

3D RNA-seq App
Day RNA-seq analysis

**The Future of
RNA-seq Analysis?**

Making it accessible to ALL!

Welcome to the June 2019 Issue of GARNish



Renier van der Hoorn
University of Oxford
Member of GARNet Advisory Committee

Welcome to the June 2019 issue of GARNish, reporting on the latest news from across the UK plant sciences community. While we are waiting the final outcome on the evaluation of our application for an extension of GARNet by the BBSRC, there are several exciting developments to highlight. As new elected member of the management committee of GARNet, it is my honour to summarize these here.

In this issue of GARNish, we feature a very useful bioinformatics tool that will make our struggles with RNA sequencing so much easier. Our colleagues from the James Hutton Institute and University of Dundee present the '3D RNA-Seq App' that introduces a robust and standardized way to analyse RNAseq data of any model organism. Now you no longer need to do the tedious specialist bioinformatics before you look at the biology of your dataset. Very useful!

Concerning conferences, ICAR2019 in China was a great success, and our workshop on improving UK-China relationships was well attended and will benefit UK research now China is improving its ties with the UK, perhaps a consequence of the declined US-China relationship?

Please note that the UK will host ICAR2021 in Belfast, an exciting event to look forward to!

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Special thanks to: Jonathan Carruthers, Isabel Mendoza, John Brown, Runxuan Zhang, Wenbin Guo, Sophie Harrington, Hannah Rees, James Hartwell, the BBSRC grant holders and the FoPD organisers.

The Spotlight in this issue is on the University of Liverpool, where 14 research labs are active in plant science. The commitment of the University to support plant science is evident from the recent hire of additional PIs and the building of new plant growth facilities. Liverpool plant science is on the way up!

Please also note the analysis of Arabidopsis publications, extracted from MASC. Rice has just beaten Arabidopsis on the number of publications, but China is steadily increasing its efforts on Arabidopsis research, while other countries probably refocused their work more on translational science. These intuitive trends are clearly supported by publication statistics.

The GARNet Committee

Steven Spoel

University of Edinburgh
GARNet Chair.
Committee member Jan 2016–Dec 2019

Jim Murray

University of Cardiff
GARNet PI from February 2015

Yoselin Benitez-Alfonso

University of Leeds
Committee member Jan 2019–Dec 2021

Daniel Gibbs

University of Birmingham
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Murray Grant

University of Warwick
Committee member Jan 2017–Dec 2019

Jill Harrison

University of Bristol
Committee member Jan 2017–Dec 2019

Andrea Harper

University of York
Committee member Jan 2018–Dec 2020

Eirini Kaiserli

University of Glasgow
Committee member Jan 2019–Dec 2021

Sabina Leonelli

University of Exeter
Ex-officio member

Sean May

Nottingham Arabidopsis Stock Centre
Ex-officio member

Sarah McKim

James Hutton Institute, University of Dundee
Committee member Jan 2018–Dec 2020

Colin Turnbull

Imperial College
Committee member Jan 2018–Dec 2020

Renier Van der Hoorn

University of Oxford
Committee member Jan 2019–Dec 2021

Geraint Parry

Cardiff University
GARNet Coordinator

We also include an important update from UKRI-BBSRC about transfer of responsive mode applications between panels. Finally we have the usual content on networks, projects, conference announcements, outreach events and a very useful evaluation of the future of genome editing after the 2018 ruling by the European Court of Justice.

I trust you will enjoy the reading.

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.

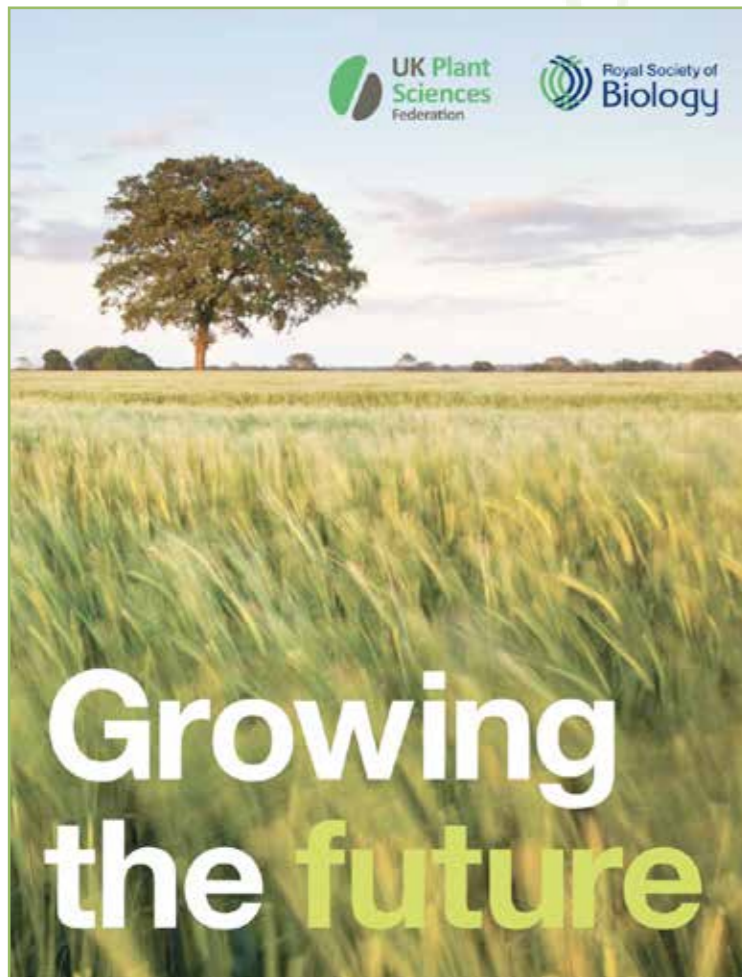
UK Plant Sciences Federation Update



Jonathan Carruthers
Royal Society of Biology

jonathan.carruthers@rsb.org.uk

The UKPSF launched its report on the future of UK plant science, 'Growing the future', in January 2019, with a breakfast meeting in the Houses of Parliament attended by MPs, Peers and around 60 members of the plant science community. The launch featured talks from Stephen Metcalfe MP, Professor Rick Mumford (outgoing UKPSF Committee chair), Professor Dale Sanders (Director, John Innes Centre) and Dr Belinda Clarke (Director, Agri-Tech East). The report is available to download at www.rsb.org.uk/growingthefuture



Professor Rick Mumford stepped down as chair of UKPSF at the end of 2018, and we thank him for his tireless work. As its new chair, the UKPSF is pleased to welcome Dr Geraint Parry. The UKPSF will host a session on careers in plant science at the RSB's Bioscience Careers Day in October 2019. The event will feature a panel comprised of people in a variety of roles in plant science, demonstrating to undergraduates the range of careers with plants.

The UKPSF's Plant Health Undergraduate Studentships programme returned this year, thanks to funding from Defra, BSPP, N8 AgriFood and the David Colegrave Foundation. Once again, nine students will have funded 10-week placements working on exciting plant health research projects with scientists around the UK. Competition for places was strong, with 198 applications submitted for the nine places.

Global Plant Council Update

Isabel Mendoza
GPC Outreach and Communications Manager
isabel@globalplantcouncil.org

This has been an exciting period for Global Plant Council! To begin with, 3 new members have joined:

- IRRI: The International Rice Research Institute (IRRI), the world's premier research organization dedicated to reducing poverty and hunger through rice science
- HeDWIC: The Heat and Drought Wheat Improvement Consortium (HeDWIC) network that facilitates global coordination of wheat research.
- MASC: The Multinational Arabidopsis Steering Committee (MASC) . composed of representatives from each country with major efforts in Arabidopsis research or coalition of countries with smaller programs.

The Global Plant Council has continued its strategy of publishing plant science news on a daily basis either in its website or blog, however rising the effort on its social strategy by increasing the posting rhythm in the established networks (Twitter, Facebook and LinkedIn) and by opening new communication channels such as the Instagram account to reach the youngest in the plant science community.

Finally, at Global Plant Council we are proud to announce that we have put in motion the Early Career Researcher International Network (ECRi). As you all well know, the early-career period is one of the most stressful stages for a researcher. The idea behind the network is based on helping ECRs with 4 essential pillars:

- job hunting,
- grant funding
- dissemination of research results
- and networking.

The network is foreseen to be a set of activities specifically address to ECRs. As for 2019, four activities have been already launched:

1. The already traditional monthly **#plantscijobs** "storm" on Twitter. During one-hour, we tweet multiple job offers from the Global Plant Council principal Twitter account with the hashtag **#plantscijobs**. Next Twitterstorm is schedule for **26th July, between 3-4 pm CEST**.
2. A Facebook group, linked to the Global Plant Council Facebook page, has been created, in order to post resources related to plant science. Those posts are posted regularly, with the hashtags **#plantscijobs**, **#plantscigrants**, **#plantsciprizes**, **#plantscinternships**. Please, consider joining the almost 800 members there.
3. In collaboration with Geraint Parry (GARNet) and Mary Williams (ASPB) we organized and hosted a science communication workshop in Wuhan (China) in the frame of the

ICAR2019 conference held there. 45 ECRs joined us to learn on how to prepare press releases and blog posts about their research and reasons to be AND be active on social media. We will publish a brief summary on our participation in ICAR2019 on our blog soon.



4. Finally, and in order to facilitate networking among the ECR, Global Plant Council will intensify its use of Plantae, as you know, a plantsci social platform powered by ASPB that Global Plant Council helped to set up. Additionally, we have set up a mailing list where ECRs can sign-in here.

Please consider contacting Barry Pogson (barry.pogson@anu.edu.au), Chair of the GPC and Isabel Mendoza (isabel@globalplantcouncil.org), Communications Officer with suggestions on ECRi.

Any offers of help in rolling out this network will be greatly appreciated!



Science Communicators at Wuhan for ICAR2019. Geraint Parry, Isabel Mendoza and Mary Williams

Plant, Cell and Environment 40th Anniversary Symposium:

Plant responses to environmental stimuli: differences, similarities and crosstalk

4th - 6th September, 2019,

Glasgow, Scotland, UK

This conference offers a holistic view on how plants respond to the environment and provides delegates with an opportunity to appreciate the wider context of their research. Marking the 40th anniversary of Plant, Cell & Environment the symposium will be a celebration of plant physiology. We offer delegates an impressive line-up of speakers and tutors who will share with you their research and expertise at the forefront of modern plant physiology.

The aim is not only to introduce a new generation of plant scientists to the breadth and importance of modern plant physiology but also to motivate scientists with a more molecular focus to embrace plant physiological techniques and embed their findings into a physiological context. Several workshops will allow participants to explore essential physiological techniques (gas exchange measurements) as well as software for

phenotyping (root system architecture) and modelling (guard cell models). Our tutors are experts in their fields and will be able to discuss your specific needs.

The training aspect of this symposium is

further enhanced by science writing workshops. These small-group sessions led by experienced editors will allow the participants to discuss how to best organise and present their research in a paper and improve writing skills.

To foster communications the delegate number will be limited to 100. Early registration is therefore recommended.

Organisers:

Anna Amtmann & Mike Blatt, Glasgow, UK

Supported by Wiley.

<https://www.wileypcsymposium.com/>

The 31st International Conference on Arabidopsis Research (ICAR2020)

University of Washington, Seattle:

Organized by the North American Arabidopsis Steering Committee (NAASC)

<http://icar2020.arabidopsisresearch.org/>

In response to community feedback we've gathered an External Advisory Board to discuss approaches to better meet the needs of plant science researchers and educators interested in a moderate sized conference such as ICAR, and that focuses on the resources, techniques, and fundamental research taking place in Arabidopsis labs and in other labs that depend on Arabidopsis knowledge and resources.

We consistently heard that attendees prioritize the chance to present their work, especially in a talk; that most want greater

diversity in the invited speakers list and in conference session topics. Therefore we anticipate a highly engaging and more diverse program in Seattle next summer.

We're now accepting proposals for community-proposed and organized mini-symposia that we expect will encompass about half the program. We especially encourage students and postdocs to make suggestions for different sessions. Deadline to apply to organize and invite speakers for a community-proposed ICAR 2020 symposium is **31 July 2019**

<https://www.surveymonkey.com/r/5ZHMYMYS>

Twitter: #ICAR2020 @ICAR_2020

The 32nd International Conference on Arabidopsis Research (ICAR2021)

International Conference Centre,
Belfast

Organized by GARNet

<http://icar2021.arabidopsisresearch.org/>

GARNet are absolutely delighted to bring the International Conference on Arabidopsis Research (ICAR) back to the UK for the first time since 2009. This meeting embraces the remarkable contribution that Arabidopsis has made to our understanding of plant science.

Information about the past 30 years of ICAR meetings can be found at website for the Multinational Arabidopsis Steering Committee (MASC).

<http://arabidopsisresearch.org/>



ICAR2021 takes place at the International Conference Centre in Belfast, Northern Ireland between 21st-25th 2021

Belfast lies within the beautiful country of Northern Ireland that was used as the backdrop for the Game of Thrones TV show.

**COME FOR THE SCIENCE
STAY FOR THE STORIES**

Twitter: #ICAR2021 @ICAR_2021

13th International Congress on Plant Molecular Biology

Cairns, Queensland, Australia -
Sunday 24 - Thursday 28 October 2021

IPMB is a triennial meeting and this is the 13th International Congress on Plant Molecular Biology.

Join what will be over 1,000 of the world's best scientists who will discuss the cutting-edge research being done to understand plant growth and development

<http://ipmb2021.org/>



 3D RNA-seq analysis - a powerful and flexible tool for rapid and accurate differential expression analysis of RNA-seq experiments for biologists

Wenbin Guo, Runxuan Zhang and John Brown

James Hutton Institute and University of Dundee.

