GARNish
December 2018: Edition 30

Opening up Global Biotech Innovation

Open MTA

Welcome to the December 2018 Issue of GARNish

Steven Spoel

GARNet Chairman

Welcome to the December 2018 issue of GARNish, reporting on the latest news from across the UK plant sciences community. The past six months have seen several exciting events, including organisation of a successful GARNet2018 conference in York. This meeting provided an excellent platform for networking between scientists that utilise fundamental and translational approaches to push the frontiers of our knowledge of plant cell signalling. In this issue you will find a report so you can relive the exciting research that was discussed at GARNet's flagship meeting.

In the past six months the GARNet Advisory Committee has also started preparing for renewal of funding. GARNet's current BBSRC support ends in just over a year's time, so a new request for funding is now in preparation. As GARNet is a network for the community and run by the community, we recently launched a survey to ask for your opinions on what aspects of GARNet you value most and what our next objectives should be. The Advisory Committee was pleased to hear from the community that there is continued support and need for GARNet in a changing political and funding landscape.

In particular the community highlighted that it would like GARNet to continue to be a strong voice for the fundamental UK plant sciences community with inclusion of all relevant model organisms. Training in new cutting-edge technologies through hands-on workshops was another element that the community would like to see more of in future. I would like to thank the plant science community for engaging with us on the current and future needs to remain a global strength in plant science.

GARNet has carefully considered all the responses we received and the Advisory Committee is now incorporating your ideas into our next request for funding.

The end of this year also marks a farewell to Advisory Committee members Saskia Hogenhout and Christine Raines who have contributed their expertise and ideas to the committee for the past three years. The keen observer will notice that my term as Chair and member of the committee should also be coming to an end. However, the committee has asked me to stay on as Chair for another year to oversee the transition of GARNet into its next phase. I am also happy to announce that your votes in our recent annual elections allow us to appoint three new Advisory Committee members: Yoselin Benitez-Alfonso (University of Leeds), Renier van der Hoorn (University of Oxford) and Eirini Kaiserli (University of Glasgow). We very much look forward to working with them over the next three years.

We hope you will enjoy reading this issue of GARNish as a welcome distraction from the continuing political turmoil around Brexit. This issue features updates from UKPSF and the Global Plant Council, reports from recent exciting meetings, a BBSRC funding update and much, much more. As always, stay up to date with the advances of the community via @GARNetweets, our website (www.garnetcommunity.org.uk), blog (http://blog.garnetcommunity.org.uk/), and YouTube channel GARNet Community.

Views expressed by authors in GARNish are their own opinions and do not necessarily represent the view of GARNet or the BBSRC.

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Special thanks to: Jon Carruthers, Isabel Mendoza, Jenny Molley, Colette Mathewman Linda Kahl, Richard Wyatt, the BBSRC grant holders, Daniel Gibbs and the plant scientists at Birmingham.

The GARNet Committee

UK Plant Sciences Federation Update

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January 2019 will see the launch of a new report from the UKPSF, entitled 'Growing the Future'. The UKPSF Committee developed the report with the involvement of experts from across the bioscience community, to demonstrate to stakeholders, the UK Government and funders the scale of opportunities and ambitions emerging from the plant science sector – and offer proposals on how to realise them.

The launch of the report will be marked with a breakfast meeting in the Houses of Parliament on 29 January 2019, with talks from Professor Rick Mumford (UKPSF Committee chair), Professor Dale Sanders (Director, John Innes Centre) and Dr Belinda Clarke (Director, Agri-Tech East). Please email ukpsf@rsb.org.uk if you wish to receive a printed copy of the report or a link to download, upon release.

The UKPSF's Plant Health Undergraduate Studentships scheme enabled nine students to undertake research projects with leading plant health researchers this summer. These placements were funded by Defra, the BSPP and N8-Agrifood; we are grateful to our funders for making it possible. The scheme has secured funding for 2019, and an initial call for project proposals will be made early in the year.

The UKPSF produces a monthly newsletter containing a round-up of plant science news and policy stories, as well as announcements about the Federation's activities. To subscribe, create a free account or log in using the Royal Society of Biology's mySociety platform, then choose 'My Subscriptions' under 'Me and the RSB', and select 'Plant Science newsletter'. You can also keep up to date with the UKPSF on twitter at @UKPSF.

Global Plant Council Update

Isabel Mendoza
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The GPC held a workshop at the Annual Meeting of the American Society of Agronomy and the Crop Science Society of America, in Baltimore, Maryland, USA, on the 3rd November. The one-day workshop was entitled "Enhancing Global Collaborations in Crop Science", and brought together over 40 researchers from all continents (except the Antarctica) to discuss how best to facilitate international collaboration between researchers, policy and communication experts in crop science.

Given the high interest in the topics addressed, GPC is organizing a collection of brief case studies about collaborations and progress in plant science in key areas for society, e.g. food production, healthy safe food, environmental stewardship. In due course, we plan to coordinate a series of white papers or a blog series. Or maybe both. The slides shared during the workshop by the speakers are available here: https://www.slideshare.net/GlobalPlantCouncil

During these past months, beginning in October, the GPC launched a short survey (https://goo.gl/Xj8QT5) to learn what the GPC members and audience think of the ongoing activities and which new actions would they be interested in. The survey will remain open until Christmas. Over 120 answers have been gathered until now, coming from all over the world, and giving a fine representation for the whole plant science community. Do not hesitate to participate!

As a direct result of the poll, during the future months, the GPC is planning to introduce new activities and open new communication channels. The most relevant novelty, an early career researchers' platform, with the aims to increase the impact of their research and to help them advance in their careers. A new knowledge exchange platform in also in development.

Don't forget, you can always keep up to date with the latest from GPC, as well as plant science events and news from around the world, by joining our 5300 followers on Twitter (@GlobalPlantGPC) or the 1000+ followers of our Spanish language account (@GPC_EnEspanol). You could also sign up to our monthly e-Bulletin newsletter (http:// tinyurl.com/GPCebulletin) or visit our website (www.globalplantcouncil.org) for more daily updates!

The Royal Microscopy Society Botanical Microscopy 2019

Oxford Brookes University

Like the World Cup or the Olympics, every four years the Royal Microscopy Society host a Botanical Microscopy meeting to highlight excellence in plant imaging. In 2019 the meeting will take place at Oxford Brookes University between April 14th-18th. This includes four days of the talks and a conference dinner at Queens College, University of Oxford.

GARNet are delighted to support this meeting by sponsoring the New Technologies session. This session includes a tribute to Ian Moore who passed away earlier this year. Earlier this decade Ian was a member of the GARNet Advisory Committee so we are honoured to contribute to this session.

GARNet are providing ten £150 grants to encourage the attendance of early career researchers to the meeting. An application form for these grants can be found on the meeting website and the closing date is **March 1st 2019**. Given the high quality of the speakers that have been invited to this meeting it would be great to see a large number of ECRs attending. The organising committee have provided plenty of opportunities for talks that will be selected from submitted abstracts.

https://www.rms.org.uk/discover-engage/event-calendar/botanical-microscopy-2019.html

Invited Speakers:

> *Keynote speaker:* Niko Geldner (University of Lausanne)
> *The Cytoskeleton:* Patrick Hussey (Durham University)
> *The Nucleus:* Ricardo Randall (University of Zurich)
> *The Endomembrane System:* Federica Brandizzi (Michigan State University)
> *The Plasmodesmata and other organelles:* Emmanuelle Bayer (Université Bordeaux Segalen)
> *Autophagy:* Diane Bassham (Iowa State University)
> *Plant Pathogen interface:* Dr. Silke Robatzek (LMU Biocenter University of Munich)
> *New Technologies:* Charlotte Kirchelle (University of Oxford)

High Value Chemicals from Plants Network. Annual Meeting

October 1st, London

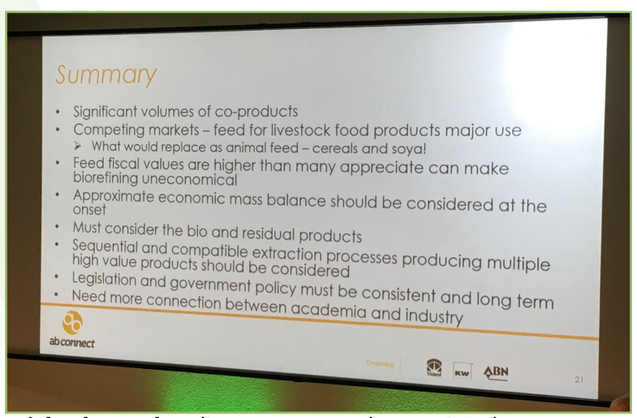
The final annual meeting in Phase I of the BBSRC-funded HVCfP NIBB network (https://bbsrc.ukri.org/research/programmes-networks/research-networks/nibb/) was held in the delightful Royal College of Physicians, close to Regents Park in London. This single day meeting was a byte-size mix of both invited talks and those provided by researchers who had received Proof of Concept (PoC) or Business Interaction Voucher (BIV) funding from the network.

From a GARNet perspective it was gratifying to hear a presentations that included preliminary work conducted in Arabidopsis, demonstrating the importance of model organisms in the development of ideas that can lead to industrial biotechnology projects. **Naomi Nakayama** at the University of Edinburgh described her labs work aimed at optimising use of Arabidopsis cell cultures as well as in developing plant stem cells as a tool for single cell factories. Secondly **Peter Eastmond** from Rothamsted Research describes the initial characterisation of the Sugar Dependent1 hydrolase enzyme that they are now developing as a potential industrial biocatalyst.

Paul Fraser from RHUL and **Mike Roberts** from Lancaster University introduced very different research projects that both use tomato plants. Long-term establishment of RIL lines have allowed the Fraser lab to identify tomato plants with increased levels of B-carotene in the fruit. This project has similarity to other attempts at vitamin A biofortification yet takes advantage of many years experitise working with tomato. These B-carotene fortified lines are now ready for the field and should be particularly important in regions with high food insecurity.

Mike Roberts has a nascent industrial collaboration with greenhouse tomato producer APS Salads. This soil-free growth of tomatoes generates a large amount of waste biomass, which is currently used for a variety of applications that rely on downstream anaerobic decomposition. It is known that mechanical disruption of plant tissue causes the release of protective defence chemicals so the Roberts lab have used BIV funding to investigate the whether macerated tomato waste has protective anti-pathogen properties. The initial characterisation of liquid fractions taken from tomato waste have given promising protective effects indicating that the mechanical disruption of the tissue generates an as-yet-unknown defense-promoting compound.

Michael Marsden provided an invited talk and made delegates re-think the idea of 'plant waste'. His company AB-Connect labels waste as '*co-products*' and it was extremely informative to learn about all the possible uses of crop co-products in an enormous range of industries. However there remains additional potential in this area as technologies continue to develop for degradation of cellulosic material and improvement of manufacturing pipelines.



Michael Marsden discusses co-products **NOT** plant waste

Sweet smelling success story of Oxford BioTrans.

Jason King from Oxford Biotrans provided the opening invited talk that was a real success story of activities that have taken place since he last presented at the in the 2015 annual HVCfP meeting (http://blog.garnetcommunity.org.uk/hvcfp-annual-meeting/). Their main product is the grapefruit flavour nootkatone that they produce from oranges using patented P450 enzymes. This industrial project was recently highlighted as a success stiry by the BBSRC (https://bbsrc.ukri.org/research/impact/natural-grapefruit-flavouring-from-industrial-biotechnology/). Oxford BioTrans are now investigating options for producing a range of other products using their set of novel P450s. Pleasingly Jason King reported that Oxford Biotrans have not had significant difficulties in obtaining funding for this project both from national funding bodies and local angel investors.

