meet these challenges.

The day began with a series of short presentations about exemplar large-scale projects in the area of stress resilience, including GPC President Bill Davies, who talked about his collaborative work in China to improve agricultural water use efficiency, and in India, where the simple 'alternative wetting and drying' technique is building a more sustainable agricultural system; Jianbo Shen from the Chinese Agricultural University, who spoke on the subject of improving the sustainability of nutrient use in Chinese agriculture; and Roberto Tuberosa from the University of Bologna on "the great project with a terrible acronym", IDuWUE: Improving Durum Wheat for Water Use Efficiency.

Inspired by hearing about these successful international projects, attendees then split off into breakout groups to discuss what they felt to be the key challenges facing stress resilience research in the world today, and the areas in which plant scientists around the world need to come together to mitigate these challenges.

Unsurprisingly, this session was lively and animated, with several differences of opinion, but each thought was a valuable and useful contribution to the assessment of the global landscape. Participants talked about the current regulatory climate, particularly surrounding GM and gene edited crops; the need for silos of knowledge to be linked and shared, and for effective technology transfer to make sure that the science we do in the lab has impact in the field – and in the fields where that science is most needed.

After a long but fruitful two days of great science, effective knowledge and ideas sharing, the Stress Resilience forum ended with a team photo and further opportunities for "networking" by the hotel pool (or for the Australian participants among us, the Argentina vs. Australia Rugby World Cup Semi Final!). The GPC is now compiling an official report, based on the discussions at the meeting, which we hope will provide a powerful and realistic call to action for stress resilience scientists across the globe to come together. Watch this space!

Thanks to Oliver Kingham and Paul Hutchinson from the SEB, Professors Vicky Buchanan-Wollaston and Jim Beynon from the University of Warwick, Professor Bill Davies from Lancaster University and Andrew Borrell from the University of Queensland for their help in making this symposium possible.



## The Microphenotron: a new phenotyping platform for chemical genetic screens

Professor Brian Forde
Lancaster University

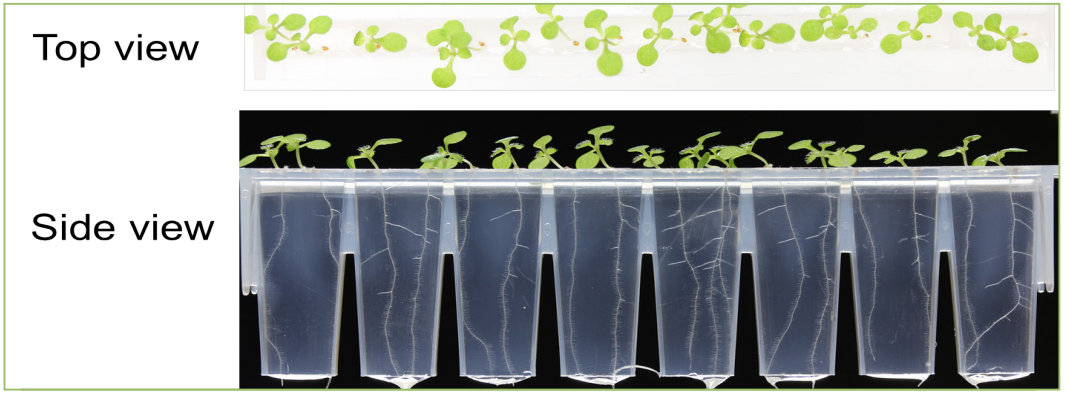
By using small molecules rather than genetic mutations to disrupt protein function, chemical genetics offers a number of advantages over conventional genetics for investigating biological processes and for gene discovery. Chemical genetics has had some notable successes in plants but has not been as widely adopted by plant scientists as by researchers in other fields. A crucial reason for this has been the difficulty of combining detailed phenotypic analysis of whole seedlings in a high-throughput format with the experimental constraints imposed by the need to treat the seedlings with thousands of different chemicals.

To address this issue, a new robotic facility has been developed with BBSRC funding at Lancaster University. The 'Microphenotron' is the result of a multidisciplinary collaboration between biologists and engineers at Lancaster and computer scientists at the University of Nottingham. The facility makes it possible for the first time to perform a detailed phenotypic analysis of both root and shoot development in a format suitable for chemical genetic screens.

At the heart of the Microphenotron is the 'Phytostrip', a custom-made strip of eight flat-sided growth tubes that are filled with nutrient agar, allowing the developing root system to be readily imaged (see figure) while chemical treatments are applied by diffusion from below. The technology is based on the same principle that was successfully used in a manual screen for antagonists of glutamate's effect on root architecture [1]. The robotic version is capable of handling up to 27 microtitre plates at a time and of automatically capturing images from >2000 individual assays each day to allow the time course of seedling development to be tracked. (A YouTube video shows the Microphenotron in action [2]). Image analysis software that will automatically quantify multiple aspects of root and shoot development is being developed by Andy French and Mike Pound at Nottingham University.

In its current form the technology will be best suited to chemical genetic screens designed around the ability of small molecules to modify one or more developmental traits (or leaf colour), but in future this can be expanded to include traits that require imaging at non-visible wavelengths. Anyone with a potential interest in using the Microphenotron for their research, either on a collaborative basis or as a service, is encouraged to contact Brian Forde (b.g.forde@lancaster.ac.uk; tel. 01524 593496).