3D RNA-seq was developed by a team of molecular and computational biologists at the University of Dundee and the James Hutton Institute. It has been designed for biologists with minimal bioinformatics experience and its ease-of-use lets lab scientists take control of the differential expression and enhanced alternative splicing analysis of their RNA-seq data and generate results themselves. It is available at: <https://ics.hutton.ac.uk/3drnaseq>

Preprint details at: <https://www.biorxiv.org/content/10.1101/656686v1>

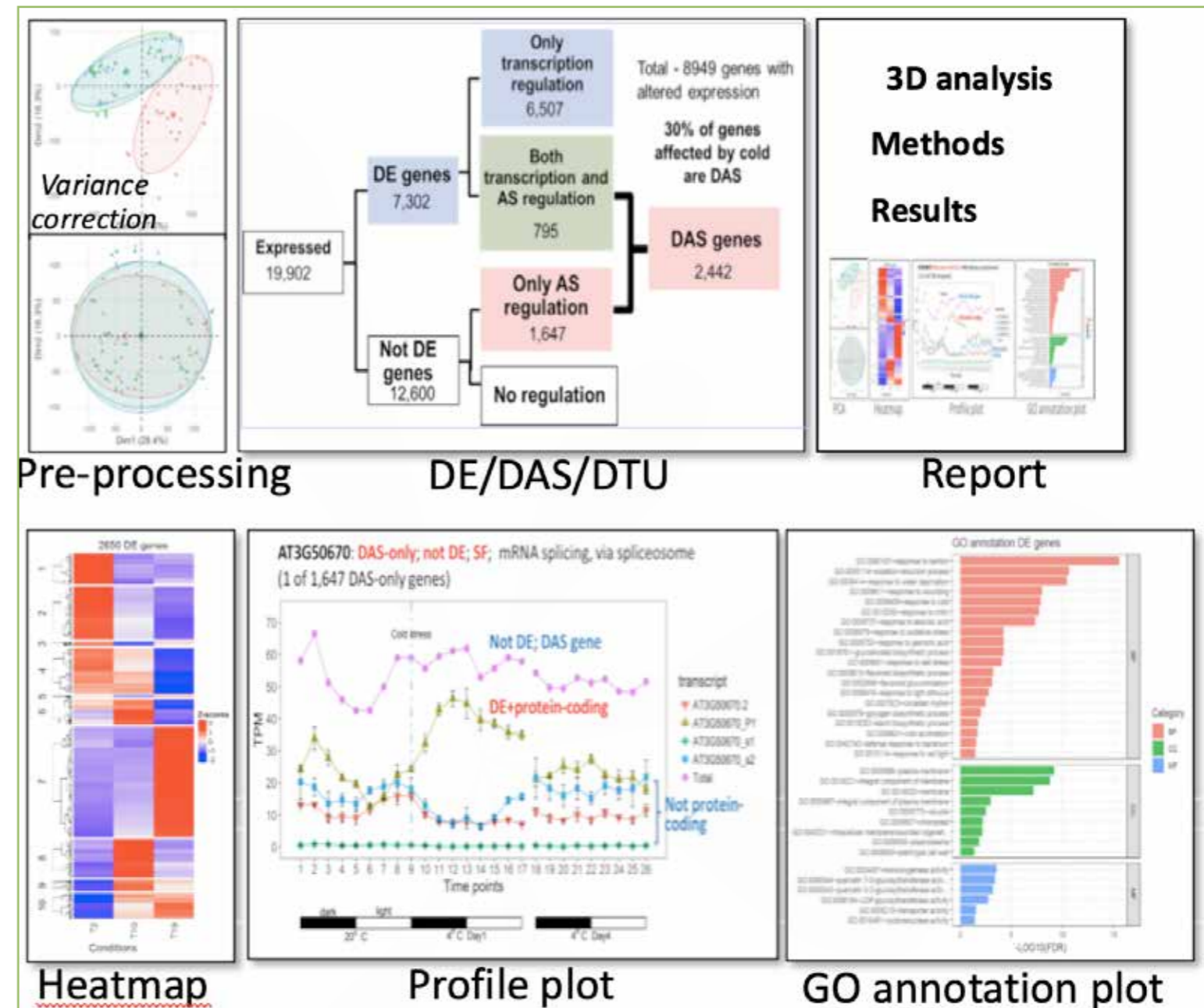
RNA-sequencing (RNA-seq) is the method of choice to analyse changes in gene expression. It is often a source of frustration for experimental biologists for three main reasons.

Firstly, once the RNA-seq read data is obtained, the differential expression analysis of the data is often a bottleneck taking many weeks or months to deliver. Most biologists have to rely on the skills of usually over-stretched bioinformaticians to process large datasets and apply complex analytical programs to experimental data.

Secondly, many RNA-seq differential analysis programs are limited to relatively simple comparisons such as pairwise comparisons between different cell-types, treatment versus control, wild-type versus mutant. They do not have the flexibility to handle complex experimental designs such as time-course or developmental series data and are error prone. There are currently a range of tools or pipelines to analyse RNA-seq and results can be inconsistent as different bioinformaticians may use different combinations of programs and parameters.

Thirdly, despite the ever-increasing appreciation that alternative splicing (AS) is an important level of post-transcriptional regulation, most RNA-seq analyses still focus on the gene expression level thereby losing important information. RNA-seq data, however, contains information that allows the quantification of expression of individual genes and transcripts and the detection of alternative splicing. New programs such as Salmon and Kallisto quantify transcript and gene level expression accurately and rapidly making thorough analysis, allows transcript level analyses to be both feasible and routine.

For Arabidopsis scientists, using AtRTD2 as transcript reference provides improved quantification of your transcripts with Salmon or Kallisto. Our motivation for 3D RNA-seq was to develop an RNA-seq analysis program designed for biologists which is easy to use, rapid, accurate and flexible. Although developed using Arabidopsis data, 3D RNA-seq can be used for analysis of RNA-seq data from any organism. 3D RNA-seq is an interactive web application tool for RNA-seq analysis implemented using



the R Shiny App. It is available as a web service and an R package (<https://github.com/wyguo/ThreeDRNaseq>).

It is hosted at the James Hutton Institute and can be accessed at: <https://ics.hutton.ac.uk/3drnaseq>

The program carries out differential expression (DE) analysis of genes and transcripts, differential alternative splicing (DAS) and isoform

switch (IS) analysis and differential transcript usage (DTU) for RNA-seq data. Isoform switches are where different transcripts from the same gene (isoforms) change their relative abundance in different conditions. DTU transcripts are those whose expression behaviour is significantly different from other transcripts of the same gene and thereby are significantly affected by AS regulation. There are five main advantages of 3D RNA-seq: **1)** accessibility, ease-of-use, extensive visualization and flexibility allows experimental

biologists to control the analysis of their own data, **2)** acceleration of RNA-seq analyses, **3)** ability to handle complex experimental designs, **4)** transcript level analysis for accurate differential expression and differential alternative splicing, and **5)** the potential to provide an analysis platform to bring consistency in RNA-seq analysis.

3D RNA-seq integrates state-of-the-art differential analysis tools and adopts current best practice. The program provides an easy-to-use graphical interface and manual to take users through the analysis. It can handle complex experimental designs and pre-processes the data to reduce technical variances. The program sets up statistical models allowing the user to specify experimental factors, comparisons (contrast groups) and parameters. It provides visualisations of intermediate and final results through graphics and tables, and generates publication quality figures of expression: volcano plots, heat-maps, expression profiles, isoform switches etc.

A final customized analysis report will be generated including all the parameters, method descriptions, tables, figures and references using R Markdown. It can be used to analyse RNA-seq data from any organism. Finally, in a typical analysis, transcript quantification takes up to two days, and the differential expression analysis and report generation using 3D RNA-seq takes a couple of hours (3-Day RNA-seq).

The impact of 3D RNA-seq is to allow biologists to analyse their own RNA-seq data quickly and accurately. It will save significant research time and cost not only of biologists but also of bioinformaticians. The acceleration of RNA-seq analysis with 3D RNA-seq potentially

reduces the time needed for a complete RNA-seq experiment to 3-4 months (generate RNA-seq data in 4-6 weeks, full DE/DAS analysis in 3 days, interpret the results in another 4-6 weeks) to allow multiple consecutive RNA-seq experiments to be conducted in a year or in the duration of a research project.

This speed of analysis will revolutionise what is achievable with RNA-seq technology.

“3D RNA-seq” was developed by Wenbin Guo with input and support from Cristiane Calixto, Nikoleta Tzioutziou, Gordon Stephen, Iain Milne, Robbie Waugh, John Brown and Runxuan Zhang of Plant Sciences, University of Dundee and the Information and Computer Sciences and Cell and Molecular Sciences groups at the James Hutton Institute.

It was supported by BBSRC funding. Wenbin Guo won the Best Innovation Award in the University of Dundee, School of Life Sciences Innovator of the Year competition (2018-2019) for 3D RNA-seq.

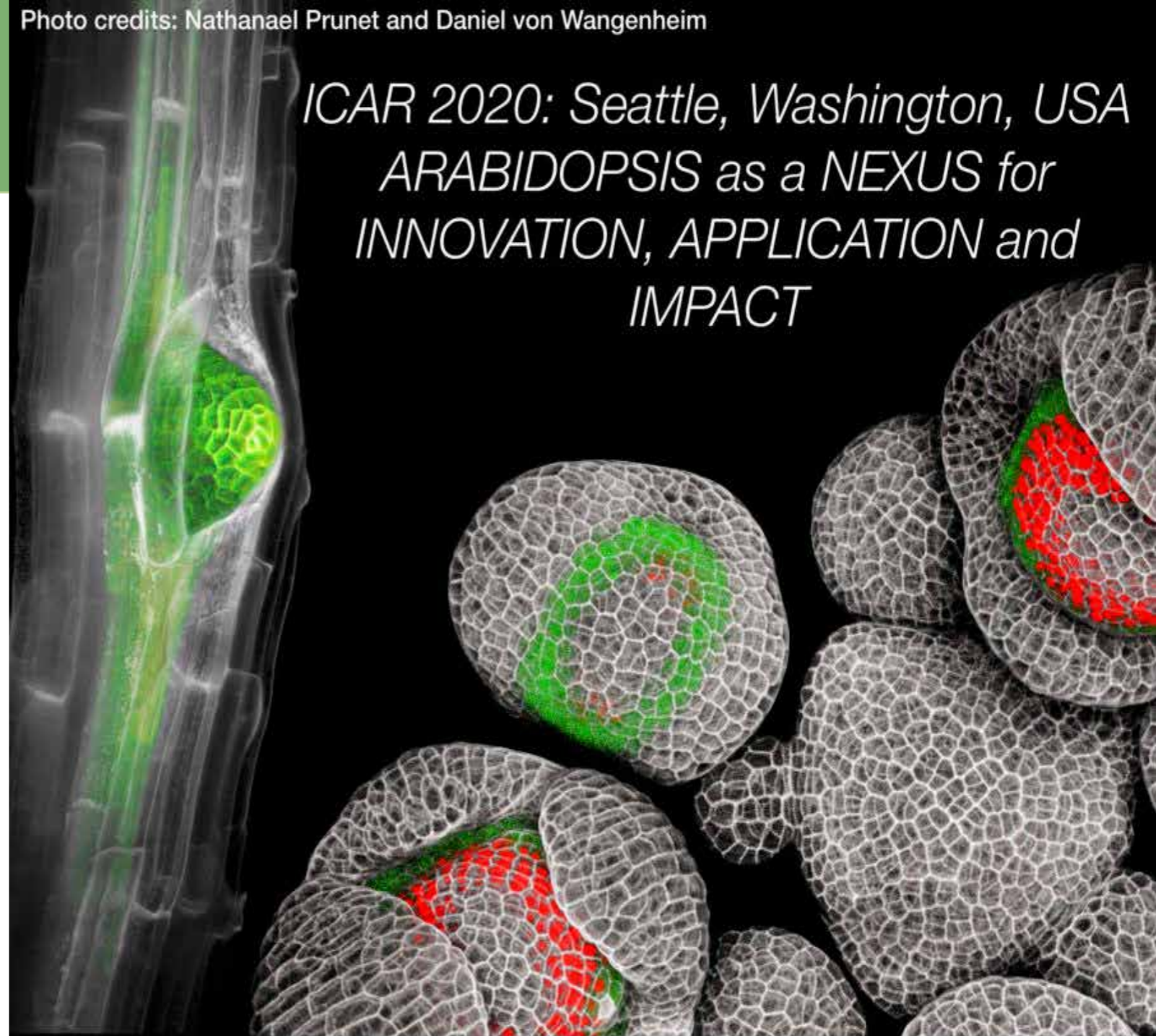
GARNet and the-3D RNA-Seq team will be organising a workshop to support new users in order to learn about the features and accessibility of this app.

This will take place on Oct 24th-25th 2019 at the University of Leeds.

Please look out for further details through all the usual GARNet channels:
www.garnetcommunity.org.uk
blog.garnetcommunity.org.uk
[@GARNetweets](https://twitter.com/GARNetweets)

ICAR 2020: Seattle, Washington, USA

ARABIDOPSIS as a NEXUS for INNOVATION, APPLICATION and IMPACT



The 31st International Conference on Arabidopsis Research

July 6th - 10th, 2020

University of Washington, Seattle

For the next ICAR the North American Arabidopsis Steering Committee (NAASC) wants your input on:

Session themes

Speakers

Broader impacts

Childcare

Inclusivity

Survey website:

<http://icar2020.arabidopsisresearch.org/>



We are soliciting proposals for concurrent session organizers. If your proposal is selected, you will have the opportunity to organize your own mini symposium on the topic of your choice, and select the session speakers for short talks. Timely research topics and proposals by early career scientists are particularly encouraged. Submit by July 31st, 2019 for full consideration.

Monogram Annual Meeting: The small grain cereal and grasses network

Sophie Harrington
John Innes Centre

This year I attended the UK Monogram conference for the third and final time in my PhD. It was a pleasure to have another opportunity to engage with the UK small grains community, both with the academics and the breeding companies that attend.

The conference opened with a brilliant plenary talk by Professor Keith Edwards from the University of Bristol, sharing his thoughts on the origin of variation within *Triticum aestivum*, hexaploid bread wheat. His talk highlighted the continuation of hybridisation between hexaploid wheat and its tetraploid parents as a result of mixed cultivation. The impacts of this hybridisation can still be seen in the genomes of hexaploid wheat varieties today.

This theme of natural genetic variation continued to thread throughout the conference, with the importance of tapping into the diversity present in landraces and wild wheats highlighted during a panel discussion session on the second day. A particularly intriguing example of variation in the grasses was discussed by Dr. Luke Dunning, when he spoke about the evidence for lateral gene transfer in the grasses. This was quite a different method for obtaining variation in grasses compared to what had previously been discussed in the conference and naturally the resounding question in the audience following his talk was how exactly such lateral gene transfer could occur! I'm sure many people are looking forward to hearing what comes out of this story in the future.

Monogram this year also had a substantial focus on methods and platforms that we can use to increase the quality and utility of our data. From the very first session, exploring the bioinformatics tools available for the cereals, it was clear that within the past few years a substantial leap in the quality and quantity of informatics tools available for wheat and barley has occurred. It

was thrilling to hear of the large new datasets available for the public, from the wheat transcriptome through to the so-called barley "variome." Moving beyond bioinformatics, we were also exposed to the potential of using machine learning in our research, as Dr. Laura-Jayne Gardiner from IBM Research highlighted the many biological and agricultural projects in which IBM has successfully applied machine learning technology. This seems to be an area that has



Sophie Harrington giving her MECEA award talk. From [@malcolmacaulay](#)

substantial potential to tap into the hidden value of the large datasets being developed particularly in cereal genomics.

Of course, without studying the plants themselves it can be difficult (if not impossible) to turn genomic data into biologically relevant information. To that end, the discussion of new phenotyping platforms and consortiums, such as the EU-funded EMPHASIS project, highlighted new ways to increase the throughput and fidelity of phenotyping data.

The importance of establishing a framework for data labelling and curation was also highlighted.

Overall, the 2019 Monogram conference was an excellent opportunity to hear about the cutting-edge research in cereals taking place in the UK and abroad. I was thrilled to have the opportunity to attend with a GARNet travel bursary, and to receive the Monogram Early Career Award for a PhD researcher. I'm already looking forward to next year!