The afternoon invited speakers provided a different perspective on some wider issues surrounding the research environment. **Kelly Vere** is working with the Science Council on the establishment of the Technicians Committment, which is an initiative to provide recognition for the vital yet often underappreciated support provided by technical staff in higher education. Over 50 universities have signed up to the charter and many are taking steps to provide this extra support. https://youtu.be/_S6tOf8ed_k

Alison Prendiville (University of the Arts London) and **Sebastian Fuller** (St George's, University of London) described their involvement with the EU-funded Pharma-Factory project.

This involves the input of numerous stakeholders associated with the use of the products generated by plant-based biofactories. These include potential patients, clinicians, regulators and researchers. They described how they are using the process of co-design (https://en.wikipedia.org/wiki/Participatory_design) to create partnerships that take into account stakeholder priorities in order to facilitate new methods of knowledge exchange. Intuitively it seems that this type of project can be challenging for bench scientists to fully appreciate so it will be interesting to observe where this project leads and their conclusions.

Due to the obvious links between the GARNet community and the type of PoC/BIV projects funded by the HVCfP network, the GARNet coordinator has attended and participated in a number of network events over the past four years. Although this annual meeting only highlighted a small set of supported projects it seems clear that the HVCfP network has succeeded in bringing together academics and industrial partners as well as supporting research in its early developmental stages.

In early November the successful five-year Phase II NIBB projects were announced and the good news is that the HVCfP will continue in a slightly alerted form as the High Value Biorenewables (HVB) Network. Details of the other five networks is here: https://bbsrc.ukri.org/news/people-skills-training/2018/181101-pr-11m-to-fund-industrial-biotechnology-and-bioenergy-networks-announced/

Opening the way for global innovation in biotechnology

Jenny Molloy
University of Cambridge
Colette Matthewman
John Innes Centre
Linda Kahl
Biobricks Foundation

Biological advances depend on efficient and wide sharing of materials such as DNA, cell lines and seeds between biotechnology practitioners from a wide range of organisations including universities, research institutions, industry and community labs. Both the donor and recipient of materials typically sign a contract known as a Material Transfer Agreement (MTA) setting out the terms of use of the material. Many MTAs are restrictive and often prohibit redistribution to other labs and use of the material in commercial projects. However, a growing number of organisations are developing open source biological tools and DNA collections with the express intention of sharing them with any interested party for any purpose.

Thanks to an initiative from San Francisco-based BioBricks Foundation and the UK-based OpenPlant Synthetic Biology Research Centre, a joint initiative between the University of Cambridge, John Innes Centre and Earlham Institute, these organisations can now use an Open Material Transfer Agreement (OpenMTA) to share their biological materials as broadly as possible. This simple, standardized legal tool relaxes restrictions on the redistribution and commercial use of biomaterials while respecting the rights of creators and promoting safe practices and responsible research. "The OpenMTA provides a permissive foundation supporting many communities and interests" explains Drew Endy, President of the BioBricks Foundation, and Professor at Stanford University "It is a critical step forward in enabling all people to benefit from next generation biotechnologies".

A major motivation for development of the OpenMTA was the many open materials emerging from the synthetic biology research community, who are compiling large collections of "DNA parts": individual promoters, coding sequences, reporters and other genetic elements that can be remixed to produce novel functions. Dr Nicola Patron, Synthetic Biology Group Leader at the Earlham Institute and a Co-Investigator in the OpenPlant Centre, describes the use of OpenMTA in sharing genetic tools for plant synthetic biology: *"We have used the OpenMTA to provide [DNA parts] developed for our own research to scientists at several international research organisations. We hope that use of the OpenMTA will enable these materials to be shared and reused by plant scientists and biotechnologists everywhere. We believe that easy access to research materials accelerates both fundamental research and the application of scientific research to agriculture, industry and medicine."*

DNA parts are one of the pre-competitive research materials for which we expect to see OpenMTA being most widely adopted. Like many such materials distributed under restrictive MTAs, the potential commercial value of individual DNA parts is quite low, there is usually no requirement for tight control of provenance for reasons of safety or security and their MTAs are unlikely to

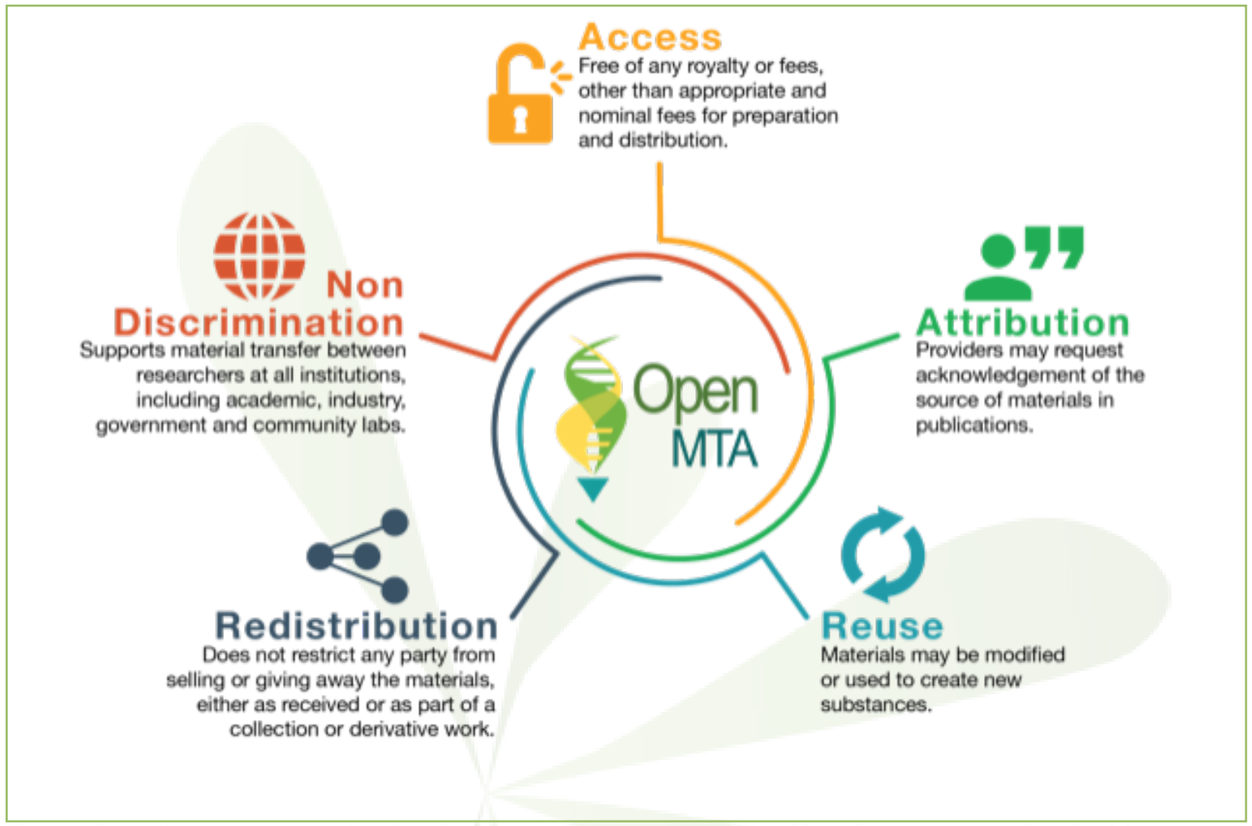


Figure 1: https://www.nature.com/articles/nbt.4263/figures/1 Image credit: Kahl et al, 2018. Licensed under CC-BY 4.0.

ever be monitored and enforced. These might be construed as reasons not to have MTAs at all but when sharing open tools it's important to institutions and researchers that their work is attributed, permissive terms of use are clearly spelled out and appropriate limitations are placed on their legal liabilities, for example if the material does not function as expected. Technology transfer professionals were therefore heavily involved in the creation of the OpenMTA framework to ensure that the new tool reflects the practical realities of their work.

OpenMTA provides a standardised master agreement that eases the administrative burden for technology transfer offices, negating the need to negotiate unique terms for individual transfers of widely-used materials and integrating seamlessly into semi-automated systems for managing MTAs. Dr Joanne Kamens, Executive Director at Addgene, a leading global charity that helps scientists share plasmids and which interacts with technology transfer offices across the globe, reinforced the potential of the OpenMTA to enable scientific exchange "Addgene is excited to see this new option becoming available to increase reagent sharing and scientific collaboration. This kind of open exchange drives innovation and accelerates research".

Open exchange is a feature that is also frequently highlighted by supporters of the

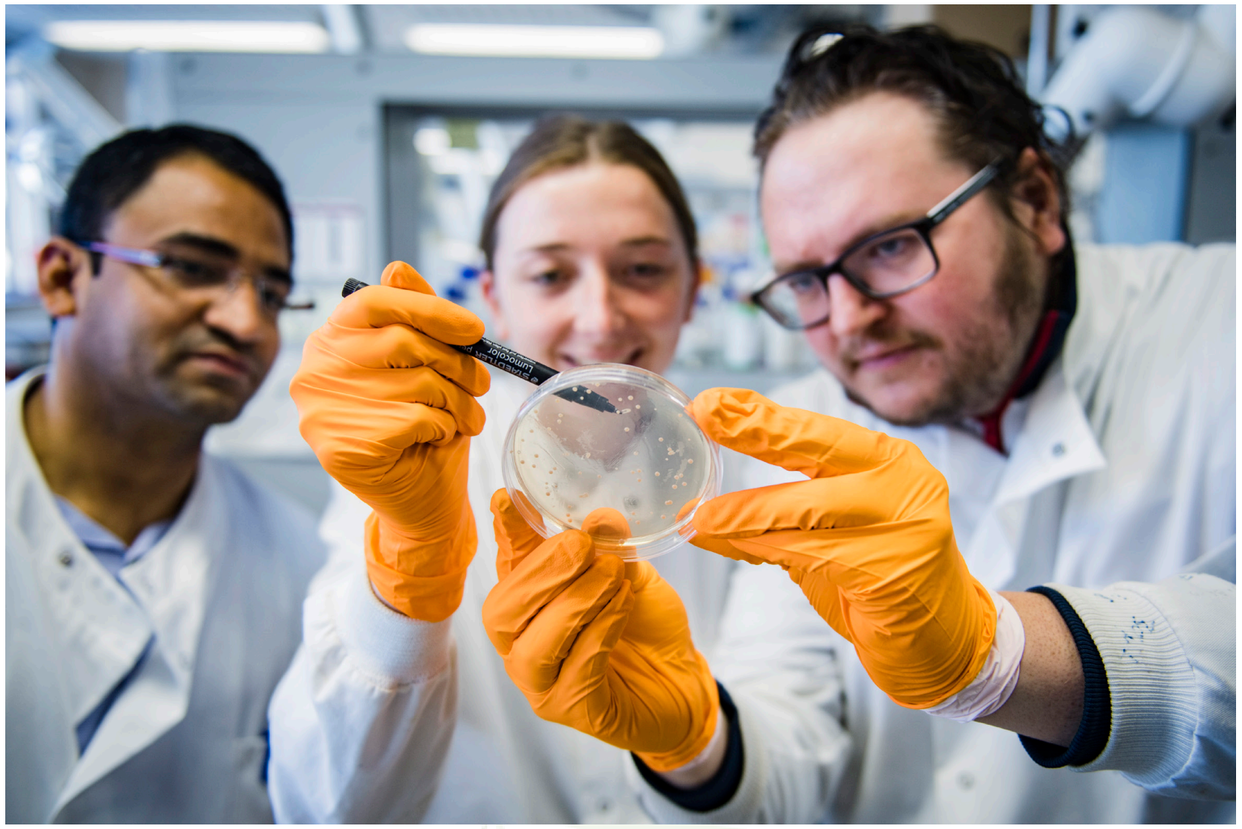


Figure 2: https://www.jic.ac.uk/media/cms_page_media/2018/10/11/Open%20MTA%20300.jpg Image credit: Photo by Phil Robinson, John Innes Centre. Shared with permission

OpenMTA who see the advantages in promoting access for researchers and individuals working in less privileged institutions and world regions. Dr Fernán Federici, an early adopter of the OpenMTA and a group leader at the Millennium Institute for Integrative Biology (iBio) in Santiago, Chile, explains: "*The OpenMTA will be particularly useful in Latin America, allowing researchers to redistribute materials imported from overseas sources, reducing shipping costs and waiting times for future local users. We are implementing it in an international project that requires sharing genetic tools among labs in four different continents. We believe, the OpenMTA will support projects based on community-sourced resources and distributed repositories that lead to more fluid collaborations.*"

This use of the OpenMTA is aligned with its design goals that were compiled by an international working group of researchers, technology transfer professionals, social scientists, and legal experts. The group determined through a workshop and series of meetings that in addition to enabling sharing in an international context through being usable by institutions worldwide, the OpenMTA should promote safe and responsible use of materials and reflect the following five goals:

(i) Access
(ii) Attribution
(iii) Reuse
(iv) Redistribution
(v) Non-discrimination

These design goals were built into the legal text of the OpenMTA Master Agreement, which is already gaining traction and includes initial signatories from academic research institutions, companies, and community labs.