1- Forde BG, Cutler S, Zaman N, & Krysan PJ (2013) Plant J. 75:1-10.
2- The Microphenotron. https://www.youtube.com/watch?v=-mnsfi2u2kY



Spotlight on:

Queen Mary University London

Kindly complied by Richard Buggs

Queen Mary
University of London

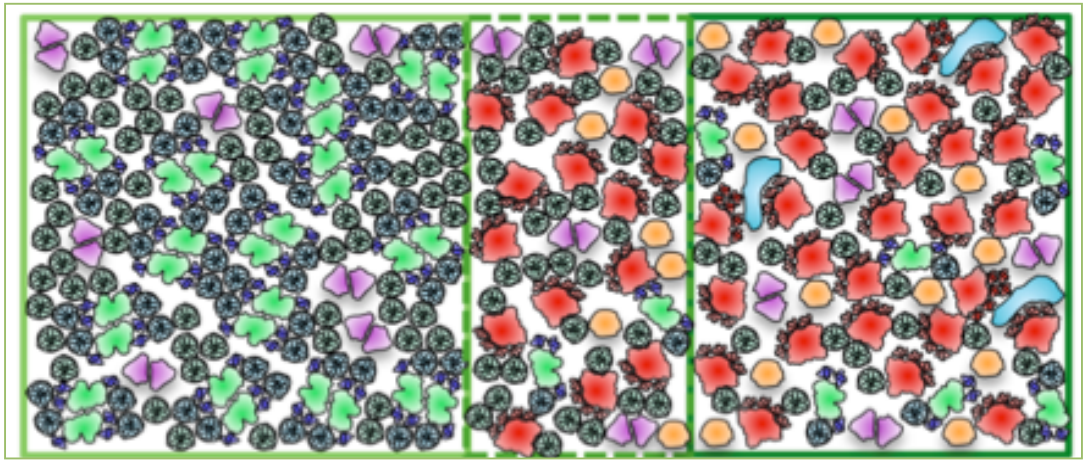
Alexander Ruban
a.ruban@qmul.ac.uk

http://webspace.qmul.ac.uk/aruban

**Alexander Ruban**

Our lab is engaged in mechanistic photosynthesis research. Our multidisciplinary approach applies molecular spectroscopy, biophysics, biochemistry and molecular biology to important problems in plant physiology. Specifically, the role of the various components (proteins, lipids and pigments) and macrostructure in the functions and adaptive mechanisms of the photosynthetic membrane related to light harvesting and photoprotection in plants and algae. In addition we are interested in the universal properties of carotenoids in biological membranes, the molecular dynamics of these molecules in the modulation of membrane protein conformation and their functions (summarised in the recent book: Ruban, A.V. (2012) The Photosynthetic Membrane: Molecular Mechanisms and Biophysics of Light Harvesting. Wiley-Blackwell).

Our research has contributed to the fundamental understanding of the molecular design of the photosynthetic light harvesting machinery and we have confirmed the key role of LHCII antenna aggregation in the major photoprotective process in the photosynthetic membrane, NPQ and introduced the concepts of light adaptation 'memory' via the allosteric action of the xanthophyll cycle, robust genetic design of the light harvesting antenna. We discovered the photoprotective molecular switch in the Photosystem II antenna that shortens the chlorophyll excited state lifetime, protecting the thylakoid membrane from photo-oxidative damage and that dynamics of antenna proteins is tuned by the polarity and structure of bound xanthophyll co-factors.



**Alexandre Ruban: Light harvesting proteins of the photosynthetic membrane**



Recently we established that the main photoprotective process in plants, NPQ, has an economic nature and developed a novel methodology for assessment of the photoprotective effectiveness of NPQ.

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**Chris Duffy**

Our focus deals with understanding the first moments of photosynthesis, the capture of energy by pigments in the antenna complex and its transfer to the reaction centres. This process is fast (occurring on a femto- to pico-second timescale) and governed by the laws of quantum mechanics. With such processes being difficult to understand from a purely experimental perspective I use my background in theoretical physics to address the question of what makes this process so efficient and, more importantly, so flexible an adaptive in a light environment that fluctuates intensely and rapidly.

My main area of interest concerns the second class of photosynthetic pigments, the carotenoids. Their roles in photosynthesis are varied. Their rigid, hydrophobic structure means they define the structure and stability of light-harvesting pigment complexes, they harvest light of wavelengths not covered by chlorophylls, they provide anti-oxidant protection, and they are involved in the photoprotective dissipation of the harmful excess energy that accumulates in the antenna following sudden bursts of high light. From a purely physical point of view these pigments are equally fascinating, being a natural example of a 'strongly correlated' system, possessing a complex electronic structure and unusual optical properties such a highly dissipative, 'dark' state intimately linked to their photoprotective function.

Theoretical modelling of photosynthetic structures has been invaluable to understanding these processes. However, their strongly correlated nature previously rendered it impossible to include carotenoids in such models. My theoretical research has rectified this, yielding the first 'all-pigment' model of plant light-harvesting complexes, allowing for the first microscopic, structure-based model of the mechanisms of excess energy dissipation in the photosynthetic antenna of plants.

This approach related the fundamental properties of these pigments to the newly-discovered aspect of the photo-protective regulation of light-harvesting, its slow or 'economic' nature, offering gentle protection to the organism without disrupting normal photosynthetic function. These mathematical tools are allowing my collaborators (both experimental and theoretical) and I to develop a general understanding of carotenoid photosynthetic function, answering questions such as: What makes the same pigment act as a light-harvester in one protein but a photoprotective dissipater in another? What factors ultimately control the incredible efficiency and adaptability of these photosynthetic systems? Can these physical principles be applied to artificial, bio-inspired or hybrid solar devices?