Annual meeting of the UK Rice Research Consortium

Geraint Parry, GARNet Coordinator

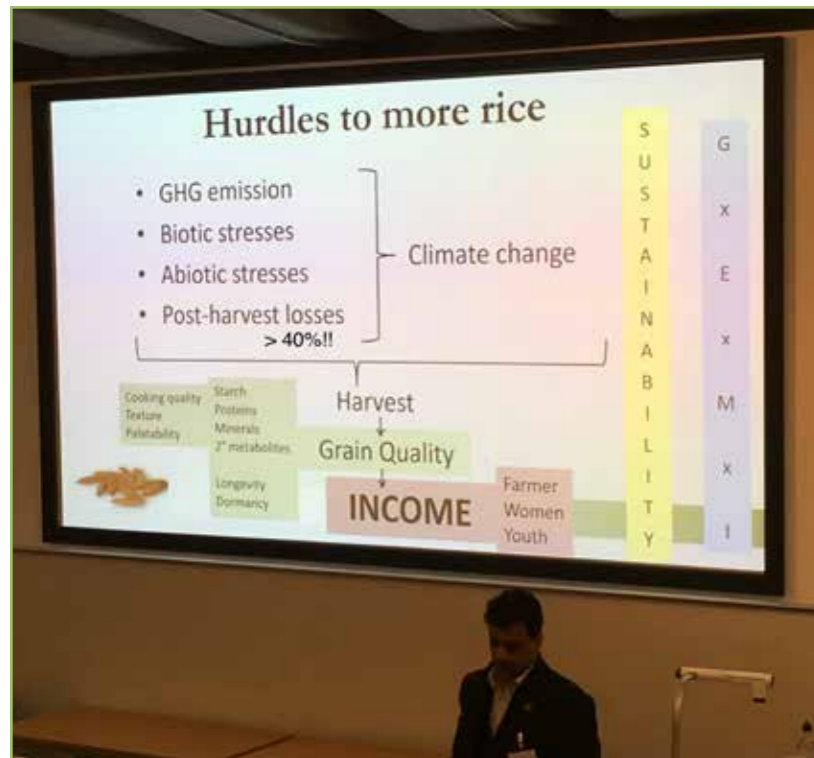
A small group of researchers is actively looking to build the UK Rice Research community so over the past two years the UKRI-BBSRC has supported a two-day meeting aimed at community-building and exploring the potential for resource development in the UK within this research area.



This years UK Rice Research Consortium meeting was held at the end of Monogram2019 at the University of Nottingham. This arrangement was successful in persuading the group of PIs to stay on and contribute to this community-building exercise. The meeting was led by Ari Sadanandom from Durham University and Erik Murchie at the host institution.

There is a surprising high amount of rice-focused research already happening in the UK. This ranges from the large groupings in (perhaps surprisingly) Aberdeen, Sheffield and NIAB through to smaller individuals pockets around the country. The UK Rice Research Consortium website (<http://ukrrc.org/>) is managed by Andy Jones at the University of Liverpool and is becoming a growing repository of information about UK-focused activities.

Arguably the biggest road-block to building this community is that rice cannot be grown in the field in the UK (at least not before significant climate change :/) and is therefore not a significant contributor to UK agriculture. However throughout the meeting it was clear that all attendees considered that the main internationally recognised strength of UK Rice research is in answering fundamental questions in plant biology. This strength will be key in the development of new varieties in collaboration with overseas institutions who have the capacity to undertake large field trials.



Ajay Kohli highlights a holistic approach to rice research

The meeting was split into two main phases: Firstly a set of speakers gave a global perspective on the current status of rice research. Rod Wing from the University of Arizona outlined his collaborations that have recently sequenced 3010 diverse accession of rice. This highlights that the diploid *Oryza sativa* genome (430Mb) is a more manageable size when compared to bread wheat (14.5Gb)! However even with the enormous amount of genome information the impression that came across from the meeting was that there currently a lack of joined-up thinking when it comes to the provision of genomic resources that will bring together this vast amount of information. With some planning the UK rice research community should be able to take an international leadership role in the development of online rice resources.

A notably international talk was from Ajay Kohli at the International Rice Research Institute (IRRI) who highlighted that 'everyone wants rice' and the importance of including

social considerations in any global strategies to advance the sustainability of more efficient rice varieties that can be used by small holders across Asia. Kohli proposed that the UK community can link with IRRI by contributing both upstream (by developing fundamental knowledge) and downstream (by providing mechanistic understanding for newly bred varieties) discoveries.

In the second phase of the meeting, Sadanandom and Murchie led a series of group discussions that had the aim of developing a roadmap for UK rice research. Overall the strengths of UK rice research are in fundamental areas of discovery, in the excellence of genomic resources, within a collaborative outlook to research and in community-facing transformation resources. The challenges include the actual growth of the plant and therefore in persuading funders of the importance of supporting something that is not currently a large portion of the UK research portfolio. Clearly there is potential for interactions between local and international agri-tech companies and the UK research community; both in the support of studentships or in providing space for downstream field trials.

Overall this second UK Rice Consortium meeting was an extremely positive experience and there is significant motivation to grow the community. Importantly UK researchers already have major overseas collaborators that support their research and the production of a 'Rice Roadmap' will define the future direction of the community.

Watch out for updates on the Consortium website and on social media at [#UKRiceResearch](#) and [@ukrrc](#). The 2020 meeting will be hosted at Rothamsted Research.

Annual meeting of the UK Brassica Research Community

Geraint Parry, GARNet Coordinator

One thing clear from the UK Brassica Research Community (UKBRC) annual meeting is that this group is greater than the sum of its parts.

Research into a variety of Brassica species is conducted at a small number of UK institutions but the integration of that research enables much greater impact. In particular this is exemplified by four collaborative programs that have been run over the past decade.

Firstly the DEFRA-funded Vegetable Genetic Improvement Network (VeGIN). This is led by the University of Warwick, where they maintain germplasm from a range of species whilst developing industrial collaborations to improve market delivery.

<https://warwick.ac.uk/fac/sci/lifesci/research/vegin/>

At this UKBRC meeting Graham Teakle from Warwick introduced a new project that is hoping to identify germplasm that is resistant to clubroot (<https://en.wikipedia.org/wiki/Clubroot>). This is a challenging prospect since it appears that this resistance isn't commonly found amongst UK germplasm.

Ian Bancroft from the University of York introduces two other Brassica projects that he leads. Firstly the OReGIN project plays a similar role to VeGIN but focused on Oilseed Rape (OSR). <http://oregin.info/>

As well as supporting the activities of the UKBRC, phase 5 of this OReGIN funding is now conducting field trials to

test promising varieties that have been identified by this and other projects. One such associated project is the BBSRC-funded sLOLA entitled 'Renewable Industrial Products from Rapeseed (RIPR)'. Although RIPR ends in 2019 they remain busy generating an OSR TILLING population generated by radiation mutagenesis.

<https://gtr.ukri.org/projects?ref=BB%2FL002124%2F1>

The Brassica Rapeseed and Vegetable Optimisation (BRAVO) project is also a BBSRC sLOLA that is managed by Dr Rachel Wells at the John Innes Centre.

<https://www.jic.ac.uk/research-impact/genes-in-the-environment/impact/brassica/>

It was extremely interesting to hear an update from this project now that is into its third year. Rachel outlined the extensive phenotyping and transcriptomic analysis that has been conducted across four sites as part of workgroup activities (JIC, Rothamsted, Nottingham, Aberystwyth). This information will be fed into the Associative Transcriptomics pipeline at York to reveal areas of interest across OSR and *Brassica Oleracea* genomes. In addition this information will populate a new Brassica expression browser



Early results from **Tom Bennett's** field trial

(Oilseed rape developmental expression resource- ORDER) that will be launched over coming months. BRAVO are also hoping to develop an eFP browser to visualise this data. BRAVO indeed!!

The UKBRC annual meeting is characterised throughout by a series of short 5 minute talks irrespective of whether the presenter is a PhD student, postdoc or PI (although it is the PIs who most often overrun their time :). These talks include a range of broad topics expanding on projects aimed at altering metabolic profiles, tackling disease resistance or improving yields.

Tom Bennett from the University of Leeds introduced his lab's work that had looked at the impact of pot size on the yield of OSR. They use pot size as a proxy for root crowding and this initially lab-based project (available at [biorxiv.org/content/10.1101/539726v1](https://doi.org/10.1101/539726v1)) has moved to the field where they are looking at the effect of cross-drilling to reduce root crowding and hopefully improve yield. The early results look promising.....

Something completely different came from Pat Heslop-Harrison from the University of Leicester, who introduced a set of cytogenetic tools that his lab has developed to look at chromosome organisation in Brassicas <https://molcyt.org/>

Back to the field and Sarah Kendall provided an interesting update on her work at ADAS with the Yield Enhancement Networks (YEN). <http://www.yen.adas.co.uk/>

These are a set of programs that work with farmers to encourage innovative ideas for yield improvement.



Mikhaela Neequaye introduces her field trial

They run a competition that is 'handicapped' to take into account local environmental conditions so that farmers compete on an equal playing field, so to speak. Seemingly this has proved very successful where several farmers have achieved yields close to the ADAS-assigned yield potentials.

It was gratifying to learn that a couple of speakers (Mikhaela Neequaye at the Quadram Institute and Henrik Stotz at the University of Hertfordshire) are successfully taking advantage of the BRAC resource at the JIC. This resource generates gene edited B.Oleracea and Mikhaela, who is looking to reduce glucopharin levels, is already testing her plants in field trials in Norwich. <https://www.jic.ac.uk/research-impact/technology-platforms/genomic-services/crop-transformation/>.

The UK Brassica community may be small but it is extremely friendly and the level of collaboration aimed at developing new germplasm resources and online analysis tools enables progress that is far beyond what would be possible by individual labs working alone.

Update from the BBSRC

Transfer of Responsive Mode Proposals

Our last GARNet meeting in Birmingham in June included a summary from UKRI-BBSRC about the responsive mode proposals transferred between BBSRC panels A, B, C and D. These transfers are a frequent frustration to applicants when submitting a proposal targeted to a specific committee for evaluation.

However, the numbers from UKRI-BBSRC are clear: transfers between committees are uncommon (<7.5% over the past 5 rounds) and committee B (Plants, microbes, food and sustainability) is actually involved with fewer transfers (moved from and received) than the other committees.

The representative from the UKRI-BBSRC explained that transfers only occur when the composition of a different panel is more appropriate to the submitted proposal.

Importantly UKRI-BBSRC has committed that any potential transfer will be discussed with the lead PI, allowing them to remove the proposal from consideration if required.

Responsive Mode Update

For whom the bell tolls: Linking protease degradomes with the proteasome through the N-end rule pathway to understand biological function.

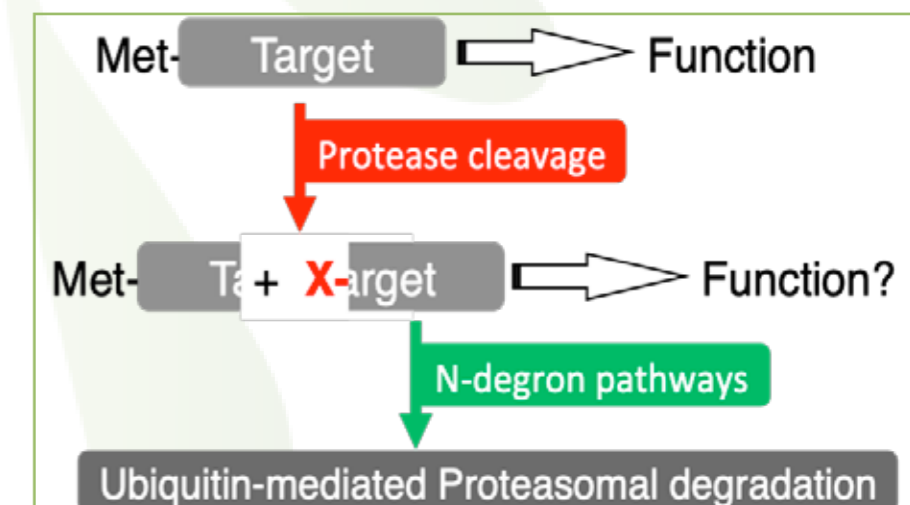
Michael Holdsworth, Rumiana Ray, Jorge Vicente:
University of Nottingham.

Kris Gevaert, Frank van Breusegem;
VIB, Gent

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Intracellular proteases cleave protein substrates to reveal polypeptide fragments. What are those fragments, do they have novel activities, and how does the cell regulate their stability? These questions are the focus of this proposal.

Endo-peptidase proteases catalyse cleavage of protein substrates that results in diverse effects



Holdsworth: Methionine (Met) is the first amino-acid of proteins after cytoplasmic translation, but protease action on 'target' proteins will result in a new Nt-residue (X). Under the right circumstances almost all revealed Nt-residues can be 'destabilising', i.e. These residues are recognised by N-degron pathways, and in animal systems have been shown to target products of proteases for ubiquitin-mediated destruction.

on function, stability and cellular location. One obvious and key effect of protease action is the general regulation of proteostasis (the total cellular protein content and turnover). The N-end rule (now N-degron) pathways represent an ancient conserved component of the Ubiquitin Proteasome System (UPS), that also has profound effects on proteostasis. N-degron pathways relate the identity of the amino terminal (Nt-) residue of a protein to its destruction by the UPS.

Although plant genomes encode large numbers of proteases (over 700 in Arabidopsis) very few substrates have been identified. In the study of the N-degron pathways, still very few substrates, and even fewer proteases that give rise to N-terminal destabilising residues have been identified. Therefore, key questions of these two fields represent two sides of the same coin. New proteomics techniques pioneered by collaborators at the VIB are revealing the landscape of protease degradomes (fragments generated from protein substrates following protease action) that provides a treasure trove of information about potential N-degron pathway substrates, as protease degradomes include the identity of the Nt-residue of cleaved products.

With the work described in this proposal we will use N-terminomics datasets derived from analysis of plant proteases and N-degron pathway mutants to identify N-degron pathway substrates. We will study how both protease and N-degron pathway activities modulate substrate stability, and the effects that this has on plant growth and development, and interactions with the environment. The project will greatly increase understanding of the roles of proteases and N-degron pathways in regulating the fate of protease substrates as part of cellular proteostasis. for the existence of alternative mechanisms by which hormones regulate plant growth and development.

Plastid terminal oxidase - a route to improving food security

Giles Johnson,
University of Manchester

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For plants, light is essential in providing energy for growth. Excess light, however, above that which can be used for photosynthesis, can damage the leaf. The excess energy absorbed drives production of reactive oxygen species (ROS) causing both localised damage to the chloroplast (photoinhibition) and more widespread harmful reactions throughout the cell. When plants are exposed to other forms of stress, such as drought, extreme temperatures or salinity, they have an increased vulnerability light stress. Plants possess an array of mechanisms to protect themselves from excess light.

One protective pathway, which was only relatively recently described, involves the plastid terminal oxidase (Ptox). Ptox was first identified in mutants of Arabidopsis (IMMUTANS) and tomato (ghost) exhibiting white sectors on their leaves (see Nawrocki *et al.*, 2015; Johnson and Stepien, 2016 for reviews). Ptox has since been shown to be a plastoquinone oxygen oxidoreductase, a diiron non heme protein showing homology to the mitochondrial alternative oxidase.