Once the Master Agreement has been signed, transfers can take place using an implementing letter. Institutions retain full discretion to handle the transfer of materials on a customized basis using the OpenMTA where appropriate and other forms of MTA for situations where the material should be restricted for reasons of safety, security, high commercial value or due to limited supply.

Unlike some other open approaches in software and copyrighted materials, the OpenMTA does not include a 'viral' clause that requires derivative materials to be shared under the same open terms. In combination, these features mean that the OpenMTA provides organisations with the maximum flexibility and choice about how they want to share their materials to maximise their dissemination and impact.

Dr Linda Kahl, Senior Counsel of BioBricks Foundation is clear on the direction she would like the initiative to head: "*In five years' time my ideal is for the OpenMTA to be the default option for the transfer of research materials. Instead of automatically placing restrictions on materials, people will ask whether restrictions on use and redistribution are appropriate and instead use the OpenMTA to promote sharing and innovation.*"

The first step to achieving this is also clear: "*We encourage organisations worldwide to sign the OpenMTA Master Agreement and start using it.*" The OpenMTA Master Agreement is now freely available to view via http://openmta.org and more information on the background, rationale and deployment of the OpenMTA is detailed in Kahl et al. (2018). Further signatories are welcome and comments are encouraged both publicly online and by email to openmta@biobricks.org.

Kahl, L., Molloy, J., Patron, N., Matthewman, C., Haseloff, J., Grewal, D., Johnson, R. and Endy, D., 2018. Opening options for material transfer.

CONNECTED: The Community Network for African Vector-Borne Plant Viruses

By Richard Wyatt, CONNECTED Communication Officer

Plant scientists: do you want access to excellent research, training and networking opportunities, whilst helping improve food security for millions of people living in some of the world's poorest countries?

If it's a '**yes**', read on to learn more about The Community Network for African Vector-Borne Plant Viruses (CONNECTED). 12 months on from the start of the project, CONNECTED is taking stock, and inviting GARNet members to join, free of charge.

CONNECTED is a transformative project, building a sustainable network of world-class researchers to develop practical solutions to tackle the devastation caused by vector-borne plant disease in Sub-Saharan Africa.

Bringing together plant scientists and entomologists from across the globe, the three-year project is funded by a £2 million grant from the UK government Global Challenges Research Fund. It is co-ordinated from the University of Bristol School of Biological Sciences: long recognised as world-leading in plant virology and vector-transmitted diseases.

Vector-borne plant diseases bring colossal challenges to Sub-Saharan African countries. When food crop production is restricted by these diseases it leads to poverty, malnutrition and food insecurity.

Take cassava, for example. It's Africa's second most important staple food, yet its productivity in East and Central Africa is hugely constrained by two viral diseases: cassava mosaic disease and cassava brown streak disease, whose combined devastation is estimated to cause annual losses worth $1 billion.

Then there's yam: in West Africa alone over 300 million people use yam as a preferred staple food, and it's a major income source for smallholder farmers. Aphids are responsible for spreading yam mosaic virus, causing the most economically damaging viral disease of yams in West Africa, and an average yield loss of 40%.

The impact doesn't end with food security. The affected countries' economic and social development is hugely impacted. And when insufficient food and crop-derived income leads to people wanting to flee the country, migration rises.

Looking to the future, a range of new factors will soon compound the situation:

- The emergence of new virus diseases
- Climate change
- Resource limitations
- A growing population.

These will impact Sub-Saharan Africa sooner and more significantly than other parts of the world.

Creating new research collaborations

A number of research projects have been carried out in recent years in different parts of the world. There is a great deal of expertise, but it's vital to bring this together, creating more effective research communities.

Chaired by the UK's Chief Plant Health Officer, Professor Nicola Spence, the CONNECTED Management Board comprises UK and Africa-based experts in vector-borne plant disease, sustainability, social and environmental science, and agricultural impact. They are working to ensure active engagement between established networks, stakeholders and research funders in the region – preventing duplication and overlap – and forging exciting new collaborations.

CONNECTED Management Board member Dr Titus Alicai addresses delegates during a field visit to The National Crops Resources Research Institute, Uganda, during The CONNECTED Africa Launch Conference

There needs to be a relentless focus on refining the most pressing research questions and targeting work to ensure academic excellence has maximum impact on the ground. This is what CONNECTED is working to achieve. By developing a network of world-class scientists and researchers the project aims to produce a pipeline of innovative disease-prevention and -control strategies that will improve food security for years to come.

Work is now underway on the first nine projects that CONNECTED is pump-prime funding: in Kenya, Rwanda, Mali, Tanzania, Nigeria, Uganda, and the United Kingdom. Full details are on the CONNECTED website where you can see the diversity of projects currently being undertaken on:

- Diseases including cassava brown streak disease, maize lethal necrosis, maize chlorotic mottle virus, and turnip mosaic virus
- Issues ranging from new low-cost surveillance methods, to novel botanical formulations for the treatment of virus vectors, through to the potential of entomopathogenic fungi as biopesticides of cassava whitefly
- Crops including maize, tomato, pepper, cassava, banana, and cabbage.

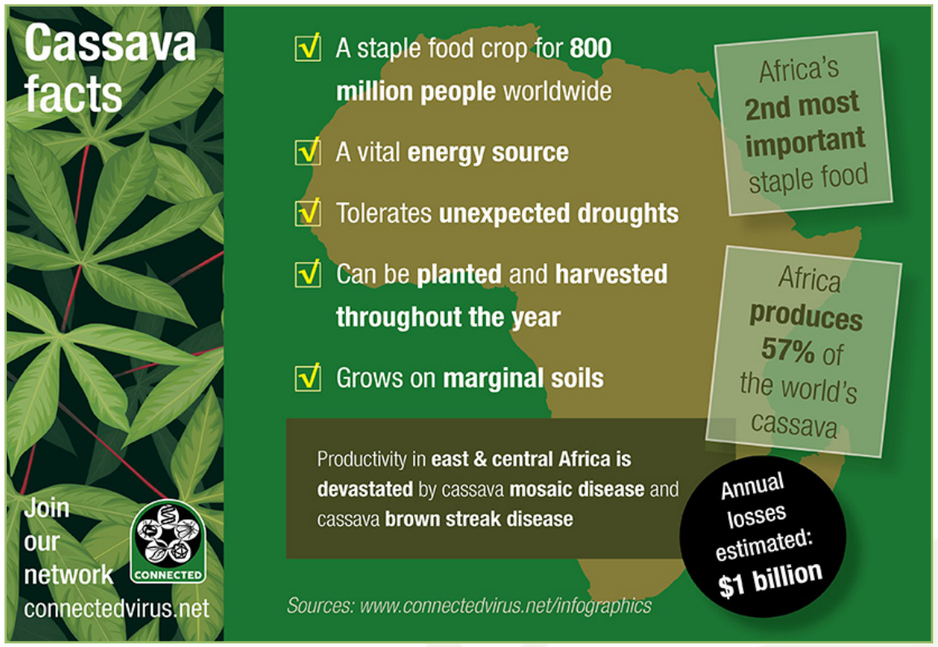
What CONNECTED offers plant scientists

The project has indeed seen positive beginnings, and CONNECTED is determined to accelerate this work, and draw more plant science researchers into its growing network.

So you would expect CONNECTED to urge you to join. But apart from the fact it's free to do so, why should you do so?

To date, members have benefited from:

- Two pump-prime research funding calls
- Two major international plant science conferences, run by CONNECTED: one in the UK;



one in Uganda with time spent in the field and workshops, as well as scientific presentations

- An Early Career Researcher training workshop in Kampala, including input on writing funding proposals
- The opportunity to attend 'An introduction to virus and vector diagnostics': a fully-funded five-day course in Kenya
- Training Voucher funding to pay for overseas laboratory visits and training courses up to the value of £3,000 per award.

In the first year of the project, membership has grown to well over 400, with people from over 40 countries getting outstanding training and research funding openings.

If you join now, you'll get full access to future opportunities which only network members can take advantage of. For example, in the next few weeks network members will receive news about:

- The next two rounds of the Training Voucher scheme: applications will open in Spring 2019
- T19: apply for funding of up to £2,000 throughout 2019, for members who see an existing training course or workshop they would like to attend which would benefit their professional development
- The CONNECTED Early Career Researcher Development Programme: our flagship, innovative, interdisciplinary programme, which will run for ten days in June 2019, and applications open soon.

As a member, you'll also have access to the member-only section of the CONNECTED website, with videos of conference presentations, infographics and other tools and resources.

Because CONNECTED is all about building new collaborations, members are able to search the member database to find others from across the world with similar interests. Interdisciplinarity is a major theme for CONNECTED, which is why the project is reaching out to develop collaborations with plant scientists, plant pathologists, entomologists and others as network activities are accelerated.

Plant scientists: what are you waiting for? CONNECTED very much looks forward to welcoming you to the network. Come and join CONNECTED.

www.connectedvirus.net

Responsive Mode Update

AUXENTRIC: a hormone-based mechanism to control chromatin state

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The fate of all cells is a function of the genes they express. In multicellular organisms, changes in gene expression underpin differentiation processes often controlled by mobile signals such as hormones that translate positional information into a cell-type specific transcriptional output.

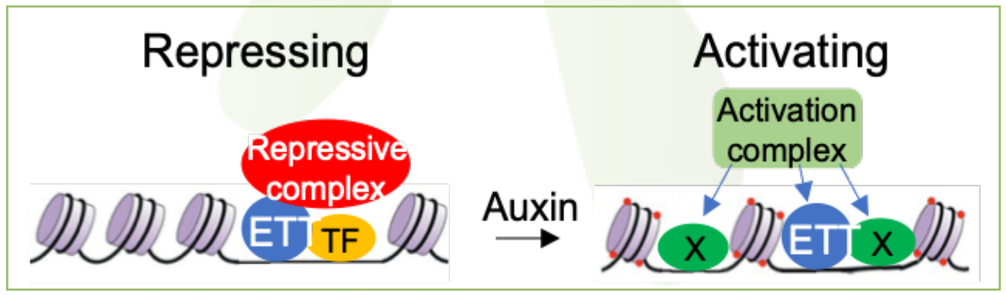
This BBSRC-funded project (BB/S002901/1) will unravel how cellular levels of the plant hormone auxin are translated into developmental outputs via dynamic control of chromatin states. Auxin is a key regulator of plant development. The text-book view of auxin signalling describes how auxin mediates its effect on gene expression by promoting the degradation of transcriptional repressor proteins. The molecular mechanism involves binding of the auxin molecule to TIR1/AFB F-box proteins. This allows interaction with AUX/IAA transcriptional repressor proteins, which – in the absence of auxin – repress Auxin Response Factor (ARF) proteins. Interaction with TIR1/AFB leads to AUX/IAA protein degradation thus relieving the ARF proteins from repression.