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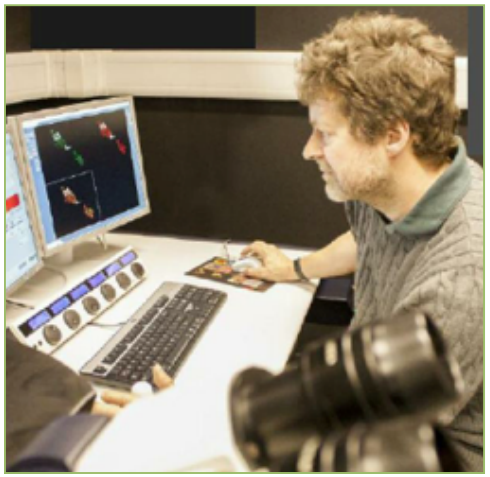
We are interested in all aspects of the cell biology of cyanobacteria. A long-standing interest is in the



**Conrad Mullineaux**

thylakoid membrane, its organisation, biogenesis and dynamics, and how these aspects relate to photosynthetic function, especially the regulation of light-harvesting and electron transport. We want to know how and where the components of the thylakoid membrane are assembled, how the different membrane components are distributed and how the membrane works as a dynamic system. Through collaborations we have extended our work from cyanobacteria to their close relatives the chloroplasts, and we also look at related problems in non-photosynthetic bacteria.

Wider interests in cyanobacterial cell biology include cell-cell communication in filamentous cyanobacteria, where we have helped to identify and characterise structures that allow small molecules to diffuse across the cell junctions.

These structures are key to the multicellular lifestyle of these complex prokaryotes. A current interest is in motility and phototaxis in the unicellular cyanobacterium *Synechocystis*, where we recently found that the cell is able to perceive light direction because it acts as a tiny spherical lens.

A key technique for all our areas of investigation is fluorescence microscopy, often combined with fluorescent protein tagging to allow us to identify the sub-cellular location and dynamic behaviour of specific cell components. We complement the fluorescence microscopy with spectroscopy and various forms of electron microscopy to give higher-resolution views of the cell.

Guy Hanke
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**Guy Hanke**

We would be dead without photosynthesis. We depend on its products in crop plants to supply our food, and in fossil plants to support most of our energy needs. When harvesting light energy, plants exquisitely regulate how this energy is distributed into different bioassimilatory, biosynthetic and protective pathways. A fundamental part of improving traditional agricultural crops and generating new microbial bioenergy crops will be to optimise energy distribution into these pathways. The aim of our research is to identify the molecular and genetic mechanisms that control energy distribution in crop plants and cyanobacteria, and to manipulate them for the improvement of agronomic traits.

Our research focuses on the interface between energy generation in chloroplasts (at the thylakoid membrane) and its distribution to soluble enzymes, both inside and outside the chloroplast. To do this we focus on electron carrier proteins, including ferredoxins and ferredoxin:NADPH oxidoreductase enzymes. There is a great abundance of genes encoding these proteins (e.g. maize genome encodes at least 10 genes for ferredoxin). Our work has shown that by manipulating the relative amounts of these different isoforms, plants can alter their energy investment into different areas of metabolism.



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We have a focus on the processes and consequences of interspecific hybridisation and polyploidisation in plants, as well as an interest on the origin and ecological consequence of plant genome sizes.
Our five overlapping themes of research are:

**Polyploidy**

I have over many years studied polyploidy in a range of species and genera, especially in Nicotiana, Triticum, Rubus, Agave, Spartina, Tragopogon and others. We have three central questions: [1] What are the genetic consequences of polyploidy for genes and genome structures? [2] Why are polyploids so successful in angiosperms? [3] What are the costs of polyploidy in ecology?

**Ecological Genomics**

The focus of this research is to study the fundamental role that genome size and polyploidy plays as a sink for both Nitrogen (N) and Phosphorous (P), and in influencing photosynthesis efficiency, both influencing plant competitiveness. We also study how genome size and polyploidy have cascading effects at multiple levels of biodiversity, from the genome to the ecosystem. Of particular importance to this study is how the huge 2,400-fold range in angiosperm genome sizes influences ecology and shapes the distribution and persistence of biodiversity, particularly in environments with limiting N and P. The

**Andrew Leith**

findings from the proposed research will be fundamental, and aims to add new dimensions to our understanding of ecology.

**Epigenetics**

Epigenetic mechanisms involved in constraining repeat amplification and mobility may not be the same across all land plants, in particular they may be different in gymnosperms when compared to angiospems and this might contribute to their more stable genomes over time (Leitch AR, Leitch IJ. 2012. Ecological and genetic factors linked to contrasting genome dynamics in seed plants. New Phytologist 194: 629-646). We have three central questions: [1] How does polyploidy perturb epigenetics processes? [2] Is gymnosperm epigenetics different, and if so in what way and what are the consequences? [3] How does RdDM impact genome evolution, in particular the evolution of giant genomes?

**Giant Genomes**

Large-scale comparative analyses of plant genome sizes have shown that plants with large genomes are at greater risk of extinction, are less adaptable

to living in polluted soils, and are less able to tolerate extreme environmental conditions, clearly demonstrating that GS has ecological consequences which shape the distribution and persistence of biodiversity. Genome size in angiosperms (flowering plants) varies by an astonishing 2,400-fold range, the largest range for any comparable group (e.g. mammals and birds vary only 5- and 2-fold respectively). We aim to understand the underlying processes that give rise to plants with giant genomes asking: [1] Which sequences make up these giants? [2] Why do plant genomes become so huge? [3] Why are many giant genomes are found in gymnosperms. [4] Why do many species with giant genomes are rare and endangered.