Ptox was recognised to have the potential to act as a “safety valve” for the photosynthetic electron transport chain, diverting electrons away from Photosystem II, preventing ROS production. However, in plants such as Arabidopsis, the protein is only normally present in very low concentrations, with barely detectable activity. Furthermore, attempts at overexpressing the protein not only did not induce significant activity,

they actually resulted in plants with increased susceptibility to oxidative damage.

Evidence for significant activity of Ptox has though been found in a small number of extremophile plants, including the alpine species *Ranunculus glacialis* (Streb *et al.*, 2005) and the model salt tolerant brassica, *Eutrema salsugineum* (Stepien and Johnson, 2009) It is work on the latter species that forms the basis of a BBSRC-funded project (BB/S009078/1) starting at the University of Manchester.

In plants of *Eutrema* grown under optimal conditions, only very low levels of Ptox activity can be detected, however, in plants exposed to saline conditions, Ptox can account for up to 30% of total electron transport activity. Work by Stepien and Johnson (2018) demonstrated that overexpressing the known Ptox gene did not result in measurable activity, however, when over-expressing plants were exposed to salt, the activity increased faster and reached a higher level. This suggests that other activation steps, possibly involving other gene productions, are required for full activity of Ptox. Furthermore, activation of Ptox was seen to involve a relocalisation of the Ptox protein in the thylakoid membrane, from the stromal lamellae to the granal stacks, bringing it into close proximity with Photosystem II.

Work to understand the processes involved in relocalisation of Ptox will form the basis of this new grant. Approaches used will include examining gene expression, using proteomic analysis of different membrane fractions, tagging of Ptox and using microscopy to examine the relocalisation.



Johnson: Salt marshes represent an extreme environment for plant growth. Lessons learnt from halophytes such as *Eutrema salsugineum* may hold the key to increasing stress tolerance in crop plants

Work will be carried out by Dr Pablo Calzadilla, currently a post-doc at the Centre d'Etudes de Saclay, near Paris, under the supervision of Prof. Giles Johnson and Dr Patrick Gallois.

By identifying the co-factors needed for Ptox activity, we may be able to transfer that activity into stress-sensitive crop species, increasing their stress tolerance.

Johnson GN, Stepien P (2016) **Plastid Terminal Oxidase as a Route to Improving Plant Stress Tolerance: Known Knowns and Known Unknowns.** *Plant and Cell Physiology* 57: 1387-1396

Nawrocki WJ, Tourasse NJ, Taly A, Rappaport F, Wollman F-A (2015) **The Plastid Terminal Oxidase: Its Elusive Function Points to Multiple Contributions to Plastid Physiology.** *Annual Review of Plant Biology* 66: 49-74

Stepien P, Johnson GN (2009) **Contrasting responses of photosynthesis to salt stress in the glycophyte *Arabidopsis thaliana* and the halophyte *Thellungiella halophila*. Role of the plastid terminal oxidase as an alternative electron sink** *Plant Physiology* 149: 1154-1165

Stepien P, Johnson GN (2018) **Plastid terminal oxidase requires translocation to the grana stacks to act as a sink for electron transport.** *Proceedings of the National Academy of Sciences* 115: 9634-9639

Streb P, Josse EM, Gallouet E, Baptist F, Kuntz M, Cornic G (2005) **Evidence for alternative electron sinks to photosynthetic carbon assimilation in the high mountain plant species *Ranunculus glacialis*.** *Plant Cell and Environment* 28: 1123-1135

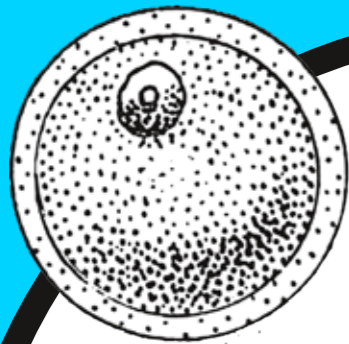
**IMPACT OF CHROMATIN DOMAINS
ON PLANT PHENOTYPES**

CELL AND PLANT SECTION SYMPOSIUM

9-11 DECEMBER 2019

REAL CENTRO UNIVERSITARIO ESCORIAL-MARIA
CRISTINA, EL ESCORIAL, MADRID, SPAIN

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ORGANISED BY

- MONICA PRADILLO (COMPLUTENSE UNIVERSITY OF MADRID, SPAIN)
- GERAINT PARRY (GARNET, CARDIFF UNIVERSITY, UK)
- ALINE PROBST (UNIVERSITÉ CLERMONT AUVERGNE, FRANCE)
- CHRISTOPHE TATOUT (UNIVERSITÉ CLERMONT AUVERGNE, FRANCE)

INVITED SPEAKERS

- ALES PECINKA (INSTITUTE OF EXPERIMENTAL BOTANY OF THE CZECH ACADEMY OF SCIENCES, CZECH REPUBLIC)
- ARP SCHNITTGER (UNIVERSITY OF HAMBURG, GERMANY)
- CÉLIA BAROUX (UNIVERSITY OF ZÜRICH, SWITZERLAND)
- CRISANTO GUTIERREZ (CBMSO, SPAIN)
- DARIUSZ PLEWCZYNSKI (UNIVERSITY OF WARSAW, POLAND)
- EIRINI KAESERLI (UNIVERSITY OF GLASGOW, UK)
- IRIS MEIER (OHIO STATE UNIVERSITY, USA)
- ISABEL BÄURLE (UNIVERSITÄT POTSDAM, GERMANY)

INVITED SPEAKERS CONT'D

- JIM MURRAY (CARDIFF UNIVERSITY, UK)
- MOUSSA BENHAMED (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE)
- NILS STEIN (IPK GATERSLEBEN, GERMANY)
- SILIN ZHONG (CHINESE UNIVERSITY OF HONG KONG, CHINA)
- STEVEN SPOEL (UNIVERSITY OF EDINBURGH, UK)
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- XUEHUA ZHONG (UNIVERSITY OF WISCONSIN-MADISON, USA)

IN COLLABORATION WITH



GARNish
FoPD2019

Fascination of Plant Day

The fifth international "Fascination of Plants Day" took place on May 18th 2019 organised under the umbrella of the European Plant Science Organisation (EPSO), coordinated by Carmel Edwards

The goal of the FoPD is to get as many people as possible around the world fascinated by plants and enthused about the importance of plant science for agriculture, in sustainability producing food, as well as for horticulture, forestry, and all of the non-food products such as paper, timber, chemicals, energy, and pharmaceuticals. There were 11 events 'official' events organised across the UK. Below are brief reports and photos from some of those events. No doubt lots of fun was had by all participants!



Oxford: Taking plants to the people

Public Engagement in the City Centre

Tegan Bennett, Oxford Botanic Garden

The Education Team have been training keen D.Phil. research students from the Department of Plant Sciences in the art of public engagement. To test all our learning we set up 'shop' at the Westgate Centre in Oxford to see if we could entice casual shoppers to engage with botany! The students showcased a short but punchy animation about their research into altering plants to make them more resistant to drought and salt stress. The Garden hooked younger visitors with some practical gardening and an investigation into the pigments in flowers; the Arboretum was represented by seeds collected by OBG's staff in Japan. All involved were pleasantly surprised by how open people were to finding out more about the research and activities of the University.

FoPD at Durham University Botanic Gardens and Dilston Physic Garden

Flora Hetherington, Durham University

We had 2 stalls arranged for the public, one was looking at root nodulation in clover and other legumes, and the other was learning about traditional medicinal plants with tea tasting and a quiz to test your senses.

Despite terrible weather reducing the number of visitors to the gardens we still had approx. 25 interested parties across a range of age groups, even including some interested teenagers(!) and some younger children. All of the visitors stayed and talked for a long time with



Durham: Plants need rain after all!

plenty of interesting conversation and positive feedback. There were also 5 visitors who signed up to take part in a 4 week 'Memory Test Study'. This trial is being conducted to test the effects of safe common plants that are reputed in history to improve our memory by Dilston Physic Garden, local medical herbalists Davina Hopkinson & Ross Menzies, Wesnes Cognition & Kew Royal Botanic Gardens, with support from Wesnes Cognition, Make My Day Better and The Ridley Family Charity.

In spite of the weather we had a great day with some fantastic interactions with the public. Those who volunteered to take part in the study will continue to engage with the research we are doing and participate directly in a research study. Many thanks to the Botanic Gardens for hosting and to all the volunteers and academics involved in running the event.



RGU in Aberdeen: Discussing the importance of plants

Collaborative Power of Plants Day

Morag McFadyen, Robert Gordon University

The Power of Plants event was held on Thursday, May 16th in the David Welch Winter Gardens Aberdeen. This collaborative workshop was run by Robert Gordon University School of Pharmacy and the Duthie Park Ranger Service.

This event enabled almost 60 pupils from two local schools to find out more about the power of plants! These pupils had the opportunity to take part in learning all about the science of extracting DNA from strawberries. While working with the Duthie Park Ranger Service, the pupils explored the David Welch Winter Gardens, discovering the variety of plants it holds, their uses and how they impact on our daily lives



The Lancaster team

Fascinating Plants and Where to Find Them

Cristina Sales, University of Lancaster

To celebrate the 5th year of FoPD, a diverse group celebrated at Lancaster Environment Centre, Lancaster University. This included three PhD students and nine staff who held the event in an open market at Lancaster city centre. Activities including "Find your Inner Plant", "Seed Race" and a "Live Plant Display" included diverse crops such as maize, cassava, cowpea, maize and soybean and attracted over 400 people of all ages! Participants were able to learn about how everyday products trace back to plants, what common food crops look like, and realise the importance of plants in everyone's lives!

The biggest challenge encountered was around the planning of many different activities, and how to find the best way to assess engagement. No doubt that in the end the event was a success and we will hopefully participate again in coming years!



Reading: Getting youngsters into lab coats!

Why are Plants Smelly?

Jonathan Mitchley, University of Reading

We invited local primary schools' groups to University of Reading to ask them why is it that some plants smell so nice and sweet while others are really quite grossly stinky?! We arranged a set of activities both in the laboratory and outside in the University of Reading's Harris Garden.

We examined the different ways in which plants try to attract pollinators while doing their best to repel others such as insect and microbes herbivores intent on eating or infecting them! All our school groups left looking at plants in a totally new way!



Reading: Inspiring the next generation of plant scientists

International
Conference on
Arabidopsis
Research (ICAR2019)



June 17th-21st

Eurasia Convention Centre Wuhan,
China Hynes Convention Centre, Boston

Hannah Rees
Earlham Institute

ICAR 2019: Exciting culture, interesting talks, enthusiastic speakers and the chance to meet researchers at the forefront of their science- what more could you ask for!

Myself and one other UK-based student (Gina Garzon from Aberystwyth) were granted a travel bursary from the Gatsby Foundation to go towards attending the ICAR conference this year in Wuhan, China. This has been a big conference leap for me; my first outside of Europe and the first I have been accepted to give a short talk.

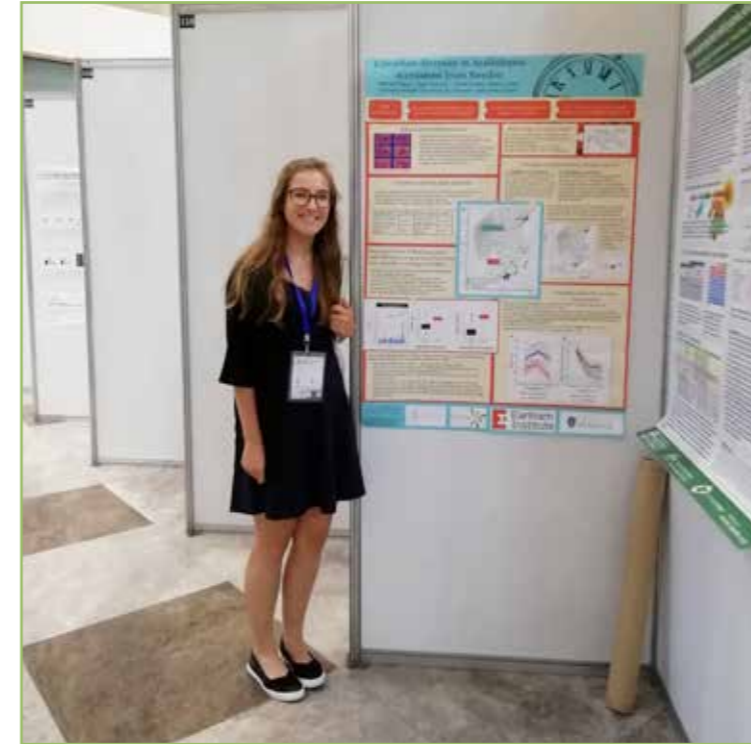


Zhihong Xu, President of School of Advanced Agricultural Science of Peking University kicks off the meeting.

Each day there were Plenary sessions followed by smaller concurrent sessions, so everyone could find something they were interested in. For me, the most interesting talks included Mary Beth Mudgett describing a new insights into how a metabolite (N-hydroxy-pipecolic acid) which can elicit systemic acquired resistance and its application in tomato bio-protection and Diane Bassham's talk about transcriptional control of autophagy under a number of stress conditions.

I really enjoyed all of the photobiology talks, especially Hongtao Liu's talk about the effects of UV on photomorphogenesis (in the root!) and a brief but intriguing talk from Alexander van der Krol which made me re-evaluate my knowledge of the circadian behaviour of PHY transcripts.

An evening workshop on 'Scientific writing and Journal publishing' was covered by several prestigious plant journals. They had some great



Hannah presenting her poster

advice about applying to journals (think about preparing summary figures for cover letters?) and on responding to reviewer's comments (go away and calm down first!).

I had some great feedback and discussions after my talk and at the poster session. Lots of researchers were excited by idea of using delayed fluorescence screening; 'no genetic modification required!' and I had some useful questions which will help me to polish my final manuscript [Once you write it: Ed].

On Tuesday night everyone was invited to a Banquet where we were treated to several rounds of traditional Chinese food. Being vegetarian I thought I might be going hungry, but I was surprised by the number of really tasty dishes that arrived at our table! They just kept on coming! A local show was performed while we ate, ranging from performances of traditional instruments to hip-hop! I left stuffed and having enjoyed quite a bit of Kiwi wine!