This mechanism elegantly explains the effect of auxin on the subset of ARF proteins that are classified as activators of gene expression. However, it is less clear why it would affect repressive ARFs. We recently identified an alternative auxin-signalling mechanism whereby auxin directly affects the activity of a transcription factor (TF) complex towards its downstream targets without the involvement of TIR1/AFB.

This mechanism, which we for simplicity refer to as the Auxentric mechanism, mediates precise polarity switches during organ initiation and patterning. A central factor of Auxentric is the ARF protein, ETTIN (ETT), which is classified as a repressive ARF.

Moreover, ETT is an unusual ARF lacking the AUX/IAA-interacting domain and the Auxentric mechanism differs from the TIR1/AFB-based auxin-signalling mechanism in three key aspects.

Firstly, the lack of a protein degradation step allows switching between states in immediate response to changes in auxin levels. In this way, the Auxentric mechanism is reminiscent of animal hormone-signalling pathways, such as the Thyroid Hormone pathway and the Wnt/ß-catenin pathway.



Ostergaard: Hypothetical model of how ETT controls gene expression through modulation of chromatin state in response to auxin. Red dots on nucleosomes indicate acetyl groups. TF indicates transcription factor; X indicates unknown protein.

Secondly, similar to these animal mechanisms, the data so far suggest that the hormone ligand in the Auxentric mechanism (Auxin) may be interacting with proteins bound to DNA. Finally, the effect of auxin on ETT-TF interactions appears to be structurally more specific than the TIR1/AFB-based mechanism as only the naturally occurring auxin, indole 3-acetic acid (IAA), is able to affect the ETT-TF interaction, while other auxinic compounds are not.

Experiments and analyses proposed in this project, are designed to answer the following overall question: What is the molecular mechanism by which ETT-containing complexes translate cellular auxin levels into transcriptional outputs to control plant development? Our preliminary data suggest that a direct effect on chromatin dynamics is at the centre of the Auxentric mechanism and we will explore this using a combination of molecular biology, developmental genetics and biochemical/structural approaches.

Over and above the elucidation of the molecular details by which the Auxentric mechanism control gene expression, the direct hormonal effect on transcription factor interactions may have far-reaching implications for the existence of alternative mechanisms by which hormones regulate plant growth and development.

Genome maintenance and the enhancement of seed vigour

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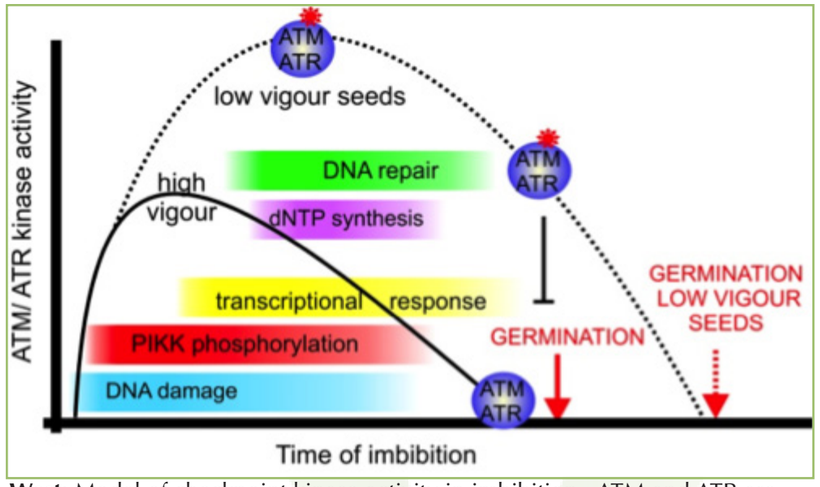
Seeds underpin sustainable agriculture, food security and play essential roles in crop propagation. Optimal yields, particularly under averse climatic conditions, require high vigour seed lots that display rapid, uniform germination tolerant of environmental stresses and robust, stress-resistant seedling establishment. Seed deterioration leads to progressively delayed germination which ultimately culminates in loss of viability.

Low germination vigour negatively impacts on final yield through reduced emergence, slower growth, weaker seedlings and reduced harvesting efficiency. Germination and seedling establishment are routinely improved in many commercial species by seed priming, which involves controlled hydration to activate pre-germinative processes without completion of germination. However, a significant drawback associated priming in many species is the reduced storability of primed seeds. In this project, we will uncover the molecular mechanisms which confer vigour enhancement in priming, and establish the genetic basis for the associated loss of seed longevity.

Recently we discovered that the mechanisms that mediate responses to DNA damage in plants play important roles in seeds by imposing the delay to germination associated with seed ageing. In dry seeds there is a steady



West: Model of checkpoint kinase activity in imbibition. ATM and ATR are activated (red star) by DNA damage early in imbibition. This leads to a rapid burst of DNA damage-responsive transcription and phosphorylation, activating DNA repair and inhibiting germination. Higher DNA damage levels in aged seeds prolongs and increases kinase activation, extending the lag phase to germination (dotted lines). Repair activities during priming are hypothesised to reduce the duration and magnitude of ATM/ATR signalling, thereby helping to increase seed vigour of primed seeds.

accumulation of background DNA damage which is exacerbated by adverse conditions during seed maturation, storage and germination. This leads to extremely high levels of genome stress experienced by the embryo upon seed rehydration, including the accumulation of chromosomal breaks (DNA double strand breaks (DSBs)), which represent a highly cytotoxic form of DNA damage. We identified that powerful DNA repair activities are required early in germination to reverse this damage before resumption of growth, as failure in repair processes results in severely impaired growth and development, mutagenesis and ultimately death of the plant.

DNA damage sensing leads to rapid activation of cellular signalling programmes early in germination that function to delay germination, allowing extended time for repair. The eukaryotic DNA damage response is orchestrated by the phosphoinositide-3-kinase-related protein kinases (PIKKs) ATAXIA TELANGIECTASIA MUTATED (ATM) and ATM AND RAD3-RELATED (ATR). These kinases integrate sensing of genome integrity with the cellular response to DNA damage, functioning to activate cell cycle checkpoints, transcriptional responses, DNA repair factors and cell death. As priming functions to reverse the delay to germination imposed by DNA damage responses, we hypothesise a central role for DNA repair and damage signalling processes in the priming mechanism.

Here we will use integrated genetic, biochemical and 'omic approaches to reveal the molecular link between genome integrity and priming, establishing the mechanistic basis of seed priming for the enhancement of seed germination. In addition, we will identify the specific factors which mitigate reduced seed storability post-priming.

The ultimate objective of this project is to develop novel lines of plants with improved seed longevity after priming through modulation of genome maintenance activities. We will test the potential of key factors to genetically improve seed germination performance in Arabidopsis and *Brassica oleracea*, a crop species important to UK agriculture. Collectively, these approaches will address the long-standing problem of the reduced storability of primed seeds, supporting sustainable agriculture.

Size matters: A systems approach to understanding cell size control in a developing multicellular tissue

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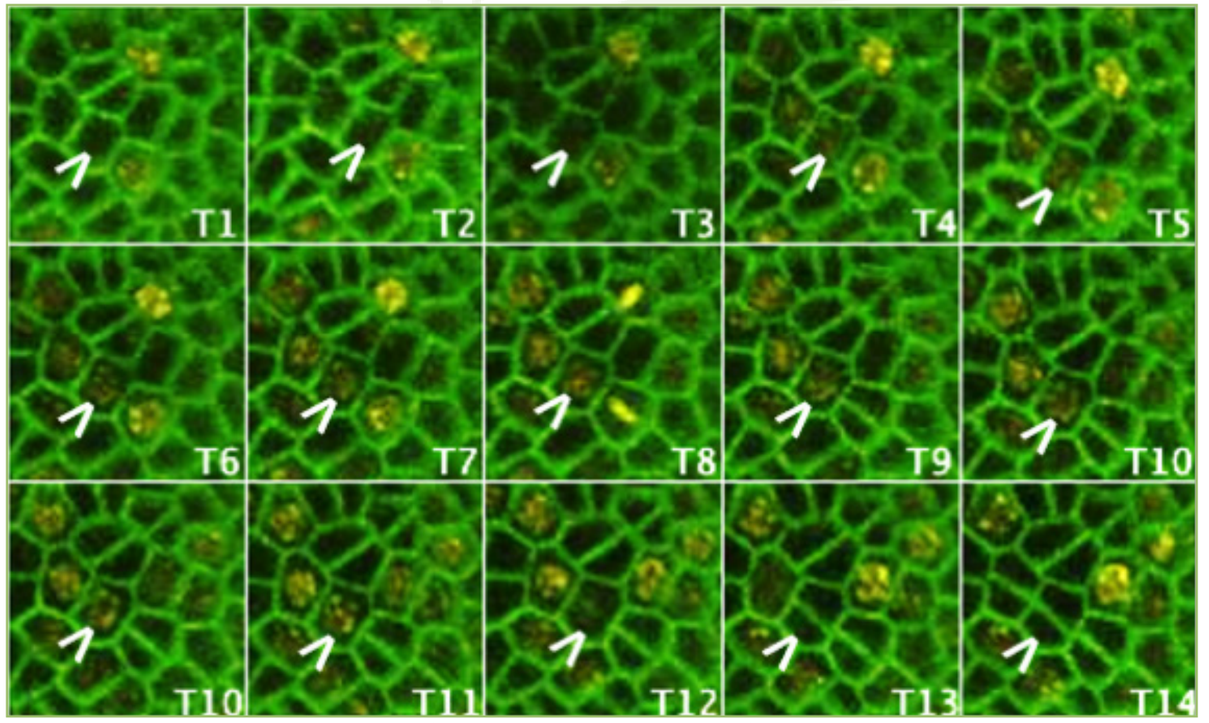
Cells are the building blocks of tissues, but how 3D structures are built from cells is a fundamental unsolved problem in biology. It is even more complex when we consider a growing tissue, in which the physical properties of the building blocks (cells) change constantly as they grow and divide.

We study the shoot apical meristem of the model plant Arabidopsis, which is required to produce new leaves and flowers as the plant grows. The early stages of organ development require efficient tissue growth and an increase in cell size is normally observed at this time. Over several years, we have developed techniques allowing us to image the meristem over extended periods in the confocal microscope.

We can follow individual cells over time and determine their growth and division. In order to divide, a cell goes through a defined series of processes known as the cell cycle. Using fluorescent reporters we have developed, we can simultaneously determine the position of all cells



Jones: Time course showing expression of a fluorescent marker (yellow) for the S-G2-M phase of the cell cycle in cells of the Arabidopsis shoot apical meristem. White arrow heads indicate a dividing cell. Cell cycle progression and growth can be measured from time courses using lineage tracking and image analysis.

in the cell cycle during imaging time courses of growing plant tissues.

Our recently published study showed that the size cells reach when they divide is on average consistent for a given tissue and set of environmental conditions, but is highly plastic when these change. For example we found that cells were smaller, and tissue growth slower, when plants were grown under environmental conditions that restrict photosynthesis. Variation in cell size arises through unequal division and has to be removed. This is done by establishing a balance between growth and division on a cell by cell basis.