**Telomeres**

We are interested in the evolution of plant telomere motifs. In particular we showed that in the divergence of the plant order Asparagales, the telomere motif (TTTAGGG)n, which is thought typical of plants was replaced with a (TTAGGG)n motif, more usually associated with vertebrates. We also showed that with the divergence of Allium (onion), this new TTAGGG-type motif was itself replaced by another, as yet unknown telomere motif. We also found that in the plant family Solanaceae, a group of closely related genera, Cestrum, Sessia and Vestia, also lost the TTTAGGG-type telomere motif, and the sequence that replaced it is also unknown. In collaboration with Dr Jiri Fajkus, we are studying the evolution of plant telomeres.

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I am interested in the mechanisms of evolution. How do new species originate? How are they maintained? What causes them to go extinct?

My lab works on genomic aspects of the evolution and conservation of plants, especially trees. We have active research programmes in three areas:

**(1) Phylogenomics of the ash tree genus Fraxinus**

Ash trees in Britain, Europe and North America are


**Richard Buggs discussing Ash Dieback Disease.**



threatened by ash dieback and the emerald ash borer. We are using phylogenomic approaches to find genetic variants in Ash species that reduce their susceptibility to these two health problems. We have sequenced the genome of a British Ash tree (*Fraxinus excelsior*) with funding from NERC (see www.ashgenome.org). Postdoc Laura Kelly is now sequencing the genomes of 35 other Ash species from around the world, funded by the BBSRC, Defra, NERC, ESRC, Scottish Government and Forestry Commission. We are screening different Ash species for susceptibility to ash dieback and the emerald ash borer, in collaboration with Forest Research (Roslin) and the United States Forest Service (Ohio). We will seek gene trees that have a topology matching the pattern of susceptibility of the species to each health problem.

**(2) Birch trees on Scottish mountains.**

Dwarf Birch is rare and found mainly above the tree line, whereas Downy Birch is widespread below the tree line. The two species hybridise a great deal. We are using new DNA sequencing methods to work out how the two species maintain their identity in the face of hybridisation, and the extent to which hybridisation impedes the conservation of dwarf birch. We are especially interested in how global warming affects the dynamics of this system. This work is funded by a Fellowship from the Natural Environment Research Council. We have recently sequenced the whole genome of *Betula nana* (www.birchgenome.org).

**(3) Hybridisation of Tragopogon species (Daisy family) in south-east England.**

We are studying diploid hybridisation between *Tragopogon pratensis* and *T.porrifolius*, which results in *T. x mirabilis*. We have found abundant hybrids in natural mixed populations in London and have preliminary evidence that they are reproducing. This work is funded by a pump-priming SYNTAX grant in collaboration with Andrew and Ilia Leitch.

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**Emily Lines**

My research is focussed on large-scale questions about terrestrial vegetation, such as how climate controls vegetation dynamics; answering such questions requires combining large datasets with biological theory on plant functioning.

A major area of research has been exploiting large forest inventory datasets to answer broad questions on the role of climate and competition on forest processes in Europe, North America and New Zealand. This has involved empirical studies, testing metabolic scaling theory with large-scale data and developing models of forest functioning. A lack of sufficient ground data in many forested areas to address these questions has led me to a second area of research: the use of Earth Observation data to understand forest functioning. Ground and remote sensing data can be integrated using data assimilation approaches coupled to radiative transfer models to retrieve information on ecosystem structure and function.

This research develops methods to integrate remote sensing data into land surface models, to understand the impact of canopy structural heterogeneity on the remote sensing signal and to use statistical emulators of radiative transfer models to improve assimilation.

Spotlight on:
University of Cranfield,
Kindly complied by Andrew Thompson

Cranfield UNIVERSITY

Food quality, safety and security are major worldwide challenges drawing increasing attention from both policy makers and businesses. At Cranfield we are well known for our closeness to industry, offering relevant, practical and transformational research, with over 80% of our business coming from sources other than Government. Agrifood is one of the University's eight key strategic themes and it is the most rapidly expanding: we expect to increase our capacities in the coming years through our substantive involvement in two of the forthcoming government-funded AgriTech Centres of Innovation viz. Agri-EPI Centre (for precision AgEng research) and the Centre for Crop Health And Protection (CHAP), where Cranfield will deliver the soil health component. These new ventures and internal funding amount to a ca. £12 million capital investment in the next two years. In addition, we will recruit ten new academics in 2016 in the areas of plant science, postharvest technology, soil science, bioinformatics and agricultural engineering and will be developing our research portfolio in basic plant and soil sciences to underpin our applied work.


The Vincent Building, home of AgriFood Research

We are an exclusively postgraduate university, with over 50 PhD students in the Agrifood Theme alone – this will double by 2018-2019, primarily through internal funding. In addition, we are a member of two Doctoral Training Centres: Soil Training And Research Studentships (STARS) and Data, Risk and Environmental Analytical Methods (DREAM). Our Agrifood MSc courses explore the integrated nature of our food supply chains and the ongoing need to increase their economic and ecological sustainability, drawing on the latest technologies and informatics tools. We also provide short courses for professionals working in the Agrifood sector.

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Leon Terry

## Postharvest dormancy, storage and shelf-life

I was appointed as the Director of Agrifood in 2014. The role focuses on leading Cranfield's activities in agriculture, food research and teaching across the University. In addition, I have established Cranfield University as one of the largest and best equipped groups dedicated to research, consultancy and education in postharvest science in the EU. My scholarship is centred on understanding the physiological, biochemical and molecular mechanisms which govern dormancy, ripening and senescence of fruits, tubers, bulbs, roots and vegetables. I am funded by the EU, overseas governments, the UK Government and its agencies (Defra, BBSRC, EPSRC, DFID, Innovate UK and AHDB), and we have continued to secure substantial repeat-funding from industry (Unilever, PepsiCo, Johnson Matthey). I am an appointed member of the BBSRC Agriculture and Food Security Strategy Advisory Panel (AFS SAP) 2015-2018.