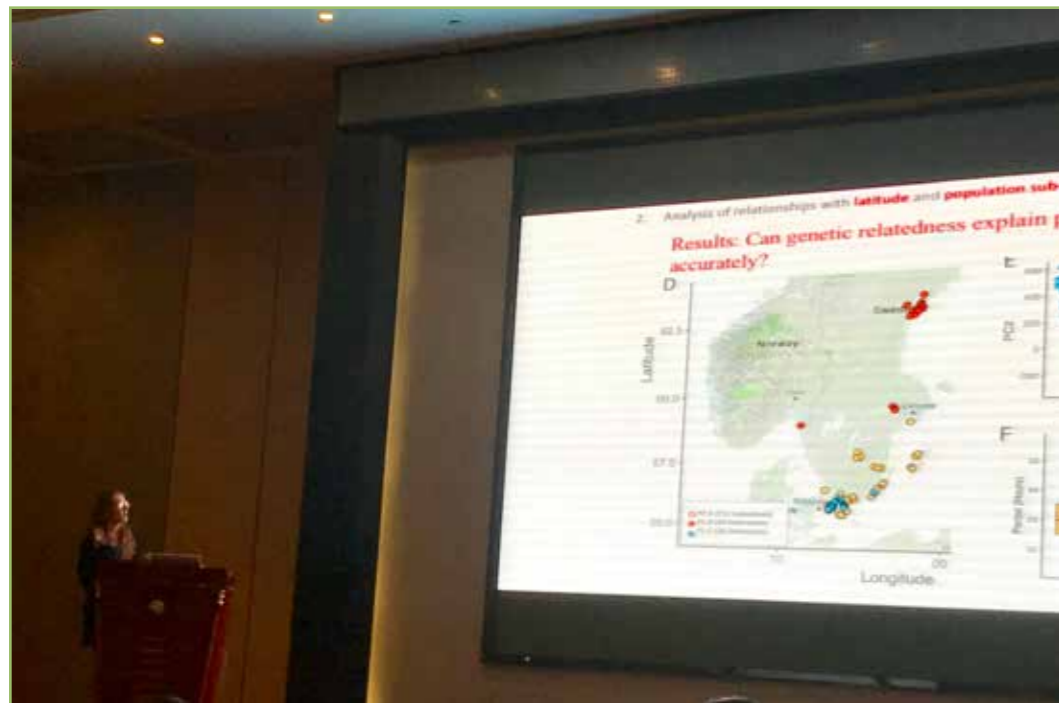
In all, the conference was a really enjoyable and constructive experience for me. I met loads of people who were very welcoming and I hope to run into them again in the future. I am really grateful for the travel bursary from the Gatsby foundation and would recommend for students to apply in the future. I am making the most of the flights out here and staying on for 5 more days to do some exploring in China!

So for now,

谢谢，再见

Thank you and goodbye!

<http://icar2019.arabidopsisresearch.org/>



Hannah presenting her research in the Photobiology concurrent session

The Future of Genome Editing in the EU

Geraint Parry
GARNet Coordinator

There was great surprise and disappointment amongst plant scientists following the July 2018 European Court of Justice (ECJ) decision on the future use of genome editing technology for the generation of novel crop varieties. Despite advice to the contrary from the Advocate General, the ECJ concluded that crops generated by genome editing should be considered equivalent to conventional transgenic crops, characterised by an addition of a foreign gene.

This decision does not consider the scientific fact that gene edits are much more precise than the mutagenesis techniques that are

routinely used during plant breeding. Perhaps more worrying is that the ECJ ruling provides scope for EU member states to **unilaterally decide** that they wish to more strictly regulate crops generated by 'conventional breeding techniques'.

The inability to generate transgenic plants is already impacting the competitiveness of EU scientists who hope to commercialise their research. An example of this are the disease resistance potatoes developed by Jonathan Jones' lab at the John Innes Centre. The commercial potential of these plants is being explored by a partner in the USA, since there is no prospect of growing these plants closer to home.

If the proposed ECJ ruling on GE stands then this will further compromise the ability of EU researchers to explore the full potential of their work. Currently non-transgenic genome-edited plants do not have the same restrictions applied to them in many other countries, meaning that

academics and companies are able to collaborate to test any GE-crops in the field without the significant regulatory and financial challenges that preclude the growth of transgenic plants. The USDA APHIS website provides an interesting list of the genome-edited organisms that have been approved for growth.

https://www.aphis.usda.gov/aphis/ourfocus/biotechnology/am-i-regulated/Regulated_Article_Letters_of_Inquiry

Regulatory developments on international level							
03-2019	No Foreign DNA				Foreign DNA		Comments
	Targeted small deletions	Targeted small additions/-edits	Targeted allele replacements	Targeted insertions	Null Segregant	Targeted Insertion	
Argentina	No	No	No	Likely Yes	No	Yes	Status: Final Consultation—60d New combination of DNA trigger
Chile	No	No	No	Likely Yes	No	Yes	Status: Final Consultation—20d New combination of DNA trigger
Brazil	No	No	No	Yes	No	Yes	Status: Final Consultation—90d New combination of DNA trigger
Colombia	No	No	No	Yes	No	Yes	Status: Proposal, Case by Case; 60 days Foreign DNA trigger
Canada	Using existing regulations—Novelty as trigger						
US (USDA)	No, if no plant pest	No, if no plant pest	No, if no plant pest	No, if no plant pest	No	No, if no plant pest	"Am I Regulated" Process Plant Pest Trigger; Secretary/Perdue issues USDA Statement on Plant Breeding Innovation 26.3.2018
Australia	No	Yes	Yes	Yes	No	Yes	Proposal to exclude SDP-3 and null segregants being issued by government will enter into force October 2019
New Zealand	Yes	Yes	Yes	Yes	?	Yes	High court decision Unlikely if GDO will challenge
FSANZ	Code under review						Australia/NZ Food Safety Authority
Israel	No	Likely No	Likely No	?	?	Yes	Status: Final Consultation New combination of DNA trigger
EU	yes	(likely) yes	(likely) yes	(likely) yes	??	Yes	According to ECJ ruling clarifying existing gm regulations; ** no formal policy
Japan (MOE)	No	No	Likely No*	?	No	Yes	Final MOE published guidance for developers *Self-donating exemption
China	?	?	?	Yes	?	Yes	No formal proposal yet

Yes=Under current biotech regulations No= Not under current biotech regulations ? = uncertain

Figure 1: The global regulatory environment for crops developed by New Breeding Technologies. Image from Petra Jorasch, European Seed Association

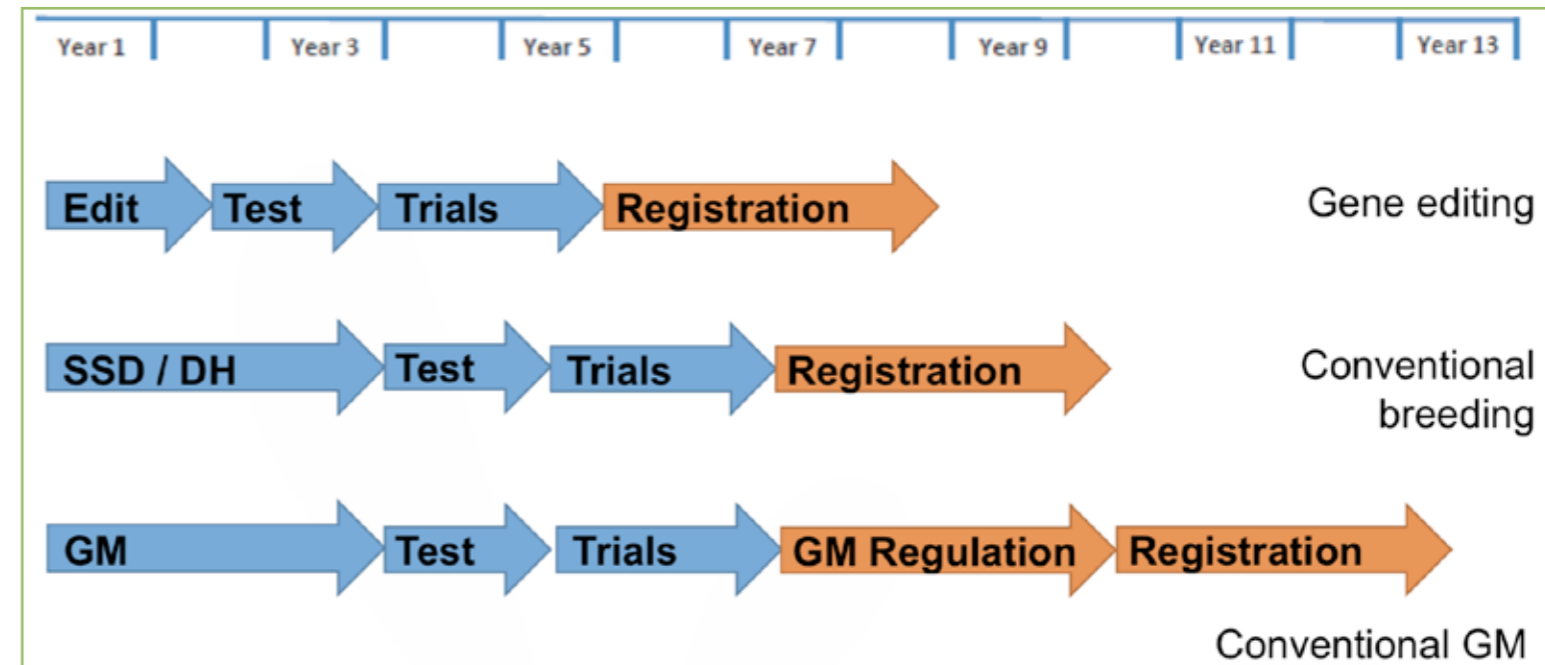


Figure 2: Genome editing can reduce the time of crop development. Image from Chris Burt, RAGT

EU and UK competitiveness is further challenged by the complex set of regulations that apply to the movement of GM/GE seed versus the movement of the products of GM/GE plants. The current head-start that international competitors have in the development of new varieties could mean that using the well established pipelines for the import of GM/GE products could make it is uneconomic to locally grow and process GM/GE plants.

In the UK the Advisory Committee on Releases to the Environment (ACRE) controls the growth of modified crops and they have been supportive of the small number of applications for field trials of GE crops, notably the Camelina developed by researchers in Rothamsted <https://www.gov.uk/government/publications/acre-advice-camelina-trial>

Following Brexit the UK regulatory environment might be more permissive regarding the growth of GE crops. However if the same restrictions exist across the EU then it will be challenging for UK companies to move GE seed across Europe.

Therefore in this current climate it is important that interested parties present an united front during the next steps in the process of convincing regulators that genome edited plants should not be regulated differently to plants developed by conventional mutagenesis or breeding.

Bringing together concerned and interested parties

To that end in early May the British Society of Plant Breeders (BSPB) organised an event at RAGT seeds in Cambridgeshire to discuss the current regulatory situation. This meeting was attended by a mixed selection of interested parties from policy fellows at the Royal Society, The Royal Society of Biology and the Earlham Institute, representatives of Syngenta and the European Seed Association (ESA), the NIAB CEO Tina Barsby and Cristobal Uauy from the JIC who has played a leading role in the development of open tools to aid generation of new wheat varieties.

Chris Black provided an introduction to activities at RAGT. It was surprising to learn of the relatively small size of the wheat market (the entire UK Winter wheat market is €26M), meaning that the seed companies are perhaps not as rich as others might imagine! However interestingly Chris confirmed that sale of UK-specific varieties **would be sustainable** to RAGT; which may be relevant if UK and EU regulations differ after Brexit.

Chris Burt leads the genotyping service at RAGT and provided a somewhat downbeat overview of the time required to bring a new crop variety to market. RAGT are taking advantage of a new TILLING resource developed by the Uauy group and others at the JIC. <http://www.wheat-tilling.com/>

These lines are generated by conventional mutagenesis so there are no extra regulations attached to use of this seed. However Chris cautioned that the need for backcrossing into Elite varieties means that it will take 8 years to get field data on these lines, which clearly represents a significant time and financial commitment. Interestingly RAGT know that conventional breeding will see a yield increase of 3.5% over 8 years. Therefore any line developed through TILLING (or gene edited) needs to have a greater yield increase to be economically viable.

This is a challenging proposition especially in the current environment where these crops might not be able to be grown in the field. Therefore seed companies will require regulatory certainty in order to commit to testing plants generated with GE technology.

Therefore the reality of using GE technologies to develop novel crop varieties might be different from the ideal pipeline that would

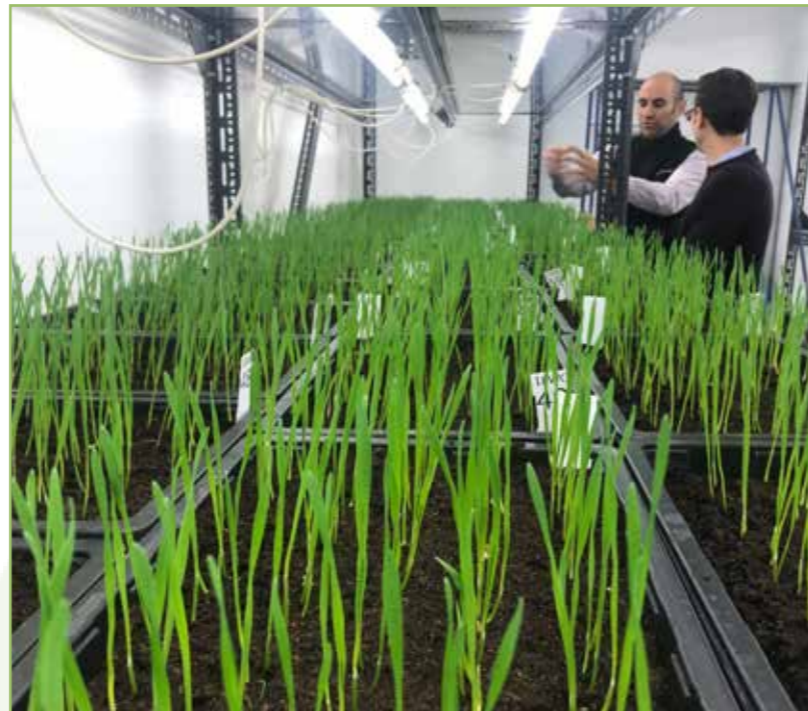


Figure 3: Cristobal Uauy and Chris Burt discussing single seed descent in wheat breeding.

see the straightforward movement from a newly discovered allele in the lab through to the farmers field.

However Chris ended with the positive message that non-transgenic genome-editing is certainly a technology worth pursuing due to the possibility of introducing edits into elite varieties, the potential targeting all homeologues in a single edit and a reduction in the need for backcrossing to reduce mutational load (as is needed in TILLING populations).

Another challenge that was only briefly discussed at the meeting is the ongoing impasse regarding the **application of patents** that might preclude commercial use of gene editing technologies. If this issue is not resolved then it would not be commercially viable for many SMEs to use this technology given the likely high cost of licencing. This needs to be resolved alongside those about discussions about amendments to the current regulatory situation.

Putting a Targeted Amendment in the crosshairs.

Petra Jorasch from ESA provided an update to the current strategic plan that is being considered by her organisation. The value of the EU seed market is approximately 25% of the \$50B global market. The ESA represents participants in this market that has 42000 different varieties available for farmers for purchase. This increases with the addition of 3500 new varieties each year! A significant fear is that member states will choose to legislate conventionally mutated crops as GMOs, an occurrence that would lead to an exodus of innovative plant breeders and a significant competitive advantage to those breeders outside of Europe.

The ESA considers that genome editing is an extra arrow in the quiver of tools that seed companies can use to development new varieties. Petra reported that ESA is advocating to push for a targeted amendment of Directive 2001/18 (on regulation of GM crops) that would exclude from its definition the products of old and new mutagenesis breeding.