The plasticity of the system leads us to consider that cell size at division is not determined by a direct "cellular ruler" but is instead determined as a consequence (or "emergent property") of the contributing processes of growth and division. This mechanism appears to be conserved from unicellular organisms which can also achieve a larger cell size and higher absolute growth rate under plentiful conditions. Regulation of cell size in these simple cells is achieved by balancing cell growth and division via the protein synthetic capacity of the cell.

We have developed a model that can predict accurately the size of plant cells based on the rate of growth and the accumulation of activity of two regulatory proteins (CDKs) as the cell grows. We tested this extensively using different mutants and growth conditions and identified the key processes that lead to cell size control. These processes appear to be the production and thresholding of CDK activity.

In this proposal we will identify the "sizer" molecules involved in these processes that establish the link between growth and division of cells and analyse their function using our state-of-the-art imaging and analysis techniques. We have a number of candidate sizers, with known roles in CDK regulation, but we will also carry out experiments to identify new candidates in an unbiased manner using a genome-wide approach based on identifying the rate at which proteins are being synthesized under different conditions.

We will use a combination of experiments and mathematics to develop a model that will allow us to understand how these sizer molecules are regulated and what effect this has on cell size control

How does PAP, a stress-induced metabolite, regulate gene expression?

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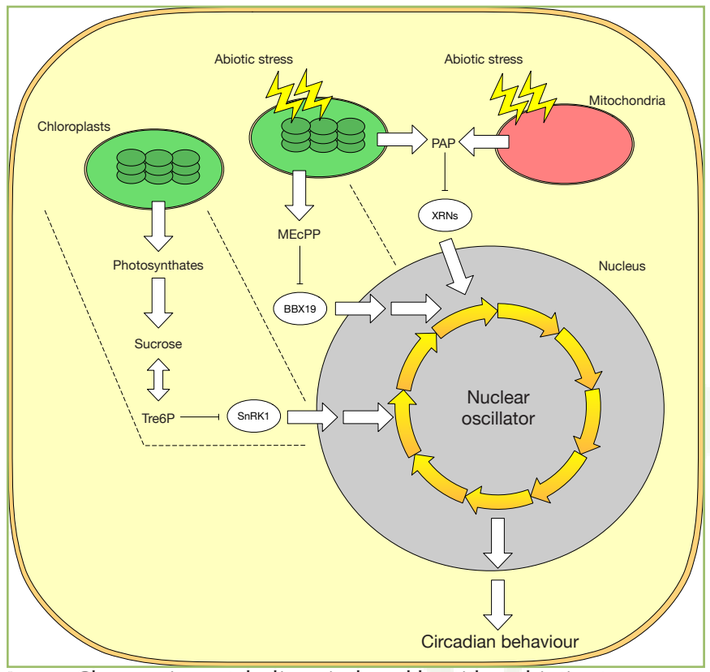
Plants thrive in a fluctuating environment. Regular daily changes in light and temperature have driven the evolution of the circadian system, a pervasive endogenous timing mechanism that coordinates gene expression and metabolism with prevailing environmental conditions. In addition to these diel changes, plants are also subjected to more infrequent environmental fluctuations (such as extremes in temperature or insufficient water) which are sufficient to limit crop yield in both field-grown and glasshouse-grown contexts. Since many of the abiotic and biotic stresses experienced by plants are predominantly associated with specific times of day, the circadian



Jones: Changes in metabolism, induced by either abiotic stresses or photosynthesis, alter nuclear circadian gene expression. 3′-Phosphoadenosine 5′-Phosphate (PAP) and methylerythritol cyclodiphosphate (MEcPP) accumulate in response to redox stress within the chloroplast and inhibit EXORIBONUCLEASES (XRNs) and BBX19 respectively. Separately, the sucrose/trehalose 6-phosphate (Tre6P) nexus regulates the activity of SnRK1 in response to photosynthetic activity.

system has been co-opted to enable anticipation of time-dependent biotic and abiotic stresses. However, the mechanisms underlying these interactions are poorly understood.

Drought confers a multifaceted stress upon plants, but one of the first metabolic consequences is the perturbation of photosynthesis, leading to increased accumulation of ROS and the subsequent development of redox stress within the chloroplast. These perturbations are communicated from organelles to the nucleus via multiple retrograde signaling pathways that alter nuclear gene expression, allowing plants to adjust their metabolism and development to tolerate environmental stress. 3'-PhosphoAdenosine 5'-Phosphate (PAP) is one such redox stress-induced metabolite that accumulates in response to drought and osmotic stress. The accumulation of PAP inhibits the activity of exoribonucleases (XRNs), leading to altered gene expression and increased transcript stability. The PAP/XRN pathway is therefore able to induce changes in nuclear transcript stability in response to redox stress in the chloroplast.

The circadian system induces rhythmic expression of approximately one third of a plant's genome but we do not have a precise understanding of how changes in metabolism (such as those induced by stress) alter the pace of the endogenous biological timer. We have recently shown that osmotic stress (as a proxy for drought) is sufficient to delay circadian timing, and that PAP accumulation correlates with this effect. As part of this project we will expand upon this phenomenon and investigate the complex interplay between environmental signals, endogenous biological timers, and metabolic changes induced by sub-optimal environmental conditions.

If we are to fully exploit the potential yield of crops it is vital that we understand how plants interact with their environment both during daily environmental fluctuations and in response to stress. Our work will advance our understanding of plants responses to osmotic stress and directly inform BBSRC's priorities to design crops with greater drought resilience that make more efficient use of available water resources.

iGEM 2018
October 25th-28th,
Hynes Convention Centre, Boston

Geraint Parry
GARNet Coordianator

Irrespective of the number of times you attend, it is extremely difficult to leave the iGEM Giant Jamboree uninspired.

This final event of the year-long International Genetically Engineered Machine (iGEM) competition is a conference like no other. Picture an international group of 3000 excited undergraduate students, for many of whom it is their first overseas trip…then add in the nerves generated by presenting their own research to a group of judges…. *and you can start to imagine the type of energy at this event!*

iGEM projects are extremely multi-disciplinary, and although the majority involve some molecular biology, they also contain significant aspects of modeling, creation of hardware and/or software, collaboration, public engagement and human practice. Students usually work on these projects from March to October and need to achieve a series of pre-defined requirements in order to qualify for Gold, Silver or Bronze medals. In addition there are other 'Track-specific' or 'Special' Awards that provide recognition for projects grouped into different categories. Finally there are overall prizes for the best High School, Undergraduate and Overgraduate (defined as teams with at least one member over 23yo) projects.


iGEM from Above: https://www.flickr.com/photos/igemhq/albums

From humble beginnings at MIT in 2003 with just 5 teams, iGEM continues to grow and grow and grow with students from 316 teams travelling to Boston for the Giant Jamboree in 2018. This year saw a significant transition as for the first time the largest number of teams came from China, rather than the USA. This clearly confirms the growing influence of China as a scientific superpower and that it is supporting the next generation in order to maintain a long-term preeminent position.

UK Participation

In 2018 twelve UK higher education institutions entered the competition with the University of Edinburgh again entering both undergraduate and overgraduate teams. This is a reduction from the 15 teams in 2017 with St Andrews and KCL returning to the competition whilst York, Kent, Bristol, Sheffield and Glasgow taking a break.

These breaks likely occur for a couple of reasons; firstly running a team requires a high amount of faculty commitment throughout the summer and secondly….***they aren't cheap.***

iGEM has a $3500 entry fee, which supports the activities of the iGEM foundation…. before you add in flights to and accommodation in Boston as well as a pricey $695 per student entry to the final giant jamboree….Then you can begin to consider any student stipends and the costs of actually doing the project.....

With this significant barrier to participation a common theme of discussion amongst advisors from across the globe revolves around different strategies to fund each years team. Many overseas teams include some aspect of iGEM for class-credit but to my knowledge, in the UK only the Edinburgh overgraduate team uses this model as they are able to fit this into their full-year masters program.

UK teams are in the fortunate position of having the opportunity to apply for support from a joint BBSRC and Wellcome Trust grant that is administered by the University of Glasgow. This fund covers half the costs of up to 10 student summer stipends and therefore requires a matched contribution from the home institution. In addition the fund provides a small consumable budget. As the BBSRC/Wellcome Trust funding is (rightly) earmarked for student stipends; the entry fee, conference and travel funds must be found from other sources.

This can clearly be a challenge.

In Cardiff the budget for a seven-student team runs to approximately £30K. This cost is for a simple project that has no expensive 'omic experiments that are a feature of the more advanced iGEM projects. UK institutions deal with these costs in different ways; some have financial support written into departmental or teaching budgets (such as Exeter or Edinburgh), others also take advantage of sources of internal undergraduate summer studentships (such as Cardiff) whilst all rely on some type of external funding or in-kind help.

Given these significant costs it is legitimate to ask whether iGEM is really worth it?

For the students?

There is no doubt participating in iGEM is a huge positive for the vast majority of students. They are involved in exciting multidisciplinary projects that are like nothing else they have or will experience in their past or future research careers.

> *iGEM projects are a buffer to poor planning.* There are plenty of both external and internal subject-specific grants available to support summer undergraduate research. However the group-dynamic of an iGEM project buffers any student against possible negative aspects of an individual placement; such as a poorly planned, difficult project or a challenging interaction with the supervisor and/or labmates. This 'buffer' should ensure students retain a positive opinion of scientific research and go on to other projects either in the host institution or elsewhere.

> *iGEM projects build independent thinkers.* These projects are usually on a student-led topic, albeit often in an area of expertise provided by the supervisor or department. The best students take ownership of the project and can take it in directions of their own design (budget allowing!). It provides self-motivated students the opportunity to flourish and take on new challenges such as modeling, web-development or public engagement. From experience it seems the only students who struggle are those challenged by the freedom of the project, which is an enormous contrast from the prescribed nature of regular lab classes. Hopefully a good recruitment process should be able to identify those students who might struggle before the project begins! Hopefully….

For the funders?

For a modest outlay (approx. £70K) the BBSRC and Wellcome Trust will surely see a

benefit from their contribution. There is little doubt that iGEM projects will motivate students to pursue higher degrees in Bioscience-related areas. In the past the University of Glasgow has kept track of student movements so hopefully are building a dataset to confirm this trend.

For the Host University?

Individual institutions likely need to take the long view to see the value of participating in iGEM. It might take several years to build a tradition of participation that will slowly filter into the consciousness of both the faculty and the student body. Any University that is considering getting involved in iGEM might consider:

1. Use iGEM as a recruitment tool.
The best advertising for iGEM is word of mouth from participating students. Over a few years the cohort of local iGEM alumi builds so that they can influence both their friends and friends of friends, some of whom might be motivated to attend that University to participate in iGEM.

2. Building a Global Reputation in Synthetic Biology.
Over 16 years the number of iGEMers scattered around the globe is significant and permeates many areas of the scientific community. The participation of both the Institution and the students will resonant with this international cohort that in turn could lead to beneficial future interactions.

3. Use iGEM as a testing ground.
For a variety of reasons some iGEM projects are not 100% student-led but rather the initial idea might come from an advisor. The students can then take the idea in different directions but any preliminary data they obtain might be useful for future, more lucrative grant applications.

4. iGEM projects lead to commercial innovative.
If given full institutional support the students can develop an advanced idea that has a clear commercial path, which can benefit both individuals and the University. At least three 2018 iGEM teams were exploring options for future commercialisation and had patents pending resulting from different aspects of their projects.