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## Plant molecular genetics: from phytohormones to rootstocks

Our research interests in abscisic acid biosynthesis have led to various projects in water use efficiency (WUE), root development, root-to-shoot signalling and studies of dormancy in storage organs and seeds. My research seeks to understand and exploit genetic variation in WUE in horticultural crops such as tomato and the vegetable brassicas using transgenic, QTL and allele mining approaches. We have developed a range of 'high ABA' germplasm that has shown increased water uptake and water use efficiency and the ability to confer salinity tolerance when used as rootstocks. The majority of fresh market tomato and melon crops are grown on rootstocks, and we are developing an understanding of genetic loci that control rootstock vigour and hormonal signalling for use in rootstock breeding. Secondary dormancy and low seed vigour can lead to poor crop establishment in drilled crops; to address this our group have collaborated with chemists to develop novel hormone biosynthesis inhibitors that break dormancy and have potential uses as seed treatments. This chemical genetic approach has also led to the discovery of new signalling pathways in root branching.


Andrew Thompson: we aim to understand the genetic basis of drought resistance and water use efficiency in *Solanum chilense*, a wild relative of tomato.

Guy Kirk
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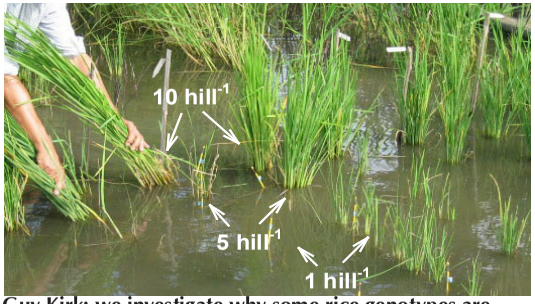
## Soil systems and processes

My research focuses on physical, chemical and biological processes in soils; how to quantify soil properties and functions; and how to model soil systems at scales from the microbial to the continental. Our current interests are in the biogeochemistry of submerged soils, trace element and metal uptake by rice plants, radionuclides uptake by plants, and plant-soil-microbe interactions controlling soil carbon balances. I collaborate widely and internationally with plant breeders and physiologists, geochemists, and mathematical modellers. My research has been continuously funded by BBSRC and NERC since starting at Cranfield in 2003. I am a Fellow of the Royal Society of Chemistry.



Guy Kirk: we investigate why some rice genotypes are much more efficient in absorbing soil zinc

Jerry Knox
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## Irrigation science and agricultural water resources management

My research interests are in the science, engineering and management of water resources for irrigated agriculture and horticulture, including understanding the relationships between resource availability, crop productivity (yield and quality)

**Jerry Knox**

and the environment, and the sustainability of production in response to abiotic stress and longer term climate variability. I am currently working on biophysical modelling, demand forecasting, precision irrigation engineering and climate impacts and adaptation in agriculture. My research is funded by UK and international public and private sector agencies including NERC, the Belmont Forum, AHDB, UN FAO and the EC.

## Paul Burgess
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### Tree and crop ecology

Our research focus is on the biological and economic modelling of crop responses in the field. My PhD was on the responses of tea cultivars to drought and temperature change in East Africa and this continues to be an area of interest. I am currently the co-ordinator of the EU-sponsored "AGFORWARD" project (www.agforward.eu) that is working with 40 farmer-stakeholder groups across 15 countries in Europe to improve the profitability and viability of agroforestry systems (farming with trees). The project includes the field-selection of durum wheat varieties adapted to shade (by INRA, France), and the development of agroforestry-adapted arable crops by the Organic Research Centre at Wakelyns Agroforestry in Suffolk. Other research in the project addresses the modelling of crop and tree yields (and their interactions) using bio-economic models, and the responses of winter wheat and oilseed rape to different minimum cultivation methods.

**Paul Burgess works on agroforestry systems**

## Fady Mohareb
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**Fady Mohareb**

### NGS informatics, machine learning and pattern recognition

Our research focuses on the development and application of computational methods in order to unravel the complexity of biological systems. This includes the application of machine learning and pattern recognition to predict quality and safety indices in food, and the development of mathematical models to detect adulteration in meat products. I also lead the NGS informatics work at Cranfield: *de novo* genome assembly of strategically important plant species, transcriptomic analysis and genotyping-by-sequencing, and I collaborate closely with colleagues working on genomics, transcriptomics and metabolomics in plant science and mycology. In addition I run the Applied Bioinformatics MSc course whose alumni now populate many molecular biology and bioinformatics labs.

## Naresh Magan
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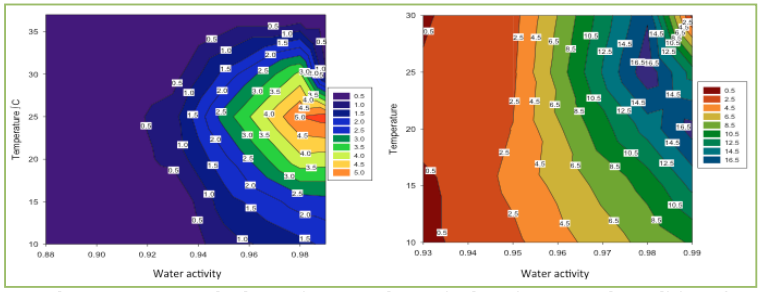
### Applied Mycology for food safety and quality

I have been carrying out research in applied aspects of mycology for over 30 years and I specialise in the application of fungal technology in the food and environment sectors. My current interests include molecular ecology and ecophysiology of spoilage and mycotoxigenic fungi in food production systems, particularly in relation to grain production and storage. I am also working on the impact of climate change factors on fungal diseases and mycotoxigenic fungi, biocontrol of fungal pathogens and pests, and electronic nose technology for early detection of microbes for food/environment/health applications.