This would align the EU with policies and rules established elsewhere in the world (**figure 1**) and create the legal certainty necessary for researchers and seed companies to ensure that excellence remains in the EU. This reasonable proposal does not aim to overturn the entire legislation but rather ensure that use of this new technology is supported.

The prospect of changing the current legislation to allow the wholesale use of transgenic plants would seem a step too far, so this proposed targeted amendment at least proposes to protect the use of this new technology. This topic is under active discussion as in late May a group of

14 EU member states requested 'a common EU approach on gene editing and called for a revision of EU GMO rules to be added to the working programme of the next European Commission'.

<https://www.euractiv.com/section/agriculture-food/news/14-eu-countries-call-for-unified-approach-to-gene-editing-in-plants/>

Although this proposal seems eminently sensible the potential time scale of its implementation is rather less encouraging. The next session of the EU parliament will not effectively begin until 2020 when the first two nations to hold the EU Presidency are Croatia and Germany. As a smaller nation is it possible Croatia will not wish to bring a controversial issue to the table whilst there has not been a huge appetite for embracing GM technology in Germany. Therefore it may be until 2021 when this targeted amendment could be brought.

However elsewhere in the world the research pipeline that leads to the development of novel crop varieties by genomic editing will not be slowing. Unfortunately this must ultimately reduce EU competitiveness in this area.

Brexit undoubtedly adds confusion to the future regulation of genome-edited crops in the UK. In response to a My Science Enquiry proposal from the Earlham institute it is likely that the UK Government Science and Technology Committee will soon open an enquiry on the future use of genome editing in agriculture. When this Enquiry begins it will be important that all interested parties submit joined-up evidence that demonstrates it is critically important for the wider UK plant science community to be able to take advantage of the outstanding UK research in genome editing.

Spotlight on: University of Liverpool

Kindly compiled by James Hartwell

Plant Science research has a long history at Liverpool. The original Botany Department played a role in the first stages of the Flora Europaea project, and the late Tony Bradshaw undertook pioneering work at Liverpool on plant evolutionary biology and its applications to land restoration. Today, Liverpool plant scientists undertake their research as members of the Institute of Integrative Biology, with additional research undertaken on the Wirral Peninsula at the University's Vet School campus at Leahurst, and at Ness Botanic Gardens. Study organisms include various photosynthetic bacteria and algae, *Arabidopsis*, barley, rice, a range of vegetable crops (with a special focus on Brassicas), various *Kalanchoë* species, and natural assemblages of species in grassland and riparian habitats.

Furthermore, plant science-related research at Liverpool also encompasses the organisms that live on and around these plants, including the soil microbiome and the animals that depend on plant communities.



The group investigate both fundamental and applied aspects of the biology and ecology of these study organisms, with a particular focus on the mechanisms used by these organisms to sense and respond to their environments, including long term adaptation to climate change.

The practical approaches employed by the group span from the structural biology of cyanobacterial photosynthetic complexes and carboxysomes, to functional genomics approaches for the dissection of higher plant photosynthetic adaptations and developmental processes, molecular modelling of complex systems, ecological and evolutionary approaches to understanding the functioning and adaptation of plants and their associated organisms in natural and semi-natural habitats, and accelerated crop molecular breeding strategies that aim to aid in humanity's response to the global food security crisis.

An area of particular focus centres on enhancing photosynthesis through studies on improving the efficiency of light harvesting and CO₂ fixation. Currently, members of the research teams are from 10 countries within the EU and further afield. Our visiting researchers range from international PhD students to senior academic staff, sponsored either by their own or the UK government.

Recent visitors have included scientists from China, Brazil, Finland, Saudi Arabia, Spain, Kuwait, Iraq, USA, India and Bangladesh.

The Institute of Integrative Biology at Liverpool occupies the Biosciences Building, which provides all of the facilities of a major, modern biosciences research centre. The plant scientists benefit from state-of-the-art transgenic glasshouse facilities that were expanded in early 2019, climate-controlled growth rooms and chambers, and specialist systems for gas exchange and luciferase and delayed fluorescence imaging. In addition, the group benefits from core facilities encompassing the latest 'omics, structural, computational and imaging technologies housed in the Centres for Genomic Research, Proteome Research, Metabolomics Research, and Cell Imaging, the GeneMill Synthetic Biology Lab,

Barkla X-Ray Laboratory of Biophysics, the Computational Biology Facility and the NMR Centre for Structural Biology.

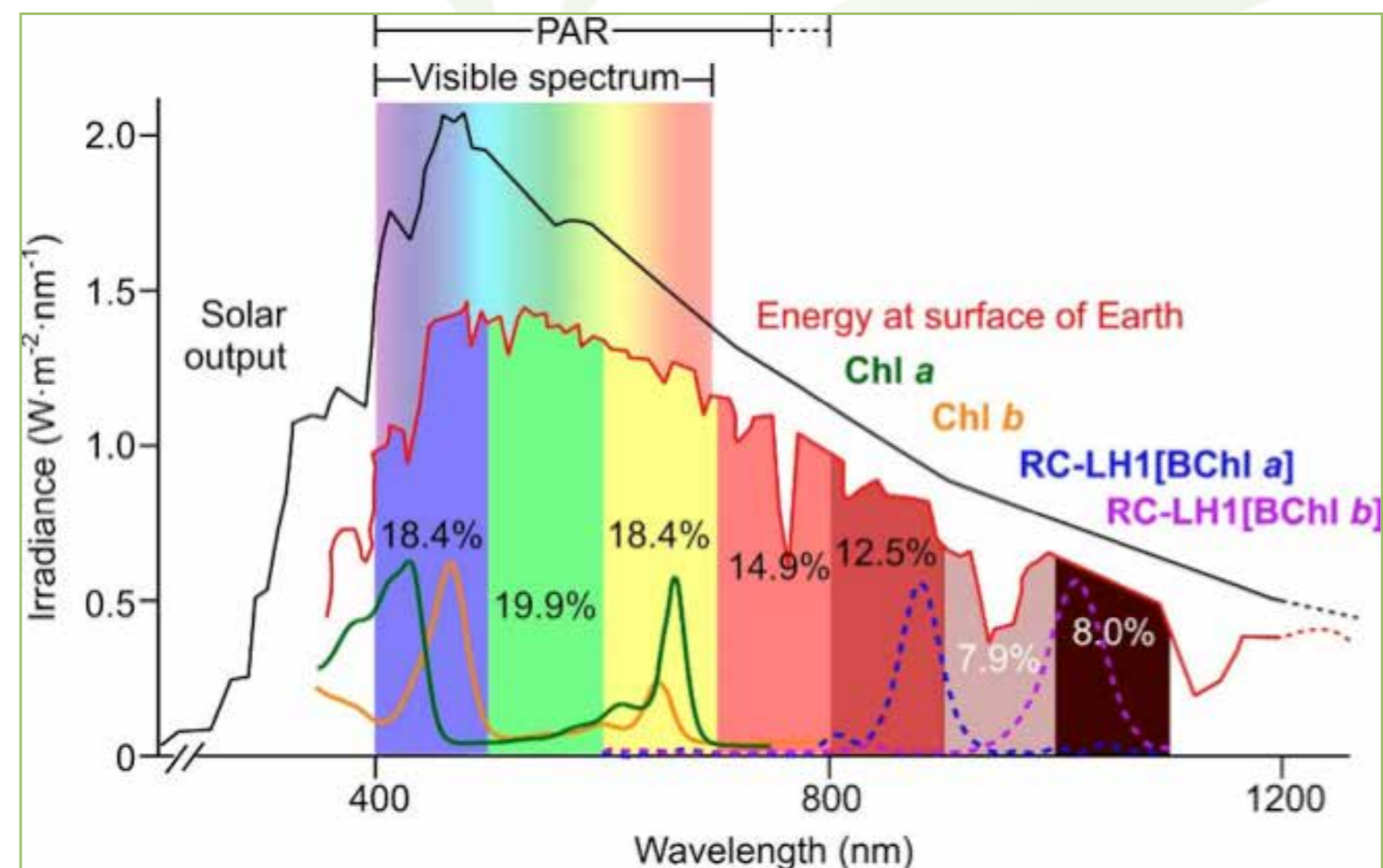
Dan Canniffe

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<https://www.liverpool.ac.uk/integrative-biology/staff/daniel-canniffe/>



Dan Canniffe is a Tenure-Track Fellow in the Department of Functional and Comparative Genomics. His research aims to improve the efficiency of photosynthesis by enhancing energy capture in underutilised regions of the solar spectrum. His lab employs molecular and synthetic biology approaches to manipulate pigment biosynthetic pathways for the production



Canniffe: Absorption profiles of common (bacterio)chlorophylls relative to available solar energy. Dashed spectra indicate the red-shifted absorption properties of bacteriochlorophyll pigments when bound in the reaction centre/light-harvesting complex 1 supercomplex (RC-LH1). Improvements to natural photosynthesis can be made in the 700–800 nm and 900–1000 nm regions, where abundant solar energy is underutilised in nature

of non-native or novel (bacterio)chlorophyll and carotenoid compounds, and in order to engineer new combinations of these pigments in bacterial protein complexes, with the long-term aim of creating new organisms for harvesting and trapping solar energy.

Alistair Darby

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Alistair is Co-Director of the Centre for Genomic Research (CGR) at Liverpool and has >15 years' experience as an applied entomologist. His main area of research in microbial/host interactions, which covers his interest in arthropod symbiosis, pathogens and microbiomes. He has extensive experience in designing and analysing genomic and RNAseq data, including arthropod genomes; e.g., *Nasonia* wasp (Science), tsetse fly (Science), mite (GigaScience), and a new high-quality version of the Diamondback moth (a major pest of Brassica crops) genome sequence using the PacBio (data at lepbase.org). He is also studies the genomics of aphids. His research also uses single cell genomics and he is the lead for the CGR single cell genomics facility.



Cristina Garcia-Perez

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Cristina is a Tenure Track Fellow at the University of Liverpool who joined Integrative Biology in 2019.

Cristina is a Plant Ecologist interested in investigating the chances of remnant forest patches



to persist, and eventually expand, across managed landscapes, in a changing world where climate extremes are expected to increase in frequency and magnitude. The ability of these fragments to cope with anthropogenic and climate-driven changes depends on their genetic diversity, and on the ecological services provided by frugivores and pollinators that transport their seeds and pollen grains (and the genes they encapsulate) across the landscape. Plant population genetics and dispersal mutualisms are, therefore, Cristina's main research topics.

The Garcia-Perez research group combines genetic and genomic tools (NGS) with long term field studies entailing thorough environmental monitoring using ecological network tools and novel modelisation approaches (such as statistics of extremes) to:

- (1) Investigate how the loss of plant dispersal ability that accompanies defaunation and fragmentation might shift plant distribution ranges;
- (2) Characterize lagged demographic and genetic population trends in response to land-use changes.
- (3) Elucidate the functional relationship between population genetic diversity and their ability to cope with increasingly frequent climate extremes. Overall, the research aims ultimately to provide scientific based guidelines to manage biodiversity, ecosystem functions, and services.

Cristina's main research interests revolve around plant-animal dispersal mutualisms, plant population genetics, landscape genetics, and plant functional responses to global change. She is interested in assessing and forecasting the outcomes of different drivers of global change, from forest loss and fragmentation to defaunation.

James Hartwell

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James is the Gatsby Plant Science Network Mentor representing the University of Liverpool, leads the Liverpool Plant Science Research Group, and coordinates the Liverpool Plant Science e-mail listserver used to communicate with the ~120 students and staff with interests in the Plant Sciences at the University of Liverpool.

Research Activities

Metabolic adaptations of photosynthesis such as CAM and C4 provide significant improvements in water-use efficiency, photosynthetic efficiency at high temperature and yield. These advantages have driven huge interest in improving the extent to which humanity can leverage these systems for sustainable crop production in the face of climate change, human population growth and diminishing agricultural resources, especially fresh water.

The Hartwell group focusses on developing a detailed understanding of the molecular-genetic blueprint underpinning CAM, with a particular emphasis on functional genomics research in model species belonging to the genus *Kalanchoë*, and on the mechanisms through which the circadian clock optimises the CAM pathway relative to the light/ dark cycle.

We have recently decoded the genomes of several *Kalanchoë* species that are capable of differing levels of CAM, including recent further enhancements of the assemblies to chromosome scale using

HiC scaffolding. We mine extensive *Kalanchoë* genomic, transcriptomic and metabolomic datasets to identify the genes and encoded proteins required for temporally optimised strong-CAM.

One of our main endeavours focusses on the generation of loss-of-function transgenic lines of *Kalanchoë* in which each candidate CAM gene has been manipulated by gene silencing or over-expression. By undertaking detailed phenotypic characterisation on these transgenic lines using physiological, biochemical and molecular assays, we are systematically deciphering the genes that are critical for CAM and its daily optimisation by the circadian clock, and those genes that are dispensable.

We are also studying the evolutionary trajectory from weak, inducible CAM to strong, constitutive CAM across the genus *Kalanchoë* through studying the molecular phylogeny of the genus, and the CAM-associated physiology and biochemistry and circadian biology within around 100 species of the estimated 125 species in the genus *Kalanchoë*.



Hartwell: Wild type *Kalanchoë laxiflora* (left) alongside transgenic RNAi lines rPPC1-A and rPPC1-B that possess either 40 % of wild type phosphoenolpyruvate carboxylase (PPC; line rPPC1-A, centre) or no detectable PPC (line rPPC1-B, right). Photo courtesy of Dr. Susanna Boxall.

Fang Huang

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Fang Huang is a Leverhulme Trust Early Career Fellow in Integrative Biology at Liverpool. Fang's interests centre on bacterial microcompartments, their gene organization, protein composition, structural assembly and applications. In particular, she focusses on cyanobacterial carboxysomes and their cellular distribution and structural organization, by using biological imaging methods such as confocal microscopy and electron microscopy, and biochemical and biophysical methods.



Improving annotation of the rice genome

In a BBSRC/Newton funded project, a new computational pipeline was used to perform "proteogenomics" analysis on rice i.e. providing protein-level evidence for predicted genes. The approach involved assembling all publicly available MS data sets for rice, and creating search databases from "official" rice gene models, as well as assembling large collections of RNA Seq data. The database design stage is crucial, since a typical MS search can only identify peptide sequences present in the database; searching a six frame translation of the genome results in an excessive loss of statistical power and an inability to identify peptides that span exons.

The pipeline applied searched >2M MS spectra, resulting in protein-level evidence for >8000 rice genes. The results also suggested potential improvements (e.g. new splice sites) for ~700 rice genes, and provided evidence for ~100 new rice genes not currently present in the existing annotation. (1) In more recent work, the group is analysing the rice transcription factor genes to understand the sub-family structure, discovery and mapping of SNPs (e.g. across 3K rice genomes) to amino acid changes in key domains. As well as improving gene models where there appear to be annotation errors. Results are due to be released shortly through a new data portal.