5. iGEM students can add future value to the department.
Participating in iGEM often will define the future research interest for the students. If a student is motivated to commit to a further degree at the home institution then there will be an immediate financial return; either from a student fee (for a masters) or from an external grant funder (for a PhD). Clearly it doesn't take many students to take up these opportunities for the institution to gain value from an initial contribution of £10-20K.

UK 2018 Successes

In 2018 UK teams continued to have success at the iGEM awards ceremony with Gold medals awarded to Cardiff, both Edinburgh teams, Imperial, Oxford, Nottingham, Newcastle and Warwick. KCL, UCL and Westminister earned Silver medals while St Andrews and Manchester won Bronze.

Each team should be proud of their achievements especially as the playing field is far from level. Whereas most UK teams have been established over the past few years the team from St Andrews started late in the year whilst the Manchester team was extremely inexperienced. Therefore obtaining a medal of any colour was a great achievement for all.


Team Cardiff win the Best Plant Synthetic Biology Award

The award of medals is an interesting process that often requires interactions that are outside of the usual 'scientific process'. The team from Munich finished second overall in the overgraduate competition due to a remarkable project that developed a cell-free bacteriophage system and novel (patent-pending) delivery system. However despite this astounding work they received a Bronze medal, presumably for not documenting something correctly during their project.

In addition to medals and overall prizes there are special awards for different 'Tracks' and aspects of a project. In 2018 the Oxford team won the extremely competitive undergraduate 'Therapeutics' track whilst the Cardiff team was awarded the undergraduate prize for 'Best Plant Synthetic Biology'. Otherwise the teams from Edinburgh UG (Foundational Advance), Newcastle (Measurement) and Oxford (Wiki, Integrated Human Practices, Entrepreneurship) received nominations for different awards. With an increased number of well-funded teams there is no doubt that competition is increasingly fierce so gaining nominations and awards is more challenging than ever.

Overall the most important thing remains that each team takes satisfaction from its own achievements, as each team's goals will be a function of the level of support and expertise provided by their advisors and host institution.

Outside of UK participation, there were some remarkable projects presented at the 2018 Jamboree. The overall overgraduate winner was the team from the University of Marburg in Germany who had developed a set of molecular tools and characterisation of *Vibrio natriegens* as an alternative chassis for synthetic biology. Vibrio has a doubling time of just 7 minutes so can potentially speed up the pace of biologically engineering. http://2018.igem.org/Team:Marburg. The winner of the undergraduate competition was the team from Valencia, whose primary achievement was to develop hardware and software tools for automated golden gate assembly and bacterial transformation. Their Printeria hardware included a heated/cooled plate where reaction reagents and bacteria are separated, mixed and moved using an electrical current. They hope that this type of hardware can reduce the cost of entry into synthetic biology for under-resourced labs. http://2018.igem.org/Team:Valencia_UPV

The Team Valencia Printeria hardware

Other projects of note were the overgraduate team from TU-Delft in Holland whose 'Adope' project developed a novel test for potential human gene-doping using a dCas9-linked to a transposase, in which specific nucleic acids can be isolated and sequenced using nanopore technology. This project has already received interest in the mainstream media and is being further developed by Dutch anti-doping authorities.

Once again attending the iGEM jamboree didn't fail to inspire both experienced scientists and scores of enthusiastic undergrads. The iGEM competition certainly has its flaws but overall there is truly nothing like it!

Get involved if you can!

Spotlight on: University of Birmingham

Kindly compiled by Daniel Gibbs

Research in the Plant Science division at the University of Birmingham is broadly focussed on the genetic and cellular control of plant growth, development, and environmental responses in model species, crops, and their wild relatives. There are currently 12 group leaders in the department, with areas of interest ranging from computational and mathematical approaches to understanding principles of plant growth and complexity, through to the dissection of abiotic and biotic stress signalling and resistance in both model and crop species.

We also have a strong focus on investigating meiosis, genome stability and the quantitative analysis of complex traits, as well as plant evolution, nutritional value, and conservation. Birmingham has recently invested heavily Plant Science research, most notably through hiring four new members of academic staff in the last year.

We are also currently developing a brand new plant growth facility, supported by the Wolfson Foundation, that will expand our current capacity for conducting controlled experiments and support ongoing fundamental and applied research efforts.

Department Twitter: @PlantSci_UoB

UNIVERSITY OF BIRMINGHAM

Professor George Bassel
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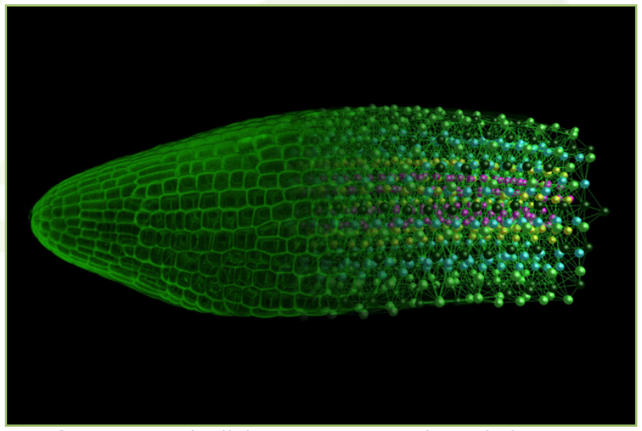
Biological complexity lab

We are interested in uncovering mechanisms of plant growth and development, in particular, how information from the environment is processed in plants across molecular, cellular and organ scales. This integrative approach lies at the interface between developmental biology, mathematics, physics and computer science, and seeks to provide meaningful strategies to rationally reprogram crop species.



Bassel: Extraction of cellular connectivity in the Arabidopsis hypocotyl

Dr Philippa Borrill
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Wheat senescence and nutrient remobilisation

Wheat is a staple food for more than 2.5 billion people around the world and provides 20 % of calories and 20 % of protein eaten by humankind. Looking to the future we need to increase the yields of wheat, however maintaining protein levels will be a challenge because in general there is a negative trade-off between yield and protein content. Research in my lab focuses on understanding the developmental process of senescence (ageing), which enables nutrient remobilisation from vegetative tissues into the developing grain, and hence is a key determinant of the balance between yield and protein content.

Through the identification of transcription factors regulating senescence and their downstream targets, we aim to escape the negative trade-off to produce high yielding, high protein wheat. This research is enabled by several resources we have recently developed including wheat expression atlases (www.wheat-expression.com; http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi), sequenced mutant populations and a high quality reference sequence.

For details on these resources and how to use them see www.wheat-training.com.

Borrill: Wild type wheat (left) and a double mutant in the NAM-A1/NAM-D1 transcription factors which regulate senescence (right).

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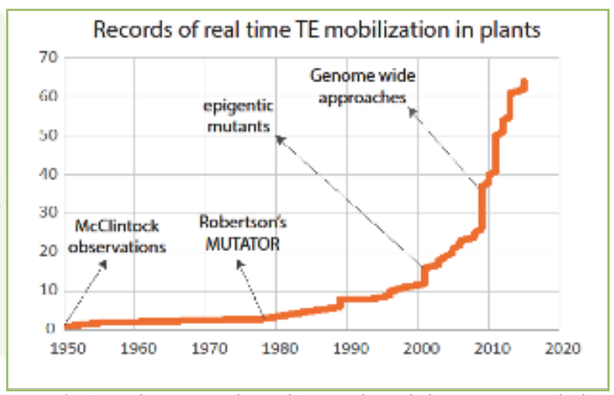
Transposable elements mobilization and genome plasticity in plants

Genome plasticity is extremely important in adaptation and plants are among the best examples of organisms able to efficiently rearrange their genome in a short evolutionary time. Genetic mobile elements (Transposable Elements or TEs) play a critical role in shaping the plant genome, and contribute to most of the genome diversity among plant species, often determining economically relevant plant traits. My research focuses on understanding the mechanisms regulating TE activation and mobilization and the effect of TE mobilization on plant genome stability and gene expression.

I am also interested in the mechanisms maintaining stable DNA methylation at TE sequences, which is the main process suppressing TE activation. The study of the effect of TE mobilization in plant models is crucial to understand their direct role in shaping the host genome, and investigate the potential use of these elements to generate gene variability and new agronomical relevant plant traits.



Catoni: Cumulative number of TEs with mobilization recorded in real time in plants, starting from the initial McClintock observations performed in maize.

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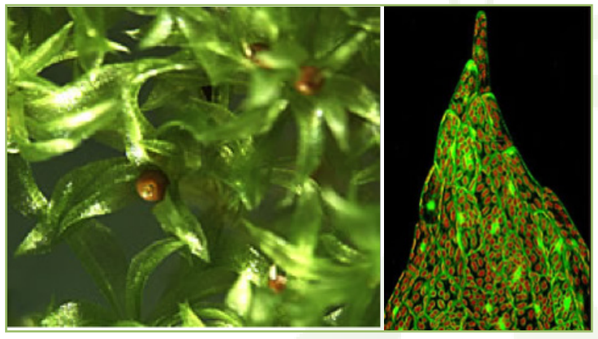
Plant evolution and development

Our research interest is in understanding plant- and algal development and evolution. The transition of plants from water to land half a billion years ago and their subsequent diversification from a single common ancestor was a critical step in the Earth's history. The acquisition of multicellularity in "green" lineages was also key in shaping our atmospheres and ecosystems. We are using flowering plants (including Arabidopsis, tomato and cereals), early-diverging plants (such as the moss Physcomitrella) and green seaweeds as model organisms to address fundamental questions about how green organisms develop and evolve.



Coates: The model moss Physcomitrella. Left: leafy gametophytes bearing sporophytes; right: Inducible GFP expressed in leafy tissue.

Recent "research highlights" include:
(i) Uncovering new molecular mechanisms that enabled early-diverging land plants to disperse and colonise the earth,
(ii) Comparisons of plant spore- and seed germination mechanisms,
(iii) Identifying new genes that enable plants to regulate their root system architecture via multicellular root development
(iv) Sequencing and analysis of the first green seaweed (Ulva) genome
(v) New understanding of how bacteria regulate seaweed morphogenesis.

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Protein degradation-based signalling

Dan is the head of plant proteolysis and signalling group at the University of Birmingham. His group studies how plants use targeted protein degradation as a mechanism for sensing and transducing signals, with a particular focus on the N-end rule pathway of the ubiquitin proteasome system. This pathway is an ancient and highly evolutionarily conserved proteolytic system that targets proteins for destruction based on the identity and chemical modification of their N-terminus, and has previously been linked to oxygen and nitric oxide perception and signalling during development and stress response.

The group uses a range of genetic, cell biology and biochemical approaches to uncover new functions and targets of this pathway. Current projects - funded by the ERC and BBSRC - are investigating links between protein degradation and co-translational quality control, and exploring how N-end rule-mediated destruction of chromatin modifying proteins regulates the epigenome in response to the environment. We are especially keen on linking the control of protein stability via this pathway to agriculturally important developmental processes and abiotic stress responses.

Gibbs: Identification of a new protein degradation component that impacts chloroplast development and function .

Dr Iain Johnston
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Stochastic Biology and organelles

Iain is head of the Stochastic Biology group in plant sciences, and his research focusses on biological processes where random influences play an important role. His group combines mathematical modelling and statistical approaches with lab- and field-based experiments to reveal the stochastic mechanisms governing plant form and function. He is particularly interested in bioenergetic organelles, with an ERC-funded research programme "EvoConBiO" exploring the evolution, cellular control, and synthetic manipulation of mitochondrial and chloroplast populations in cells.

Other research projects include elucidating the evolutionary dynamics leading to C4 photosynthesis, the physical and electrochemical behaviour of mitochondria in plant and animal cells, and stochastic bet-hedging in germination. Many of his publications, which have appeared in Nature, PNAS, eLife, Cell Systems and other top journals, and in the UK and international press, are summarised at mitomaths.blogspot.com .