**Naresh Magan: We study the optimum and marginal environmental conditions for mycotoxin production and fungal growth in the context of climate change.**

### Soil Sciences at Cranfield

Cranfield has expertise in soil systems, soil and land management, spatial geosciences, and soil spatial information. Rob Simmons recently won a prestigious KTP award for his work on establishing a Soil Information Management System 'Soil-for-Life®' which allows Produce World to map, assess and monitor soils across their business. He is also undertaking multiple projects investigating practical and adoptable soil erosion control options for maize and UK row crops. Jane Rickson's interests include the costs of soil degradation and loss of ecosystem goods and services. Ruben Sakrabani is working on application of organic amendments to soils. The focus of Mark Pawlett's research is on the interface between the plant and soil biological systems, targeting sustainable management practices (agricultural, horticultural, turfgrass, restoration) to improve soil health. Lynda Deeks is a BBSRC/NERC Horticulture and Potato Knowledge Exchange Fellow with research interests in soil structure, the causes and amelioration of soil compaction and the control of diffuse pollution; Jacqueline (Jack) Hannam focuses on understanding how soils change spatially, using digital soil mapping techniques to predict soil type and properties in the landscape.

### Agri-informatics at Cranfield

Cranfield has expertise on the role of computational analytical approaches and data-driven processes and methodologies for addressing key pressing societal challenges across the environmental, agricultural and biological domains. Researchers in this group include Abdul Mouazen who is combining cutting-edge sensor and system control technology with predictive modelling of the soil-plant-water system at field/sub-field scales; he has led numerous projects around precision bio-engineering of farming systems. Toby Waine's expertise is in developing predictive intelligence from crop and soil data from a wide range of data sources including the utilisation of earth observation (EO) and satellite navigation space assets. Stephen Hallett is responsible for Cranfield's National Land Information System (LandIS), containing comprehensive soil and related near-earth environmental information for England and Wales. Cranfield also provides a safe repository for the World Soil Survey Archive and Catalogue (WOSSAC). Ron Corstanje is focused on developing the modelling tools (statistical or quasi-mechanistic) that can assemble, manipulate and communicate meaningful outcomes from large soil datasets; Thomas Mayr is an expert in digital soil mapping who has recently completed the first phase of the Irish Soils Information System.

Spotlight on:

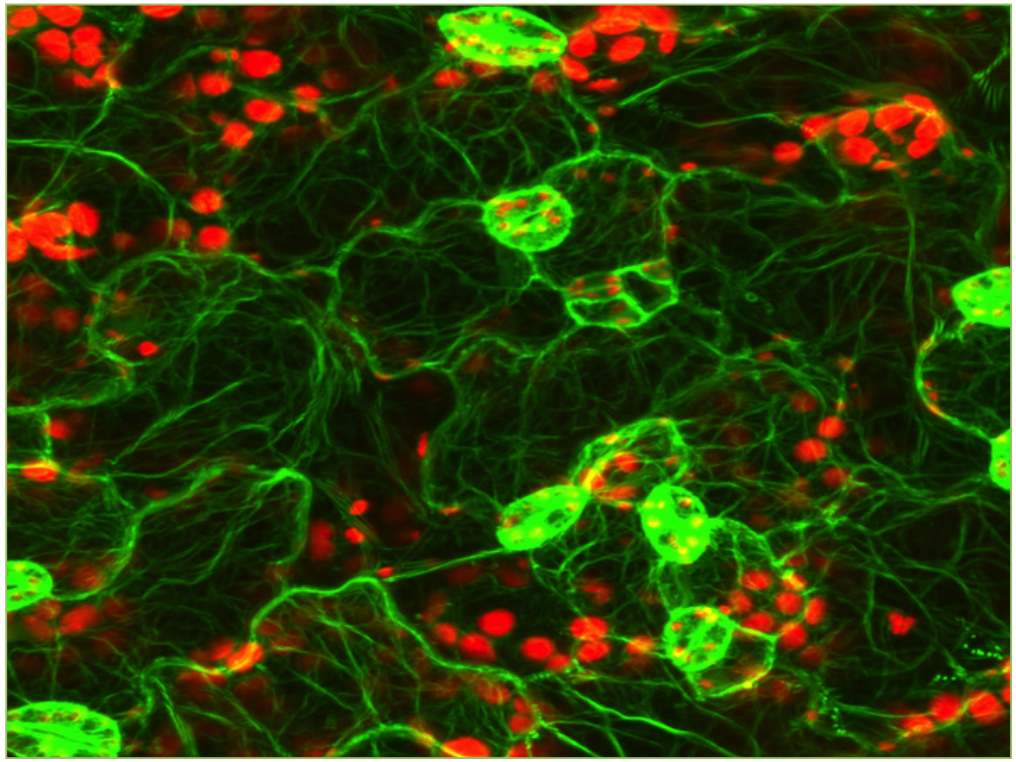
Bioimaging at Oxford Brookes University.

Kindly complied by Joe McKenna

OXFORD BROOKES UNIVERSITY

They say seeing is believing and that is a view we follow at Oxford Brookes. Plant cell biology is one of the key research groups located within the department of Biological and Medical Sciences and was established in 1989. We have a wide range of expertise in electron and light microscopy coupled with world class bioimaging systems.