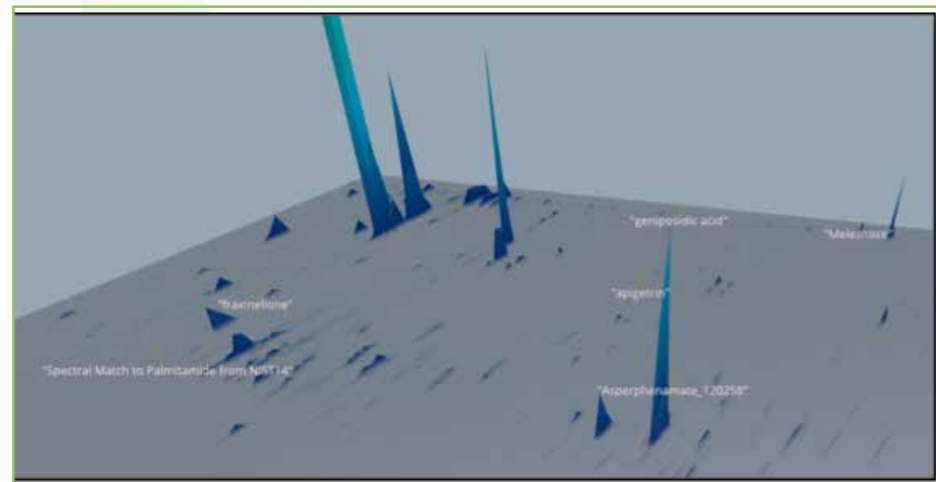
Andy Jones

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Development of computational tools and analysis of omics data for plants

The Jones group develops new software and databases for analysing omics data, particularly related to mass spectrometry (MS) for proteomics and metabolomics (e.g. new 3D visualisation software lcmsWorld), although the group also works increasingly on genomics data. These tools have been applied to human systems in the context of immunogenetics, eukaryotic pathogens such as *Toxoplasma gondii* and more recently the group has turned its attention towards plants, and particular crops such as rice.



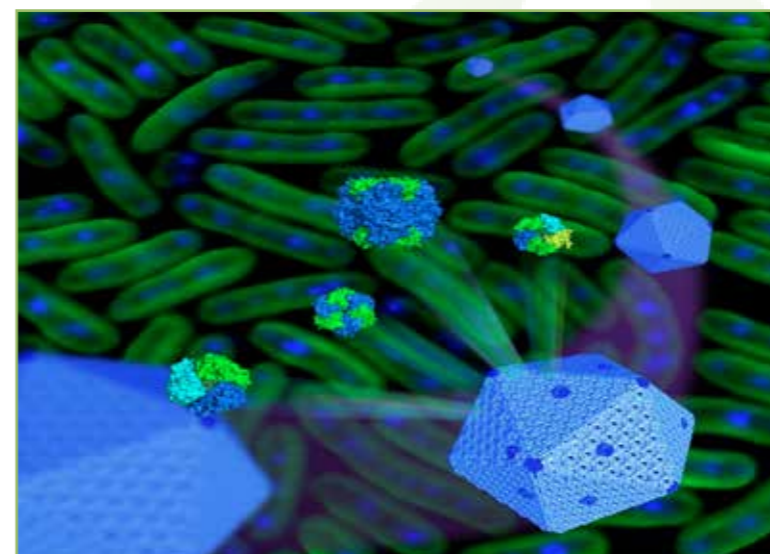
Jones: High-performance 3D visualisation software lcmsWorld for proteomics and metabolomics, here used to visualise metabolite profiling

Understanding post-translational modifications in plants

The group performed a comparative study of phosphorylation sites, motifs and pathways to discover the conservation of phosphorylation-mediated signalling from model dicot *Arabidopsis thaliana* to model monocot *Oryza sativa* (rice). The results demonstrated that despite monocots and dicots diverging ~150 million years ago, there was high conservation of phosphorylation motifs enriched in the same biological pathways. The results also showed evidence for cross-talk for phosphorylation motifs, with apparent stronger cross-talk between different phosphorylation motifs co-occurring in *Arabidopsis* (pairs of motifs present in individual proteins), indicating different kinases functioning in tandem (2). The group is now focussing on analysing a wider range of post-translational modification (PTM) types to understand how they have evolved across the plant kingdom to understand their function, particularly in relation to loss or gain of PTM sites through SNPs.

1. Ren, Z., Qi, D., Pugh, N., Li, K., Wen, B., Zhou, R., Xu, S., Liu, S., and Jones, A. R. (2019) Improvements to the Rice Genome Annotation Through Large-Scale Analysis of RNA-Seq and Proteomics Data Sets. *Mol Cell Proteomics* 18, 86-98

2. Al-Momani, S., Qi, D., Ren, Z., and Jones, A. R. (2018) Comparative qualitative phosphoproteomics analysis identifies shared phosphorylation motifs and associated biological processes in evolutionary divergent plants. *J Proteomics* 181, 152-159



Liu: Bioengineering of microcompartments

Luning Liu

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Bioenergetic machinery: structure, function, biogenesis and engineering

Cells have evolved specific machineries in a defined cellular environment to boost metabolic activities. By exploiting state-of-the-art molecular biology, biochemistry, high-resolution microscopy and synthetic biology, the Liu Lab aims to explore the molecular basis underlying the self-assembly and functional regulations of bioenergetic machineries, including photosynthetic apparatus and carbon-fixation organelles.

(1) Photosynthetic machinery

Without photosynthesis, no complex ecosystems and higher life forms including man would exist." Thylakoid membranes are the sites for photosynthetic reactions and physiological adaptation in cyanobacteria, algae and higher plants. The Liu Lab perform direct visualisation of the structural organization and dynamics of thylakoid membranes. Knowledge of cyanobacterial thylakoid membrane structure and formation could be extended to chloroplasts and mitochondrial membranes, with the aim of delineating membrane biogenesis and establishing artificial photosynthetic device for energy production.

(2) CO₂-fixing organelles

Carboxysomes are the central carbon-fixation organelles in all cyanobacteria. They represent a type of self-assembling proteinaceous microcompartments found in bacteria, resembling virus capsids. Carboxysomes sequester Rubisco within a selectively permeable shell, and the exceptional architecture enables high levels of CO₂ around Rubisco for enhanced carbon fixation. The Liu Lab seek to understand the molecular principles underlying the formation, function and modulation of carboxysomes, and

use synthetic biology approaches to generate new nanoreactors and scaffolding systems in other host cells (such as plants), to improve metabolism and productivity.

Hugh McAllister

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Hugh McAllister has studied groups of plants, especially woody genera, in which knowledge of their chromosome numbers would help understand their evolution and phytogeography. The University Botanic Gardens at Ness provided the growing space for trees received as seed to reach maturity so that flowering and fruiting specimens could be studied and, at the same time, their conservation significance evaluated and their value for landscaping and horticulture assessed. Several new species have been described, and many more reduced to synonymy, and this work continues as recent acquisitions reach maturity.

Major current projects

1) Taxonomic revision of *Spiraea* – Cultivation and study of all available species with the target of the publication of an RHS monograph on the genus.

2) Follow-up work on *Sorbus* (rowans), *Betula* (birches), *Hedera* (ivies), *Campanula rotundifolia* (harebell, Scots bluebell), (and) following publication of monographs.

3) Projects on *Alnus* (alders), *Malus* (apples), *Cotoneaster*, *Deschampsia cespitosa* (tufted hair grass) and *Festuca rubra*.

Current international collaborations with - Dr. Matthew Bowser, Kenai Wildlife Refuge, Alaska (*Betula*, *Campanula*); Dr. Tim Dickinson, London, Ontario, Canada (*Apomixis*, *Pyraea*); Dr. Brittany Sutherland, Tucson, Arizona (*Campanula*); Dr. Roman Ufimov, Komarov Botanical Institute, St. Petersburg, Russia (*Pyraea*); Dr. Nian Wang, Assistant Professor, Shandong Agricultural University, China (*Betula*).

Selected Publications

McAllister, H.A. (2005) The Genus *Sorbus*. A Botanical Magazine Monograph. London. Kew Publishing.
 Ashburner, K.B. & McAllister, H.A. (2016) The Genus *Betula*. (Reprinted with corrections and additions to first printing) A Botanical Magazine Monograph. London. Kew Publishing.
 Wang, N., Hugh McAllister, H.A., Bartlett, P. & Buggs, R. (2016) Molecular phylogeny and genome size evolution of the genus *Betula* (Betulaceae). *Annals of Botany* 117: 1023–1035.
 McAllister, H. & Marshall, R. (2017) *Hedera*, the complete guide. RHS Horticultural Monograph. London

Martin Mortimer

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Martin Mortimer is an agricultural ecologist at the Institute of Integrative Biology at the University of Liverpool. He is a Director of the Centre of Excellence in Sustainable Food Systems at the University of Liverpool that develops private-public partnerships for global food security.

Martin's research interests and experience focus on agro-ecosystem functioning in response to climate change and the development of sustainable cropping systems in direct seeded rice in south and south-east Asia, together with decision support frameworks and technology transfer in agricultural systems particularly wheat and rice. He is the author of three books and over 100 peer reviewed publications.

Siobhan O'Brien

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Ecology and Evolution in microbial communities

Dr O'Brien is an evolutionary microbiologist, interested in understanding the interplay between species interactions and evolutionary change in microbial communities.

Understanding how microbial communities evolve and function is a key global challenge, with implications for human health, agriculture and biotechnology. The O'Brien lab employs real-time experimental evolution of soil microbial communities to ask key questions about how microbes respond and adapt to stress.

This is particularly relevant in light of global climate change and intensive agricultural practices. Crucially, ecological and evolutionary responses to stress in microbial communities can have important consequences for ecosystem functioning, such as the ability of the soil microbiome to protect plants from pathogens.

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Reproductive Organ Development and Photosynthesis

We are interested in understanding the molecular mechanisms underlying the specification, growth, and differentiation of floral organs. We are focused on the roles of

transcription factors in this process and aim to understand which of their activities are conserved or diverged between flowering plants.

In particular, we are interested in how the leaf developmental program has been reshaped to generate floral organs. Interestingly, floral organs and fruits are capable of photosynthesis, which is important for seed and fruit viability/quality. We are using comparative genomics and genetics to understand how floral organs and fruits acquire the ability to photosynthesise as they mature.

Natasha Savage

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Plant Development: Patterning in the root

Dr Savage is currently working, as a modeller, in collaboration with two Labs; The Bishopp Lab, Sutton Bonington, University of Nottingham, and The Etchells Lab, University of Durham.

The Bishopp and Savage work is focused on root hair patterning. Within the project the group address previously unanswered questions by considering expression data in individual 3D root topologies. *In-vivo* data obtained by the Bishopp Lab using state of the art imaging techniques. The Savage Lab generate multi-dimensional root models. The topology of each model is set using imaging data, enabling 1to1 comparisons between in-vivo and in-silico results.

Etchells and Savage are currently building a model to understand cell division control with regard to vascular tissue development. The modelling work is done by Kristine Bagdassarian, a PhD student in the Etchells Lab.

Peter Glen Walley

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He is the Brassica crop group coordinator for the H2020 project 'Breeding for Resilient, Efficient and Sustainable Organic Vegetable production' (bresov.eu) and he coordinates the Working Group for Genetic Resources, Breeding, and Seed Production for the European Vegetable Institutes Network. His group has projects on molecular breeding in wild rocket, optimising lettuce growth for vertical farming, and breeding for acid tolerance and metabolite profiles in barley. Peter is an N8 AgriFood Fellow representing the University of Liverpool.

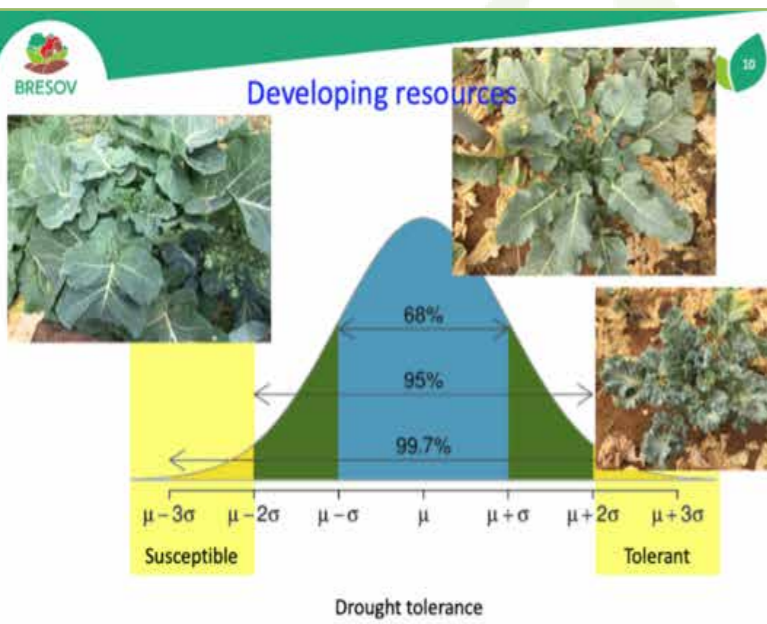
Crop Genetic Improvement

Peter Walley's research group aims to decipher the genetic basis of plant adaptations to stress, and to use this information to enhance the growth and quality of our crops. He has a particular interest in the use of landrace and crop wild relatives as sources of genetic variation.

We use high throughput sequencing to define and track genetic variation in large core collections. This work is enhanced through interaction with the Centre for Genomic Research and their team of bioinformaticians.

The group develop genetic resources that feed into pre-breeding programmes. This includes new germplasm, genetic markers, genetic maps, and genetic markers linked to genetic variation for favourable characteristics.

Peter's primary focus is vegetable genetic improvement, particularly the vegetable brassicas.



Walley: The focus is vegetable genetic improvement, particularly the vegetable brassicas.

Raj Whitlock

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Climate change threatens the integrity and diversity of natural and man-made ecosystems and the variety of services—food, clean water, pollination, carbon storage, nutrient cycling—that they provide. Work in Raj's group aims to understand how plant populations and plant communities respond to environmental change, and in particular the ecological and evolutionary mechanisms underpinning resistance



Whitlock: Buxton Climate Change Impacts Lab

to drought and global warming. Understanding these resistance mechanisms is fundamental to predicting how natural and agro-ecosystems will respond to change. Much of the work in Raj's group makes use of the Buxton Climate Change Impact Lab, the longest running climate manipulation applied to a natural ecosystem in the UK. Established in 1993, the experimental treatments (summer drought, increased rainfall, winter warming) have now been applied continuously to calcareous grassland for 25 years.

Regular surveys of the vegetation at BCCIL have made a major contribution to our understanding of how plants respond to, and can resist climate changes. The experiment is recognised as a globally important resource for our understanding of climate impacts on plants and soil microbes and fauna. Raj chairs the scientific steering group that runs BCCIL.

The research group uses a wide range of techniques to understand responses to climate change from all levels from the gene to the ecosystem, using field surveys, climate manipulation experiments in the common garden, transcriptomics, genomics, quantitative genetics, ecophysiology. A current key focus is on understanding whether evolutionary responses will be sufficient to buffer species and communities against the effects of anticipated climatic change.