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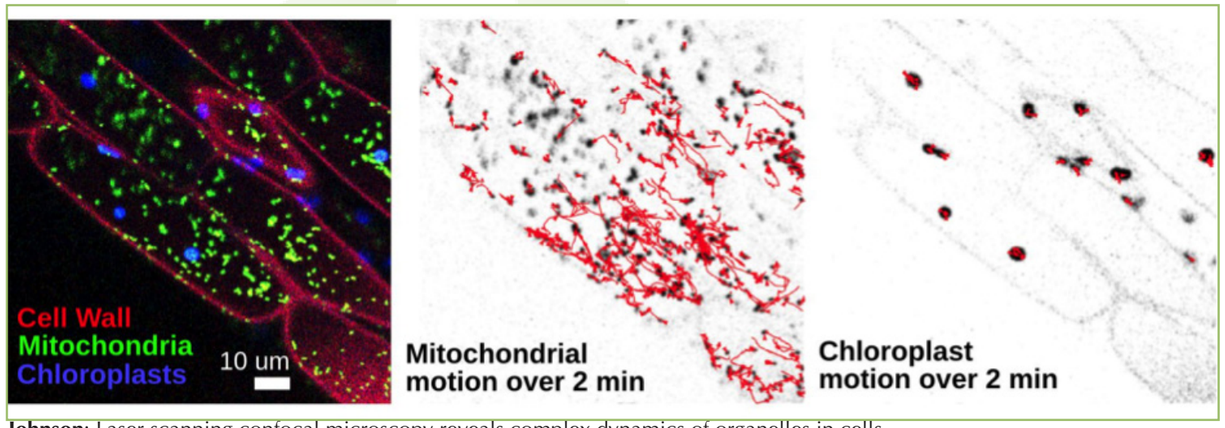
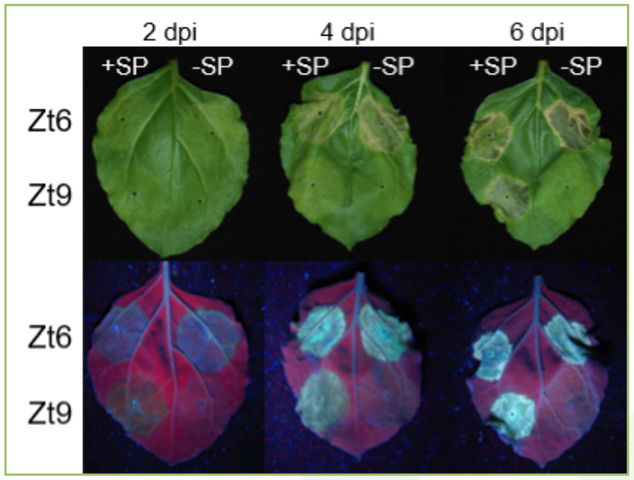
Molecular plant pathology

Plant pathogens present significant challenges to agriculture, reducing crop yields and in the case of tree diseases, potentially altering the landscape for centuries. Understanding the molecular basis of how pathogens successfully parasitize plants offers hope for the development of novel control solutions. *Zymoseptoria tritici* is a fungal pathogen of wheat, and causative agent of *Septoria tritici* blotch (STB) disease. My recent work has explored the secreted proteins (effectors) used by this fungus during its colonisation of wheat plants and attempted colonisation of non-host plants. Understanding the determinants of effector



Johnson: Laser scanning confocal microscopy reveals complex dynamics of organelles in cells



Kettles: *Z. tritici* effectors induce cell death in the non-host plant *Nicotiana benthamiana*

recognition may offer new ways to enhance wheat resistance to this important pathogen.

The second part of my research focus is on current and emerging tree pathogens, and how their impact might be exacerbated by climate change. I work in collaboration with the Birmingham Institute of Forest Research (BIFoR), making use of the unique Free-Air CO2 Enrichment (FACE) facility in Staffordshire.

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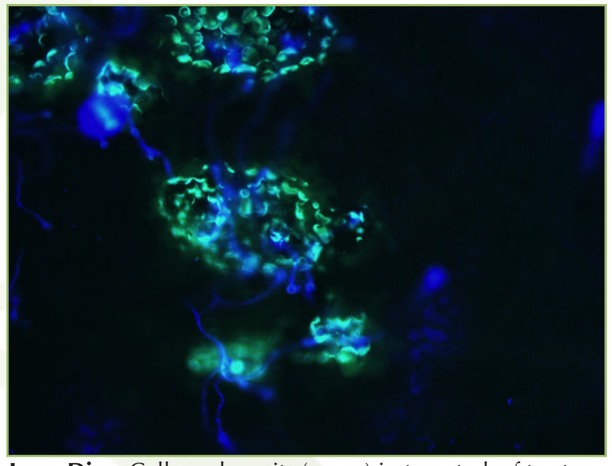
Plant defence

My group studies priming of defence, a phenomenon defined as an increase sensitivity to certain stimuli due to prior experience. Priming can be understood somehow as a plant vaccine because after an initial stimulus that warns of an upcoming attack, plants are able to activate their defence mechanisms faster and stronger upon subsequent attack. The group works in three lines of research: (1) we exploit the immune system of tomato plants to tackle emerging filamentous diseases in leaves and fruit; (2) we work to understand the infection strategies of the fungal pathogen *Fusarium oxysporum*; and (3) through our link with the Birmingham Institute of Forest Research and the Free Air CO2 Enritchment (FACE) experiment, we study priming of defence in forest trees. Our interdisciplinary work explores priming in models, crops and trees and we take into consideration the pathogens and the environment in order to gain a wider vision of the arms race between plants and pathogens.



Luna-Diez: Callose deposits (green) in tomato leaf to stop growth of *Botrytis cinerea* (blue)

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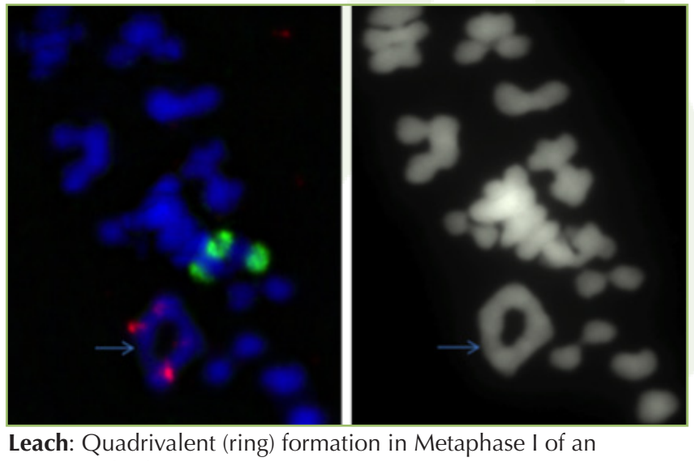
Twitter: @LindseyJLeach

Statistical genetics and complex traits

My research group is centred on developing and using statistical genetics approaches to dissect complex trait phenotypes into their underlying genetic components, in plant, animal or human populations. This central goal in statistical genetics consists of multiple interrelated parts, including genetic and epigenetic studies to identify genomic variants involved, and transcriptomics to explore the genome-wide expression patterns related to trait variation. We are particularly fascinated by the evolution of polyploid species that possess multiple copies of the genome, creating sophisticated patterns of chromosome behaviour and thus inheritance, and posing a major challenge to genetic analyses in these species.

Work in my group includes investigations on: (i) development of new statistical methods for mapping Quantitative Trait Loci (QTL) in autotetraploid species, and applying these methods to map the genetic basis of complex traits in some of the world's most important crops, particularly potato (Solanum tuberosum); (ii) comparative genomics of diploid and autotetraploid species, including patterns of chromosome pairing behaviour and recombination during meiosis using molecular cytogenetic approaches (see image); (iii) the genetic mechanisms of adaptation to environmental change in the environmental genomics model organism Daphnia; (iv) pedagogical research into teaching and learning of statistics across diverse disciplines in higher education. Websites: www.statisticalgenetics.info and https://www.birmingham.ac.uk/research/activity/transform/index.aspx



Leach: Quadrivalent (ring) formation in Metaphase I of an autotetraploid potato meiosis.

Prof. Zewei Luo
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Theoretical and experimental strategies for dissecting complex traits

Research interests of my team focus on understanding the genetic architectures and mechanisms that underlie complex quantitative genetic variation in both diploid (Arabidopsis, yeast, humans) and autotetraploid (potato) species, using both theoretical and experimental approaches. Specifically, our recent projects include:

- Methods for quantitative genetic analyses in autotetraploids

Chen J, FJ Zhang, L Wang, LJ Leach and Zewei Luo (2018) Orthogonal contrast based models for quantitative genetic analysis in autotetraploid species. New Phytologist 220: 332-340.

- Genetics of quantitative traits through a multi-omics approach

Fang Ou, XH Hu, L Wang, N Jiang, J. Yang, B Li and Zewei Luo (2018) Amn1 governs post-mitotic cell separation in Saccharomyces cerevisiae PLoS Genetics e1007691. doi: 10.1371

- Ploidy driven change in meiotic recombination frequency

Wang L and Zewei Luo* (2012) Polyploidization increases meiotic recombination frequency in Arabidopsis: a close look at statistical modeling and data analysis BMC Biology 10: 30.

- Statistical methods for integrating multi-omics sequence data and unveiling molecular underpinnings of non-small cell lung cancer

Liu TC, XP Wu, T Chen, Zewei Luo and XH Hu (2018) Downregulation of DNMT3A by miR-708-5p Inhibits Lung Cancer Stem Cell–like Phenotypes through Repressing Wnt/beta-catenin Signaling. Clinical Cancer Research 24(7): 1748-60.

Dr Nigel Maxted
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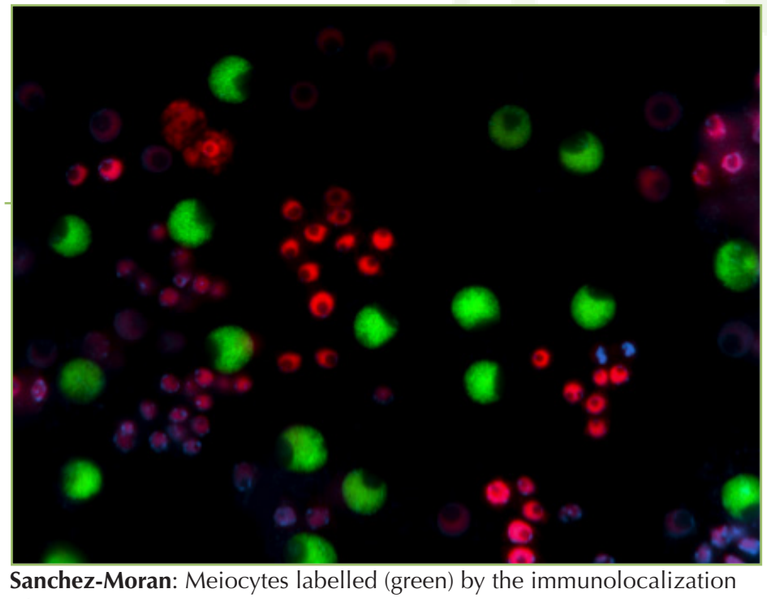
Plant conservation for Food Security

Food Security is a major global challenges confronting humankind today. The Plant Genetic Resource Group's (PGR) research is helping to secure food supplies, mitigate the impact of climate change and maintain consumer choice, impacting governments, commercial breeders, farmers and the public globally. PGR research on development and implementing agrobiodiversity conservation strategies, specifically on crop wild relatives' (CWR) and landraces' (LR) in situ and ex situ conservation, has helped national and international agencies meet their convention and treaty obligations, and underpinned food security.