The department recently invested in a Zeiss 880 confocal microscope equipped with Airyscan, allowing us to perform live cell super resolution imaging. In addition, through BBSRC funding and in collaboration with the university of Oxford we have a Serial Block Face Scanning Electron Microscope (SBF-SEM) system. This allows high resolution 3D reconstructions of cells and tissue, allowing us to probe the inner workings of the plant cell at unprecedented detail. These systems have put us at the cutting edge of light and electron microscopy and are being used for a number of research areas within plant science as detailed below. Recently the prestige of our research groups was highlighted when we were chosen by Zeiss as a lab in location, an honour bestowed on only two departments in the UK.



**Actin cytoskeleton in an *Arabidopsis thaliana* cotyledon. Image taken by Joe McKenna**



In addition to the onsite facilities we also have an STFC funded programme access grant and collaborations which allow access to the Research complex located at Harwell. This allows us to perform STED super resolution imaging, TIRF single molecule tracking, optical tweezers and fluorescence resonance energy transfer (FRET) techniques. Furthermore, with the department securing a major renovation grant, the bioimaging unit will be moving into a purpose built facility in 2016. The plant cell research being undertaken at the university is divided into three main themes. It is an exciting time for cell biology with all the recent innovations in the field and we believe this area can offer unprecedented advantages in advancing plant science in the UK and globally.

http://oxfordbrookesbioimaging.weebly.com/

@OBBU_microscopy

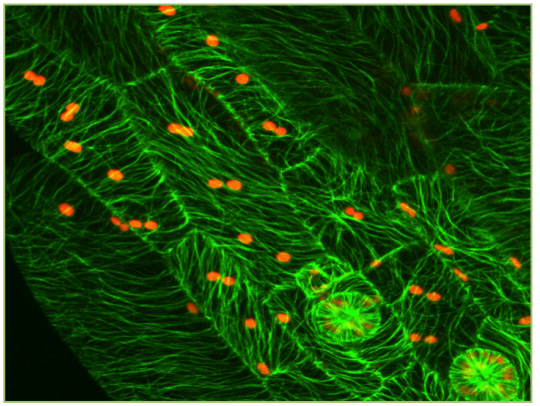
## Nuclear envelope

### David Evans and Katja Graumann

**David Evans**

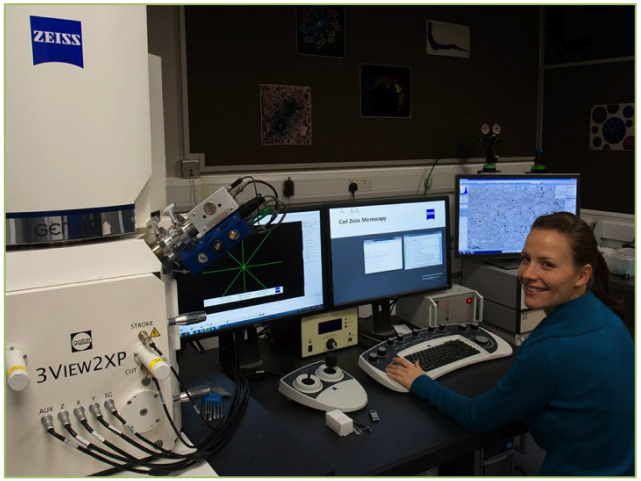
The plant nuclear envelope is a surprisingly poorly understood system and the research of the group is concentrated on identifying native plant nuclear envelope proteins and studying their properties. The nuclear envelope is a dynamic system that undergoes massive changes in the cell cycle and is closely interlinked with the nucleoskeleton and cytoskeleton. Following the discovery and characterisation of the first members of the Sad1/UNC-84 (SUN) domain protein family in various plant species we are working with the Arabidopsis homologues of AtSUN1 and AtSUN2. The SUN domain proteins are inner nuclear membrane localised proteins, which, in non plant systems, form part of the Linker of Nucleoskeleton and Cytoskeleton (LINC) complex.

**Katja Graumann**



**Microtubules in Arabidopsis thaliana Hypocotyl. Image taken by Joe McKenna**

With our collaborators in the USA (Iris Meier, Ohio State) and France (Christophe Tatout, Blaise Pascal), we have identified SUN-domain interactors of the KASH domain family as well as novel nuclear envelope associated proteins. With Sue Armstrong (Birmingham) we have identified a role for the SUN domain proteins in meiosis and we continue to describe novel functions for the plant LINC complex in chromatin structure and gene expression and nuclear movement and architecture. We are coordinators of the International Plant Nuclear Consortium (IPNC) http://bms.brookes.ac.uk/ipnc and organise the SEB Nuclear Dynamics Special Interest Group (http://www.sebiology.org/cell/Nuclear_Dynamics.html). Our next major meeting is Dynamic Organisation of the Nucleus in July 2016 at the SEB meeting in Brighton (http://www.sebiology.org/meetings/Brighton_2016/Cell.html#nucleus).




**Postdoctoral researcher Maike Kittelmann using the SBF-SEM recording volume datasets of Arabidopsis thaliana root tips**

## Plant endomembrane system

**Chris Hawes**

### Chris Hawes

### @HawesChris

The plant secretory pathway is responsible for the synthesis, modification and quality control of most of the building blocks of plant cells. Therefore, it is the basis for most of our food chain. Research in the endomembrane group is split into two main areas:

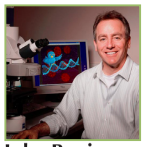
1) The organisation of the endoplasmic reticulum in plant cells:

The cortical endoplasmic reticulum (ER) in plant cells is a highly structured dynamic network of tubules and small cisternae over which, in some tissues such as leaf epidermis, the Golgi bodies move. Our research is focussing on modelling ER structure in plant cells. We are currently investigating the role of two families of ER membrane proteins, the reticulons and RHD3 proteins, in the establishment of the cortical ER during cell plate and plasmodesmata development and the maintenance of the cortical network in interphase cells. For our research we are applying biochemical methods, confocal and 3D electron microscopy as well as FRET-FLIM and optical tweezer technology. We are organising a session on the plant ER at the SEB meeting in Brighton July 2016.