Sharon Zytynska

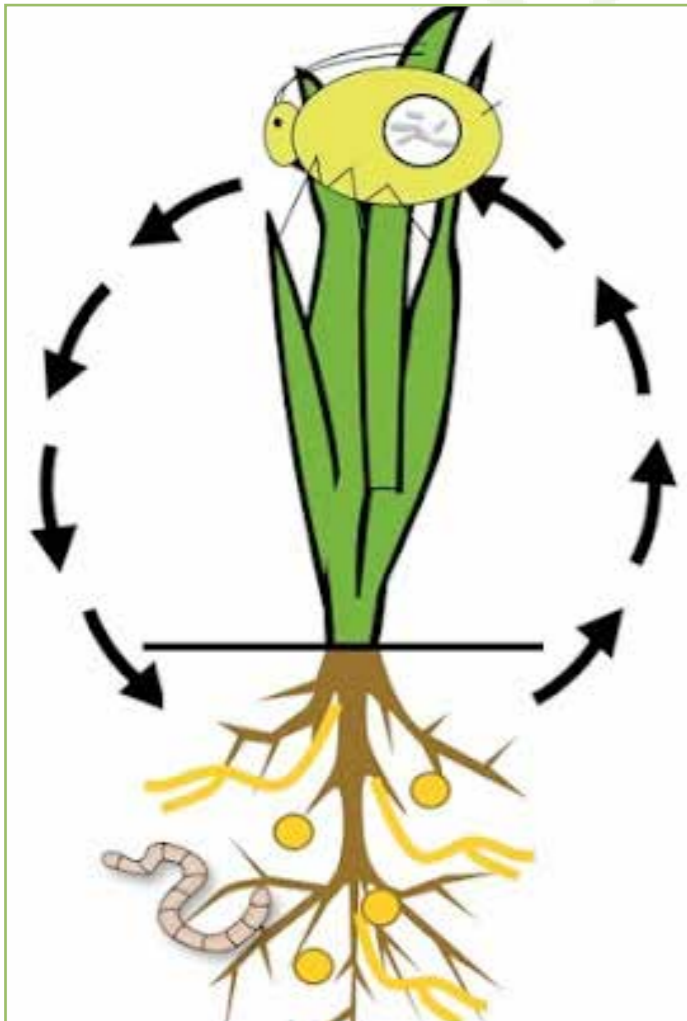
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Sharon Zytynska will join the University of Liverpool as a BBSRC David Phillips Fellow in October 2019.

Sharon's research centres around understanding the phytobiome (a plant along with its associated interacting organisms). The phytobiome is an important target for next-generation crop breeding strategies. Increasing evidence shows that the performance of plant varieties not only depends on traits coded in the plant genome, but also on those encoded in the genomes of interacting organisms.



Root-associated bacterial communities of plants can be highly dynamic and plants can actively recruit beneficial bacteria from the surrounding bulk soil in response to variable environmental conditions. This can quickly increase a plant's tolerance to adverse conditions within a growing season, including drought, high salinity, or insect attack. Other organisms in the soil, such as ecosystem engineering earthworms, have the potential to modify interactions between plants and their root bacteria. Sharon's research aims to unravel the impact of plant growth-promoting-rhizobacteria and interacting earthworms on barley plant growth and pest suppression of aphids.

She also studies the response of these interacting factors to elevated CO₂ and O₃ environments in order to determine the impact of future climate change on these beneficial interactions.

The aphid pests themselves host symbiont bacteria, which can increase the aphid's survival chances against specialised natural enemies including parasitic wasps and entomopathogenic fungi. Under monoculture cropping systems, the diversity of natural enemies is reduced and this can select for the most protective combination of aphid symbionts. This in turn further reduces the effectiveness of top-down pest control services by natural enemies.

Sharon's work in this area aims to understand the impact of plant diversity on the diversity of protective symbionts in aphids, and the potential of these factors for improving pest control services in field crop systems.



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Analysis of Arabidopsis Publications



This analysis is taken from the Annual Report of the Multinational Arabidopsis Steering Committee. The full report can be downloaded here:

arabidopsisresearch.org/images/2019_MASC_Report_FINAL.pdf

Following a high point in 2014, the annual number of publications in Pubmed journals that include 'Arabidopsis' in the Title or Abstract has since stabilised at approximately 4200 papers. However 2018 sees an important change that may prove informative with regard the future direction of global plant science research. For the first time there are more papers published in PubMed journals that include the words 'rice' or 'oryza' in the Title or Abstract than those that include 'Arabidopsis'. The recent plateau in the number of 'Arabidopsis' papers means that this change has been coming for a while. In addition papers that include either 'maize/corn' or 'wheat/triticum' continue to increase and over the coming years we might expect 'Arabidopsis' papers to slip to fourth in these rankings.

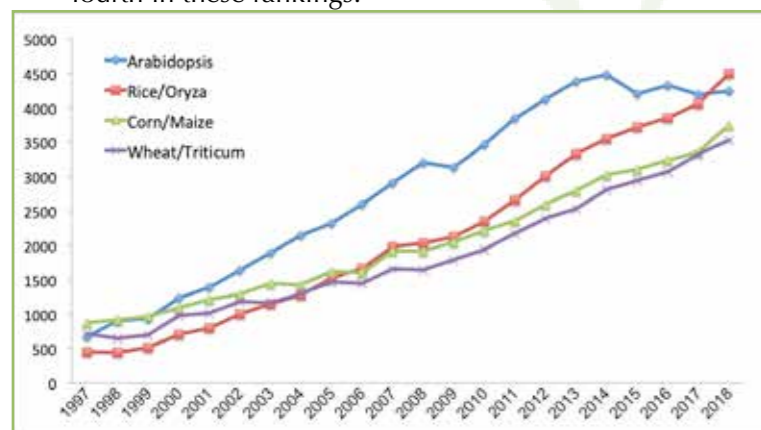


Figure 1. Papers published in Pubmed journals globally with Arabidopsis, rice/oryza, corn/maize or wheat/triticum in the Title/Abstract.

Over the past twenty years, when considering the trend of the lines in Figure 1 it is legitimate to draw a conclusion that the research achievements made using Arabidopsis have enabled subsequent improvements in the amount of publishable research using those other species. However this might not be a direct relationship as the increase in fundamental knowledge gained through use of Arabidopsis has also occurred alongside a myriad of technological improvements. These improvements have allowed more rigorous analysis of plants with larger and complex genomes using experimental techniques that previously might only have been possible in Arabidopsis.

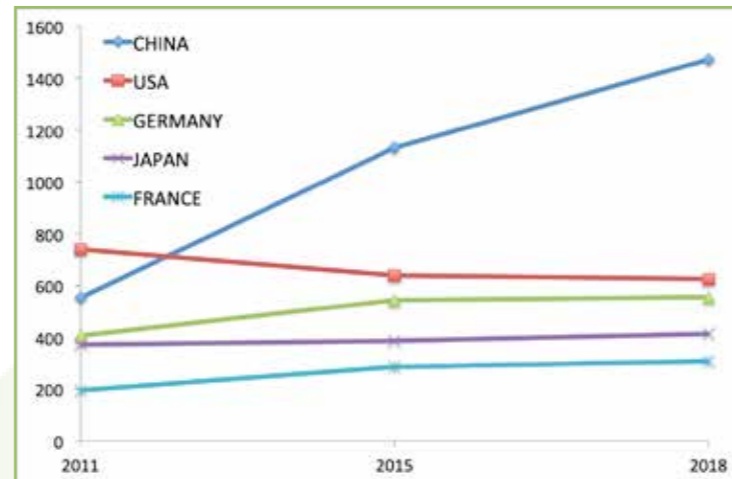


Figure 2. Papers published in Pubmed journals with Arabidopsis in the Title/Abstract since 2011. Globally These countries are have the highest number of publications.

These technical improvements might include but aren't limited to:

- 1- Improvements in next generation sequencing for genome and/or expression analysis
- 2- Advances in bioinformatics analysis of big datasets
- 3- Improved techniques for bulk transformation
- 4- Generation of TILLING mutant populations in multiple plant species
- 5- Improvements in the ability to perform large-scale field-level phenotyping

The pre-eminence of Chinese Plant Research

The overall number of papers shown in Figure 1 is highly dependent on the papers that are published by Chinese researchers. Approximately one-third of all Arabidopsis papers include research from China and over the last four years the number of 'Chinese' Arabidopsis papers continues to increase (figure 2). However in the other four countries with the most Arabidopsis publications (USA, Germany, Japan, France) the number of papers has plateaued (figure 2).

In general, European countries show a small increase in Arabidopsis publications (figure 3) whereas in Oceania and Asia there is a general plateauing, with the exception of India and Singapore that both see an increase (Figure 4). The Americas are a mixed cohort with Canada showing a similar plateau to their neighbours in the USA whilst Mexico, Brazil and Chile show increases, albeit from a lower level (Figure 5).

Although it is outside the scope of this analysis to fully evaluate the myriad reasons behind these trends, they might be broadly attributed to the development of scientific infrastructures in each country. As research infrastructure becomes more developed, such as in China or India, then the number of publications appears to show an equivalent increase. Those countries with already well-

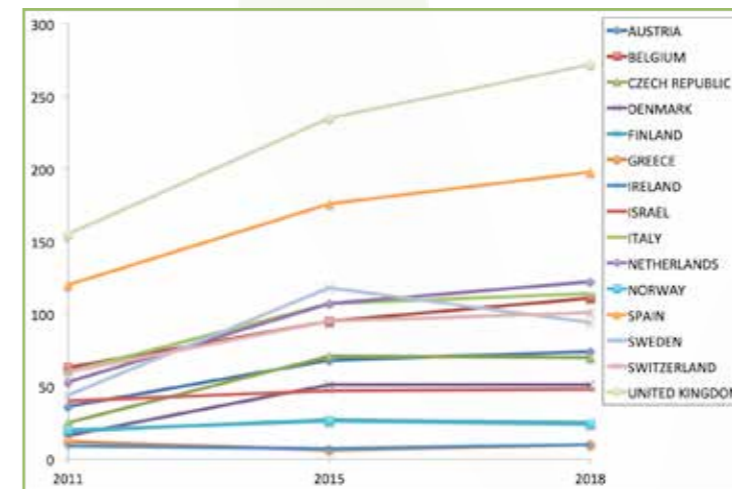


Figure 3. Papers published in Pubmed journals from different European countries with Arabidopsis in the Title/Abstract.

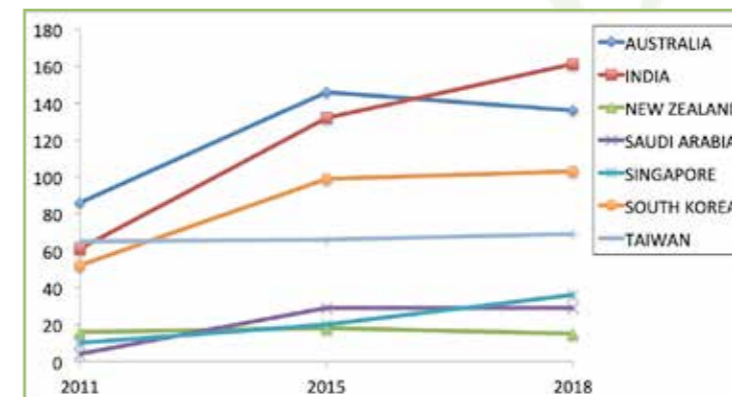


Figure 4 Papers published in Pubmed journals from different Oceania or Asian countries with Arabidopsis in the Title/Abstract.

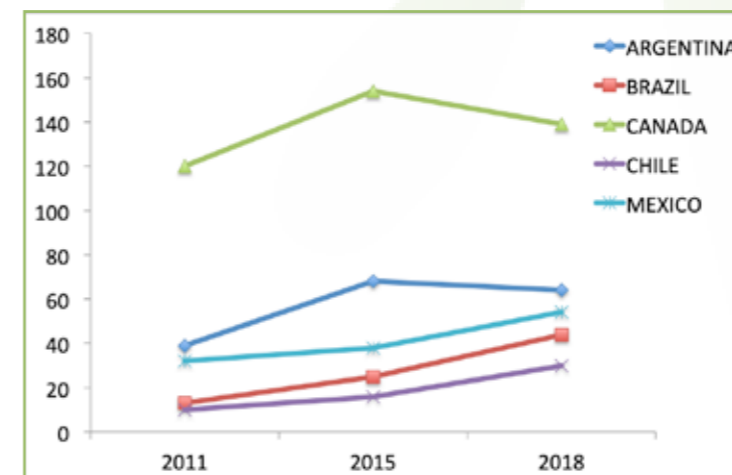


Figure 5 Papers published in Pubmed journals from different American countries with Arabidopsis in the Title/Abstract.

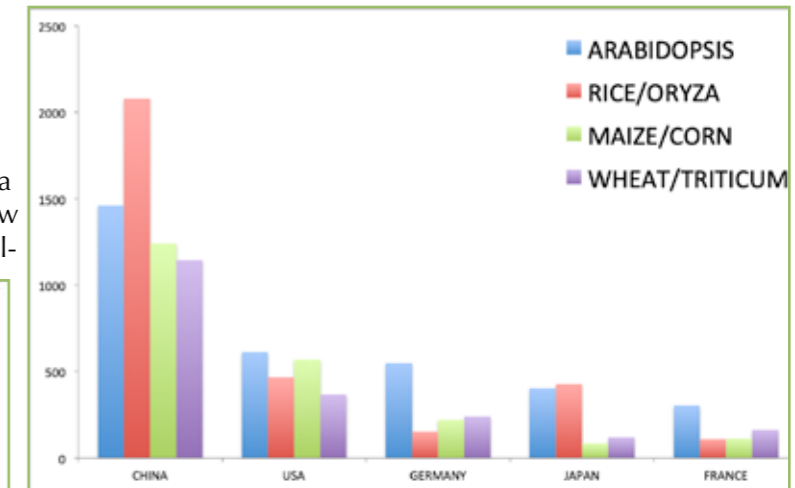


Figure 6 Papers published in Pubmed journals from different countries with Arabidopsis, rice/oryza, corn/maize or wheat/triticum in the Title/Abstract. These are the countries with the highest number of Arabidopsis publications

developed research infrastructures, such as across Europe or in North America, are now observing a plateau or small decrease in the number of publications that feature Arabidopsis research.

In 2018 the number of publications that include research in other plant species is also significantly influenced by Chinese research since a high proportion of overall global publications include research from that country (46% for rice, 33% for maize, 32% for wheat). This reflects anecdotal discussions with Chinese researchers who confirm that the majority of their research funding is for projects that have a more applied focus and are rarely specifically earmarked for Arabidopsis.

This information makes the continued production of Chinese Arabidopsis papers all the more remarkable if funding is not largely allocated for that purpose.

From these trends shown in these figures we can make a strong case that the increase in publications featuring other plants are a result of discoveries made possible by the strength of the knowledge base and research infrastructures that were developed over previous decade(s) of Arabidopsis research. The continued success of this 'discovery pipeline' is surely dependent on maintaining support for Arabidopsis research, which still underpins more applied research. However as outlined within many country submissions in this and in previous MASC annual reports (<http://arabidopsisresearch.org/index.php/en/publications>) there is global concern that funding for Arabidopsis and other fundamental plant science research is in decline.

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