Currently we are working with UN Food and Agriculture Organisation to establish a global network for CWR in situ conservation, European Commission to create an inventory of traditional crop varieties and the UK government to include CWR and LR diversity in environmental stewardship schemes, actions taken based on the group's advice. This involves expertise in field conservation, GIS, population management, on-farm conservation, gene flow and genetic diversity studies.



Sanchez-Moran: Meiocytes labelled (green) by the immunolocalization of meiotic axis protein ASY1

Dr Eugenio Sanchez-Moran
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Control of meiotic recombination

Our research is focused in understanding the control of meiotic recombination in plants in order to manipulate the frequency and localization of meiotic crossovers. Meiotic recombination is initiated by the formation of numerous programmed double-strand breaks in chromosomal DNA, a small proportion of which are processed to form crossovers. Thus, genetic variation generated by a single round of meiotic recombination is limited.

Furthermore, the distribution of crossovers in plants with large genomes, which include most crops, is highly biased towards the ends of chromosomes. As a result, extensive interstitial and centromere-proximal chromosome regions rarely recombine. Yet, these large genome areas contain roughly one-fifth of the genes in maize and even larger gene fractions in some other crops like wheat, which presents a serious impediment to plant breeding and food security. Our research uses genetics, cytology, biochemistry and microscopy approaches in order to understand and manipulate meiotic recombination in plants.

GARNet2018: A Plant Science Showcase

University of York: September 18th-19th 2018

by Geraint Parry

Meeting Website: https://garnet2018.weebly.com/

The biannual GARNet meeting was hosted by GARNet committee member Andrea Harper in the Ron Cooke Hub at the University of York. The aim of this two-day meeting was to showcase current technology and expertise both in UK and international plant science. To that end the GARNet Advisory Committee developed a program that included a mix of early career researchers and more established faculty. In order to support ECRs the meeting included fifteen two-minute flash talks that allowed delegates to introduce their posters before the official poster session. Added to the 10 speakers selected from submitted abstracts, the meeting gave opportunities for 25 registered delegates to present their work in a short talk.

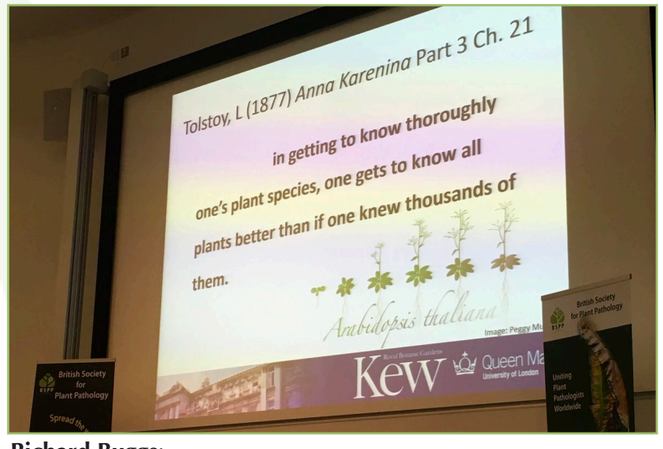
The meeting was split into five sessions and was introduced by the GARNet chairman Jim Murray who highlighted GARNet achievements over the past four years and our plans for the future . The first session was entitled 'Large Scale Biology' and was highlighted by Cristiane Calixto from the James Hutton Institute who provided an exciting, enthusiastic talk about their development of a new annotation for the Arabidopsis genome that provides additional support for alternatively spliced variants. In particular they are interested in plant responses to cold temperature as highlighted in a recent publication in The Plant Cell .

Cristiane confirmed that all of the data they have produced is freely available to the community which dovetailed nicely with the next presentation provided by Professor Andrew Millar who gave an introduction to the principles and benefits of open data in a talk entitled 'Being more Open by Being more Productive'. Professor Millar's talk is available online at the GARNet YouTube page . In addition to this formal talk Andrew also hosted a lunchtime discussion session in which attendees gave their personal and institutional experiences of using and providing open data.

Lucia Strader from Washington University in St Louis provided the opening talk in the second session that was entitled 'Innovations in Hormone Signaling' where she gave an overview of her group's discoveries of novel aspects of the auxin response. Tom Bennett (University of Leeds) also gave a thought-provoking talk about the ways in which plants decide the number of flowers and branches that it ultimately forms.

Branching was the theme of the keynote talk that was provided by Ottoline Leyser who, as a previous GARNet PI and academic at the University of York , returned 'home' to give an overview of her group's work on the hormone signals that control the growth of lateral buds.

The highlight of Session III: Interacting with the environment was a talk by Richard Buggs from Kew Science and QMUL that updated his current work that aims to tackle the progression of Ash



Richard Buggs:

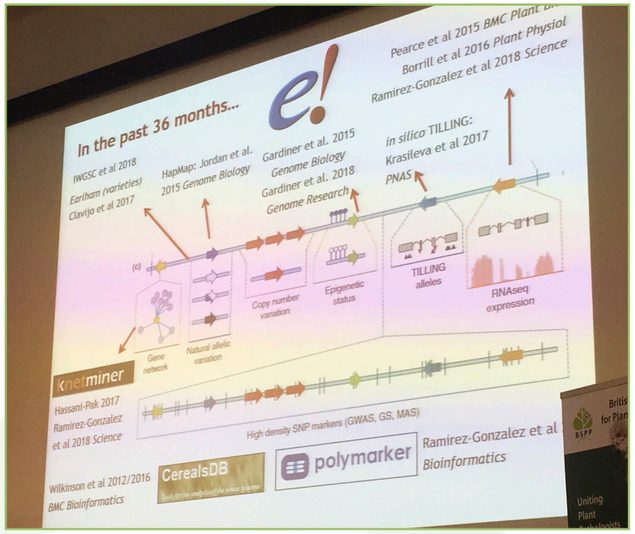
Dieback. He started his talk with an amended quote from Tolstoy's Anna Karenina that promoted the importance of model organisms and in particular Arabidopsis:

'….in getting to know thoroughly one's plant species, one gets to know all plant better than if one knew thousands of them….'.

Richard's talk was really enthusiastic and highlighted why he has been such an excellent advocate for ash dieback research in the UK and beyond.

Contrary to some thoughts, GARNet activities support more than just research in Arabidopsis and Session IV: Out of Arabidopsis highlighted the great UK research occurring in Wheat and Brassica. Cristobal Uauy (John Innes Centre) and colleagues in the global wheat community have produced a remarkable set of genomic, mutant and phenotyping resources. These new tools are now establishing wheat as a viable model to conduct both mutant studies and the type of cell and molecular biology analysis previously only possible in more accessible genetic models . Also working at the John Innes Centre, Rachel Wells is the project coordinator of the BBSRC-sponsored BRAVO project that aims to improve reliability, yield and quality in Brassica oilseed crops and includes a broad consortium of UK researchers .

George Bassel (University of Birmingham) chaired the final session that was broadly titled 'Novel methods in Cell Biology and Imaging' and also presented an exciting talk on his work that aims to quantify the factors that control interactions between cells and allow them to arrange into organs. The final plenary was provided by Minako Ueda who travelled from Nagoya for the meeting. Minako excitedly presented her outstanding live images of the events that occur during zygote formation and early embryogenesis. It was a fitting end to a



Cristobal Uauy

meeting that was characterised throughout by excellent science.

The approximately 80 delegates who attended the meeting included a majority of people from Northern universities; Leeds, York and Edinburgh. Very few delegates travelled from major plant science centres in the south of the UK. It is unclear whether the schedule was not of interest or whether researchers didn't want to venture too far north! However this geographic distribution of delegates does highlight the importance of GARNet arranging events all around the UK.

Following the meeting we circulated a survey to delegates. The majority of respondants very much enjoyed the meeting. However some aspects weren't perfect especially with the scheduling and arrangement of the second poster session.

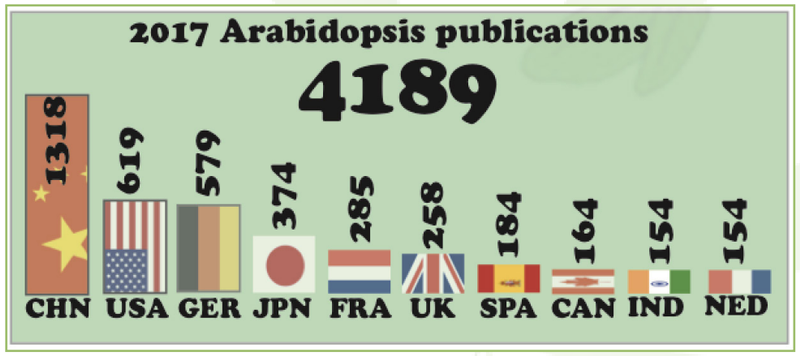
Thanks to SEB, British Society of Plant Pathology, the High Value Compounds from Plants Network and all our other sponsors for their support.

https://garnet2018.weebly.com/sponsors.html

30th Interanational Conference on Arabidopsis Research (ICAR2019)

June 16th-21st Wuhan China

Chinese researchers publish a lot of papers in which Arabidopsis is the primary organism of study. The 2018 MASC annual report showed that in 2017 Chinese researchers published 1318 papers, which was over double the number published by researchers in the USA.



This is the exciting backdrop for the 30th International Conference for Arabidopsis Research (ICAR) that will take place in Wuhan on June 16th-21st 2019.

The conference website went live last weekend:
http://icar2019.arabidopsisresearch.org/index.html

ICAR is the largest annual conference that focuses almost exclusively on discovery-led fundamental plant research. The only time ICAR has been held in China was for ICAR2007. This remains the highest ever attended ICAR with over 1400 delegates yet took place at a time when Chinese researchers published 'just' 248 papers, which was a 1/3 of the number published by US researchers.

At that time China was beginning its research relationship with fundamental plant science but in 2019 it will be very much the most productive nation. There is understandable excitement for ICAR2019 as it will undoubtedly be the most highly attended ICAR and will introduce excellent Chinese research to a global conference that is conducted in English.

The organisers have kept student early bird registration cheap at just $350. However be aware that this deadline is early in the year on February 1st. Abstract submission for an oral presentation is on March 1st. General registration ends on May 1st.

International attendees require a VISA to enter China so make sure you apply early to your home consulant. More information on this can be found here: http://icar2019.arabidopsisresearch.org/visa.html

To encourage UK PhD students to attend the meeting GARNet are administering a set of 4 £500 studentships. If you are interested in these awards please contact Geraint Parry geraint@garnetcommunity.org.uk

Botanical Microscopy 2019

14 - 18 April 2019, Oxford Brookes University, UK

Scientific Organising Committee:

Chris Hawes, Beatrice Satiat-Jeunemaitre, Verena Kriechbaumer, Katja Graumann, Louise Hughes & Imogen Sparkes

The 11th edition of the International Botanical Meeting will be held in the new lecture and conference facilities at Oxford Brookes University with accommodation in the famous Queen's College, Oxford.

The topics covered will include a mix of state-of-the art microscopy and the latest developments in plant cell biology, including organelle dynamics, nuclear structure and function, and autophagy.

Guest Lecturer

Prof. Niko Geldner, *Université de Lausanne*

Other Speakers include:

Prof. Patrick Hussey, *University of Durham*
Dr Célia Baroux, *University of Zurich*
Prof. Federica Brandizzi, *Michigan State University*
Prof. Emmanuelle Bayer, *Université Bordeaux Segalen*
Dr Diane Bassham, *Iowa State University*
Prof. Dr. Silke Robatzek, *LMU Biocenter University of Munich*

We look forward to welcoming you to the famous University City of Oxford.

www.rms.org.uk/botanical-meeting

GARNet

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