2) Plant Golgi dynamics and biogenesis:

We have previously shown that in many plant cell types the Golgi bodies are dynamic travelling over the ER network as distinct secretory units. Live cell imaging utilising fluorescence recovery after photobleaching technology (FRAP) has demonstrated cargo transport between the ER and Golgi. Several interlinked projects are currently being undertaken on the plant Golgi. The distribution of transferases and other enzymes within the Golgi stack are being investigated by live cell imaging and the differential fate of Golgi membranes and proteins upon Golgi destruction and biogenesis is being established. A number of peripheral Golgi "matrix" proteins have been identified and their role in maintenance of Golgi structure and in Golgi biogenesis is being investigated. Interactions between the Golgi matrix proteins and between matrix proteins and regulatory GTPases (Rabs) are being investigated using live cell imaging, optical tweezers and fluorescence resonance energy transfer (FRET) techniques.

## The Cell Surface Continuum



**John Runions**

### John Runions

### @JohnRunions

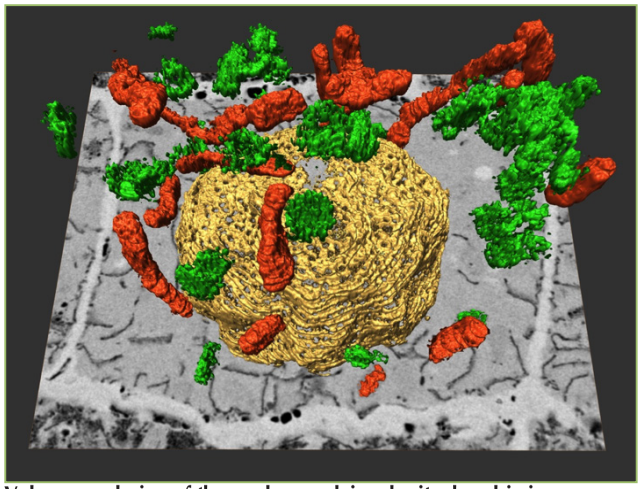
Research in the Runions laboratory focuses on the cell biology at the surface of plant cells. The surface is composed of a continuum which includes the cell wall, plasma-membrane and cytoskeleton. This continuum is extremely important throughout the development and life cycle of a plant as it is the first point of contact between the plant cell and all external stimuli. Furthermore, every molecule entering the cell has to pass through the cell wall and plasma-membrane. Rather a lot is known about how proteins in the plasma-membrane and the actin cytoskeleton regulate the composition and structure of the cell wall, however until recently little was known about how and if the cell wall regulates the plasma-membrane. Previous work in the laboratory has demonstrated that the cell wall regulates the lateral mobility of proteins in the plasma-membrane. Therefore, our currently research focuses are:

1) How is the mobility of proteins affected by the cell wall?

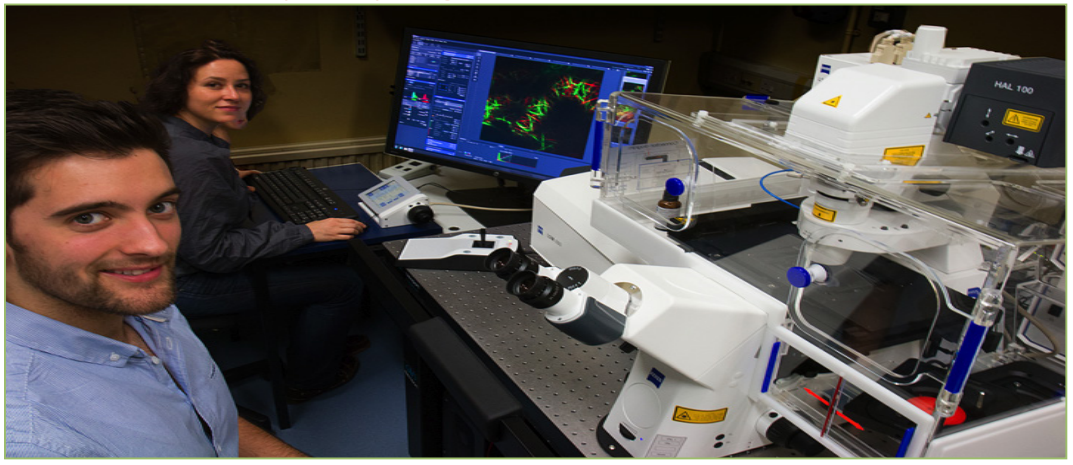
2) Does the cell wall have a role in regulating the cytoskeleton?

3) What is the function of proteins spanning through the plasma-membrane and interacting with the cell wall and cytoskeleton?

We perform the majority of our research in the model plant *Arabidopsis thaliana* and use a range of advanced live cell imaging techniques including confocal microscopy, total internal reflection fluorescence (TIRF) single molecule imaging and a number of super resolution technologies.



**Volume rendering of the nucleus, golgi and mitochondria in an *Arabidopsis thaliana* root cell. Image rendered by M Kittelmann**




**Verena Kriechbaumer and Jake Richardson imaging Arabidopsis thaliana cytoskeleton on the Zeiss LSM880**

# GARNet2016: Innovation in the Plant Sciences

**Sessions include:**

- Fronters in Imaging
- Advances in Synthetic Biology
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- Workshops on 'Araport' and 'Introduction to crispr-cas'
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*Image: George Bassel*

## Cardiff: Sept 6-7th 2016

Information: www.GARNet2016.weebly.com